

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Dumas Milne Edwards, J., et al.
Application. No. : To be assigned
Filed : Herewith
For : **FULL-LENGTH HUMAN cDNAs ENCODING
POTENTIALLY SECRETED PROTEINS**



SEQUENCE SUBMISSION STATEMENT

Assistant Commissioner for Patents
Washington, D.C. 20231

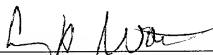
Dear Sir:

A copy of the Sequence Listing in computer readable form as required by 37 C.F.R.
§ 1.821(e) is submitted herewith.

As required by 37 C.F.R. § 1.821(f), the data on the enclosed disk is identical to the
Sequence Listing in the application filed herewith.

Respectfully submitted,

Dated: 12/7/00

By: 
Craig Worthem
Patent/Legal Assistant
Genset Corporation
875 Prospect Street
Suite #206
La Jolla, CA 92037
(858) 551-3031

SEQUENCE LISTING

<110> Dumas Milne Edwards, Jean Baptiste
Bouqueleret, Lydie
Jobert, Severin

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<151> 1999-12-08

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ctg	agt	gcc	aca	ttt	caa	ggc	cac	ccc	atg	aac	gac	cct	acc	agg	act	582
Leu	Ser	Ala	Thr	Phe	Gln	Gly	His	Pro	Met	Asn	Asp	Pro	Thr	Arg	Thr	
			135				140						145			
ttt	gcc	aat	ggc	agc	ctg	gcc	ttc	agg	gtc	cag	gcc	ttt	tcc	agg	tcc	630
Phe	Ala	Asn	Gly	Ser	Leu	Ala	Phe	Arg	Val	Gln	Ala	Phe	Ser	Arg	Ser	
			150			155				160				165		
agc	cga	cca	gcc	caa	ccc	cct	cgc	ctc	ctg	cac	aca	gca	gac	acc	tgt	678
Ser	Arg	Pro	Ala	Gln	Pro	Pro	Arg	Leu	Leu	His	Thr	Ala	Asp	Thr	Cys	
				170					175					180		
cag	cta	gag	gtg	gcc	ctg	att	gga	gcc	tct	ccc	cgg	gga	aac	cg	tcc	726
Gln	Leu	Glu	Val	Ala	Leu	Ile	Gly	Ala	Ser	Pro	Arg	Gly	Asn	Arg	Ser	
			185					190						195		
ctg	ttt	ggg	ctg	gag	gta	gcc	aca	ttg	ggc	cag	ggc	cct	gac	tgc	ccc	774
Leu	Phe	Gly	Leu	Glu	Val	Ala	Thr	Leu	Gly	Gln	Gly	Pro	Asp	Cys	Pro	
			200				205						210			
tca	atg	cag	gag	cag	cac	tcc	atc	gac	gat	gaa	tat	gca	ccg	gcc	gtc	822
Ser	Met	Gln	Glu	Gln	His	Ser	Ile	Asp	Asp	Glu	Tyr	Ala	Pro	Ala	Val	
			215				220					225				
ttc	cag	ttg	gac	cag	cta	ctg	tgg	ggc	tcc	ctc	cca	tca	ggc	ttt	gca	870
Phe	Gln	Leu	Asp	Gln	Leu	Trp	Gly	Ser	Leu	Pro	Ser	Gly	Phe	Ala		
			230			235				240				245		
cag	tgg	cga	cca	gtg	gct	tac	tcc	cag	aag	ccg	ggg	ggc	cga	gaa	tca	918
Gln	Trp	Arg	Pro	Val	Ala	Tyr	Ser	Gln	Lys	Pro	Gly	Gly	Arg	Glu	Ser	
				250					255					260		
gcc	ctg	ccc	tgc	caa	gct	tcc	cct	ctt	cat	cct	gcc	tta	gca	tac	tct	966
Ala	Leu	Pro	Cys	Gln	Ala	Ser	Pro	Leu	His	Pro	Ala	Leu	Ala	Tyr	Ser	
			265				270						275			
ctt	ccc	cag	tca	ccc	att	gtc	cga	gcc	ttc	ttt	ggg	tcc	cag	aat	aac	1014
Leu	Pro	Gln	Ser	Pro	Ile	Val	Arg	Ala	Phe	Phe	Gly	Ser	Gln	Asn	Asn	
			280				285						290			
ttc	tgt	gcc	ttc	aat	ctg	acg	ttc	ggg	gct	tcc	aca	ggc	cct	ggc	tat	1062
Phe	Cys	Ala	Phe	Asn	Leu	Thr	Phe	Gly	Ala	Ser	Thr	Gly	Pro	Gly	Tyr	
			295			300				305						
tgg	gac	caa	cac	tac	ctc	agc	tgg	tcg	atg	ctc	ctg	ggg	gtg	ggc	ttc	1110
Trp	Asp	Gln	His	Tyr	Leu	Ser	Trp	Ser	Met	Leu	Leu	Gly	Val	Gly	Phe	

[illegible]

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actggggctc ctctcgacca cctgcccggga ccgctaccgt caggaccccc agctcggcag 1183
gacactggcc agcctgcagg ctgagtagca ggtgctggcc agcctggagc tgcaggatgg 1243
tgaggacgag ggctacttcc aggagctgct gggctctgtc aacagcttgc tgaaggagct 1303
gagatgaggc cccacaccag gactggactg ggatgccgct agtgaggctg aggggtgcca 1363
gcgtgggtgg gcttctcagg caggaggaca tcttggcagt gctggcttgg ccattaaatg 1423
gaaacctgaa ggcaaaaaa aaaaaaaaaa a 1454

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<210> 6
<211> 1639
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 111..1154

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<220>
<221> sig_peptide
<222> 111..197
<223> Von Heijne matrix
score 4.68065944212013
seq LGLPLMAACFTFC/LS

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gtgggagttg tgtctgccac tcggctgccg gaggccgaag gtccttgact atg gct 116
Met Ala
ccc cag agc ctg cct tca tct agg atg gct cct ctg ggc atg ctg ctt 164
Pro Gln Ser Leu Pro Ser Arg Met Ala Pro Leu Gly Met Leu Leu
-25 -20 -15
ggg ccg ctg atg gcc gcc tgc ttc acc ttc tgc ctc agt cat cag aac 212
Gly Pro Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser His Gln Asn
-10 -5 1 5
ctg aag gag ttt gcc ctg acc aac cca gag aag agc agc acc aaa gaa 260
Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser Thr Lys Glu
10 15 20
aca gag aga aaa gaa acc aaa gcc gag gag gag ctg gat gcc gaa gtc 308
Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu Leu Asp Ala Glu Val
25 30 35
ctg gag gtg ttc cac ccg acg cat gag tgg cag gcc ctt cag cca ggg 356
Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu Gln Pro Gly
40 45 50
cag gct gtc cct gca gga tcc cac gta cgg ctg aat ctt cag act ggg 404
Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu Gln Thr Gly
55 60 65
gaa aga gag gca aaa ctc caa tat gag gac aag ttc cga aat aat ttg 452
Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn Asn Leu
70 75 80 85
aaa ggc aaa agg ctg gat atc aac acc aac acc tac aca tct cag gat 500
Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr Ser Gln Asp
90 95 100
ctc aag agt gca ctg gca aaa ttc aag gag ggg gca gag atg gag agt 548
Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu Met Glu Ser
105 110 115
tca aag gaa gac aag gca agg cag gct gag gta aag cgg ctc ttc cgc 596
Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val Lys Arg Leu Phe Arg
120 125 130
ccc att gag gaa ctg aag aaa gac ttt gat gag ctg aat gtt gtc att 644

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Pro Ile Glu Glu Leu Lys Lys Asp Phe Asp Glu Leu Asn Val Val Ile
135 140 145
gag act gac atg cag atc atg gta cgg ctg atc aac aag ttc aat agt 692
Glu Thr Asp Met Gln Ile Met Val Arg Leu Ile Asn Lys Phe Asn Ser
150 155 160
tcc agc tcc agt ttg gaa gag aag att gct gcg ctg ttt gat ctt gaa 740
Ser Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala Leu Phe Asp Leu Glu
170 175 180
tat tat gtc cat cag atg gac aat gcg cag gac ctg ctt tcc ttt ggt 788
Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp Leu Leu Ser Phe Gly
185 190 195
ggg ctt caa gtg gtg atc aat ggg ctg aac agc aca gag ccc ctg gtg 836
Gly Leu Gln Val Val Ile Asn Gly Leu Asn Ser Thr Glu Pro Leu Val
200 205 210
aag gag tat gct gcg ttt gtg ctg ggc gct gcc ttt tcc agc aac ccc 884
Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala Ala Phe Ser Ser Asn Pro
215 220 225
aag gtc cag gtg gag gcc atc gaa ggg gga gcc ctg cag aag ctg ctg 932
Lys Val Gln Val Glu Ala Ile Glu Gly Gly Ala Leu Gln Lys Leu Leu
230 235 240
gtc atc ctg gcc acg gag cag ccg ctg act gca aag aag aag gtc ctg 980
Val Ile Leu Ala Thr Glu Gln Pro Leu Thr Ala Lys Lys Lys Val Leu
250 255 260
ttt gca ctg tgc tcc ctg ctg cgc cac ttc ccc tat gcc cag cgg cag 1028
Phe Ala Leu Cys Ser Leu Leu Arg His Phe Pro Tyr Ala Gln Arg Gln
265 270 275
ttc ctg aag ctg ggg ggg ctg cag gtc ctg agg acc ctg gtg cag gag 1076
Phe Leu Lys Leu Gly Gly Leu Gln Val Leu Arg Thr Leu Val Gln Glu
280 285 290
aag ggc acg gag gtg ctg gcc gtg cgc gtg gtc aca ctg ctg tac gac 1124
Lys Gly Thr Glu Val Leu Ala Val Arg Val Val Thr Leu Leu Tyr Asp
295 300 305
ctg gtc acg gag aag atg ttc gcc gag gag taggctgagc tgaccaggga 1174
Leu Val Thr Glu Lys Met Phe Ala Glu Glu
310 315
gatgtcccca gagaagctgc agcagtatcg ccagggtacac ctcttgccag gcctgtggga 1234
acagggctgctg tgcgagatca cggcccacct cctggcgctg cccgagcatg atgcccgta 1294
gaagggtgctg cagacactgg gcgtcctcct gaccacctgc cgggaccgct accgtcagga 1354
ccccagctc ggcaggacac tggccagcct gcaggctgag taccaggtgc tggccagcct 1414
ggagctgcag gatggtgag acgagggcta ctccaggag ctgctgggct ctgtcaacag 1474
cttgcgaag gagctgagat gagggcccac accaggactg gactgggatg ccgctagtga 1534
ggctgagggg tgcacgcgtg ggtgggcttc tcaggcagga ggacatcttg gcagtgctgg 1594
cttgggcatt aaatggaac ctgaaggcaa aaaaaaaaaa aaaaa 1639

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<210> 7
<211> 1768
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 66..1256

<220>
<221> sig_peptide
<222> 66..173
<223> Von Heijne matrix
score 4.89555877630516

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seq LLLLLRLNDAALRA/LQ

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agaggagggtg gcgggtgggtgg ccctcgccctg tggccccctg gctgcttgca ctgcaactcg      60
tcgcc atg gag gag ctc cag gag cct ctg aga gga cag ctc cgg ctc tgc      110
      Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Gln Leu Arg Leu Cys
      -35                    -30                    -25
ttc acg caa gct gcc cgg act agc ctc tta ctg ctc agg ctc aac gac      158
Phe Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp
      -20                    -15                    -10
gct gcc ctg cgg gcg ctg caa gag tgt cag cgg caa cag gta cgg cgg      206
Ala Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro
      -5                    1                    5                    10
gtg att gct ttc caa ggc cac cga ggg tat ctg aga ctc cca ggc cct      254
Val Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro
      15                    20                    25
ggg tgg tcc tgc ctc ttc tcc ttc ata gtg tcc cag tgt tgt cag gag      302
Gly Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu
      30                    35                    40
ggc gct ggt ggt agc ttg gac ctt gtg tgc caa cgc ttc ctc agg tct      350
Gly Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser
      45                    50                    55
ggg cct aac agc ctc cac tgc ctg ggc tca ctc agg gag cgc ctc att      398
Gly Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile
      60                    65                    70                    75
att tgg gca gcc atg gat tct atc cca gcc cca tca tca gtt cag gga      446
Ile Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly
      80                    85                    90
cac aac ctg act gaa gat gcc aga cat cct gag agt tgg cag aac aca      494
His Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr
      95                    100                    105
gga ggc tat tct gaa gga gat gca gta tca cag cca cag atg gca cta      542
Gly Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu
      110                    115                    120
gag gag gtg tca gtg tca gat cca ctg gca agc aac caa gga cag tca      590
Glu Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser
      125                    130                    135
ctc cca gga tcc tca agg gag cac atg gca cag tgg gaa gtg aga agc      638
Leu Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser
      140                    145                    150                    155
cag acc cat gtt cca aac aga gaa cct gtt cag gca ctg cct tcc tct      686
Gln Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser
      160                    165                    170
gcc agc cgg aaa cgt ctg gac aag aaa cgt tca gtg cct gta gcc act      734
Ala Ser Arg Lys Arg Leu Asp Lys Lys Arg Ser Val Pro Val Ala Thr
      175                    180                    185
gta gaa ctg gaa gaa aag agg ttc aga act ctg cct tta gtg cca agc      782
Val Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Ser
      190                    195                    200
ccc cta caa ggc ctg acc aat cag gat tta caa gag gga gaa gat tgg      830
Pro Leu Gln Gly Leu Thr Asn Gln Asp Leu Gln Gly Glu Asp Trp
      205                    210                    215
gag caa gaa gat gag gac atg gac ccc aga tta gaa cac agt tcc tca      878
Glu Gln Glu Asp Glu Asp Met Asp Pro Arg Leu Glu His Ser Ser Ser
      220                    225                    230                    235
gtt caa gaa gat tct gaa tcc cca agt cct gaa gat ata cca gac tac      926
Val Gln Glu Asp Ser Glu Ser Pro Ser Pro Glu Asp Ile Pro Asp Tyr
      240                    245                    250

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ctc ctg caa tac agg gcc atc cac agt gca gaa cag caa cat gcc tat      974
Leu Leu Gln Tyr Arg Ala Ile His Ser Ala Glu Gln Gln His Ala Tyr
255 260 265
gag cag gac ttt gag aca gat tat gct gaa tac cgc atc ctg cat gcc      1022
Glu Gln Asp Phe Glu Thr Asp Tyr Ala Glu Tyr Arg Ile Leu His Ala
270 275 280
cgt gtt ggg act gca agc caa agg ttc ata gag ctg gga gca gag att      1070
Arg Val Gly Thr Ala Ser Gln Arg Phe Ile Glu Leu Gly Ala Glu Ile
285 290 295
aaa aga gtt cgg cga gga act cca gaa tac aag gtc ctg gaa gac aag      1118
Lys Arg Val Arg Arg Gly Thr Pro Glu Tyr Lys Val Leu Glu Asp Lys
300 305 310 315
ata atc cag gaa tat aaa aag ttc agg aag cag tac cca agt tac aga      1166
Ile Ile Gln Glu Tyr Lys Lys Phe Arg Lys Gln Tyr Pro Ser Tyr Arg
320 325 330
gaa gaa aag cgt cgc tgt gag tac ctt cac cag aaa ttg tcc cac att      1214
Glu Glu Lys Arg Arg Cys Glu Tyr Leu His Gln Lys Leu Ser His Ile
335 340 345
aaa ggt ctc atc ctg gag ttt gag gaa aag aac agg ggc agc      1256
Lys Gly Leu Ile Leu Glu Phe Glu Glu Lys Asn Arg Gly Ser
350 355 360
tgaagtatc aaggaattt ttgagcctct gcttagtgaa acacaaagga acaaaagcagc      1316
tataaactaa atagaatgca actatctgct tttcttatgc tgaccactgg agtccatggg      1376
ggcaagtaga gagctgctct aggttcttga gggttggttt tcattattaa tttttagggt      1436
atgggcactg tgcaaaagact ccatagctgt gcttaggagt ctaggaaaag tgacagaggc      1496
ttggcttttt taccttttagt tcagccaagt cattttcaag tcctgagaaa tgacatcatc      1556
ttcaggataa aataatgagg acattagaca aaccaaacta tgatgaatttt agcctggtag      1616
cctctctaag gaacacagtaa taataacttc tgataagagt taaaagaact tgtagcatac      1676
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catggctaaa aaattaaaaa aaaaaaaaaa aa      1768

<210> 8
<211> 1510
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 190..1398

<220>
<221> sig_peptide
<222> 190..252
<223> Von Heijne matrix
score 5.8172934575094
seq ALLWAQEVGVLA/GR

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acgggtggcc tggcagcgcg cgaggctggt gagtcggcag cccctgtggca gccggcgggc      60
tgggtttccat ggttgcacga ttaggaaacca ccagctgctg catcccatgg ccagggggtgg      120
cgtccaggtg gcagagcagc taggaacgca aggcctgaac ctggggccag acaccctgct      180
ctcccggccc atg gtc aac gac cct cca gta cct gcc tta ctg tgg gcc cag      231
Met Val Asn Asp Pro Pro Val Pro Ala Leu Leu Trp Ala Gln
-20 -15 -10
gag gtg ggc caa gtc ttg gca ggc cgt gcc cgc agg ctg ctg ctg cag      279
Glu Val Gly Gln Val Leu Ala Gly Arg Ala Arg Arg Leu Leu Leu Gln
-5 1 5
ttt ggg gtg ctc ttc tgc acc atc ctc ctt ttg ctc tgg gtg tct gtc      327

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Phe Gly Val Leu Phe Cys Thr Ile Leu Leu Leu Leu Trp Val Ser Val	
10 15 20 25	
ttc ctc tat ggc tcc ttc tac tat tcc tat atg ccg aca gtc agc cac	375
Phe Leu Tyr Gly Ser Phe Tyr Tyr Ser Tyr Met Pro Thr Val Ser His	
30 35 40	
ctc agc cct gtg cat ttc tac tac agg acc gac tgt gat tcc tcc acc	423
Leu Ser Pro Val His Phe Tyr Tyr Arg Thr Asp Cys Asp Ser Ser Thr	
45 50 55	
acc tca ctc tgc tcc ttc cct gtt gcc aat gtc tgc ctg act aag ggt	471
Thr Ser Leu Cys Ser Phe Pro Val Ala Asn Val Ser Leu Thr Lys Gly	
60 65 70	
gga cgt gat cgg gtg ctg atg tat gga cag ccg tat cgt gtt acc tta	519
Gly Arg Asp Arg Val Leu Met Tyr Gly Gln Pro Tyr Arg Val Thr Leu	
75 80 85	
gag ctt gag ctg cca gag tcc cct gtg aat caa gat ttg ggc atg ttc	567
Glu Leu Glu Leu Pro Glu Ser Pro Val Asn Gln Asp Leu Gly Met Phe	
90 95 100	
ttg gtc acc att tcc tgc tac acc aga ggt ggc cga atc atc tcc act	615
Leu Val Thr Ile Ser Cys Tyr Thr Arg Gly Gly Arg Ile Ile Ser Thr	
110 115 120	
tct tcg cgt tcg gtg atg ctg cat tac cgc tca gac ctg ctc cag atg	663
Ser Ser Arg Ser Val Met Leu His Tyr Arg Ser Asp Leu Leu Gln Met	
125 130 135	
ctg gac aca ctg gtc ttc tct agc ctc ctg cta ttt ggc ttt gca gag	711
Leu Asp Thr Leu Val Phe Ser Ser Leu Leu Leu Phe Gly Phe Ala Glu	
140 145 150	
cag aag cag ctg ctg gag gtg gaa ctc tac gca gac tat aga gag aac	759
Gln Lys Gln Leu Leu Glu Val Glu Leu Tyr Ala Asp Tyr Arg Glu Asn	
155 160 165	
tcg gtg agt gag tac gtg ccg acc act gga gcg atc att gag atc cac	807
Ser Val Ser Glu Tyr Val Pro Thr Thr Gly Ala Ile Ile Glu Ile His	
170 175 180 185	
agc aag cgc atc cag ctg tat gga gcc tac ctc cgc atc cac gcg cac	855
Ser Lys Arg Ile Gln Leu Tyr Gly Ala Tyr Leu Arg Ile His Ala His	
190 195 200	
ttc act ggg ctc aga tac ctg cta tac aac ttc ccg atg acc tgc gcc	903
Phe Thr Gly Leu Arg Tyr Leu Leu Tyr Asn Phe Pro Met Thr Cys Ala	
205 210 215	
ttc ata ggt gtt gcc agc aac ttc acc ttc ctc agc gtc atc gtg ctc	951
Phe Ile Gly Val Ala Ser Asn Phe Thr Phe Leu Ser Val Ile Val Leu	
220 225 230	
ttc agc tac atg cag tgg gtg tgg ggg ggc atc tgg ccc cga cac cgc	999
Phe Ser Tyr Met Gln Trp Val Trp Gly Gly Ile Trp Pro Arg His Arg	
235 240 245	
ttc tct ttg cag gtt aac atc cga aaa aga gac aat tcc ccg aag gaa	1047
Phe Ser Leu Gln Val Asn Ile Arg Lys Arg Asp Asn Ser Arg Lys Glu	
250 255 260 265	
gtc caa cga agg atc tct gct cat cag cca ggt gca ggg cct gaa ggc	1095
Val Gln Arg Arg Ile Ser Ala His Gln Pro Gly Ala Gly Pro Glu Gly	
270 275 280	
cag gag gag tca act ccg caa tca gat gtt aca gag gat ggt gag agc	1143
Gln Glu Glu Ser Thr Pro Gln Ser Asp Val Thr Glu Asp Gly Glu Ser	
285 290 295	
cct gaa gat ccc tca ggg aca gag ggt cag ctg tcc gag gag aaa	1191
Pro Glu Asp Pro Ser Gly Thr Glu Gly Gln Leu Ser Glu Glu Glu Lys	
300 305 310	
cca gat cag cag ccc ctg agc gga gaa gag gag cta gag cct gag gcc	1239
Pro Asp Gln Gln Pro Leu Ser Gly Glu Glu Glu Leu Glu Pro Glu Ala	


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gttggtgtaag ggtaggcttt gttgaaaaag aaagaaagat tgaactacag gtgcatagca 1319
agcactcttt ctgggtaact aggtctgctgg ttttaattac cctcagattt caccataaaa 1379
aacgcacaat tgtattattt tacagagatg tgtccagcgc cccctgtggt gtgtgagaga 1439
aagcagctgc aactcaagtg actaggtggg ccagctggc ttctgtcagg agggcacggt 1499
gggtgagcca ttctcgccat tctcatgtca gactgaaagg agggcctggg ccagctttga 1559
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ctccaggtgt agaaaaattc aaaacaaaat gtcaggaatc tagcagtggt gtctgccctg 1679
gagcaaacaa acagtatgtg attttgcttc gcctattttt ttttctttt ttgggggaag 1739
ataattaaag gcagaatgac tgcgtttgta aaagaaggac caccaactat actgacattt 1799
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<210> 11
<211> 565
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 55..468

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<220>
<221> sig_peptide
<222> 55..99
<223> Von Heijne matrix
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      seq FTLLFLAAVAGA/LV

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                                         Met
                                         -15
aaa ttt acc act ctc ctc ttc ttg gca gct gta gca ggg gcc ctg gtc 105
Lys Phe Thr Thr Leu Leu Phe Leu Ala Ala Val Ala Gly Ala Leu Val
                                         -10
                                         -5
                                         1
tat gct gaa gat gcc tcc tct gac tgg acg ggt gct gat cct gcc cag 153
Tyr Ala Glu Asp Ala Ser Ser Asp Ser Thr Gly Ala Asp Pro Ala Gln
      5      10      15
gaa gct ggg acc tct aag cct aat gaa gag atc tca ggt cca gca gaa 201
Glu Ala Gly Thr Ser Lys Pro Asn Glu Glu Ile Ser Gly Pro Ala Glu
      20      25      30
cca gct tca ccc cca gag aca acc aca gca gcc cag gag act tgg gcg 249
Pro Ala Ser Pro Pro Glu Thr Thr Thr Thr Ala Gln Glu Thr Ser Ala
      35      40      45      50
gca gca gtt cag ggg aca gcc aag gtc acc tca agc agg cag gaa cta 297
Ala Ala Val Gln Gly Thr Ala Lys Val Thr Ser Ser Arg Gln Glu Leu
      55      60      65
aac ccc ctg aaa tcc ata gtg gag aaa agt atc tta cta aca gaa caa 345
Asn Pro Leu Lys Ser Ile Val Glu Lys Ser Ile Leu Leu Thr Glu Gln
      70      75      80
gcc ctt gca aaa gca gga aaa gga atg cac gga ggc gtg cca ggt gga 393
Ala Leu Ala Lys Ala Gly Lys Gly Met His Gly Gly Val Pro Gly Gly
      85      90      95
aaa caa ttc atc gaa aat gga agt gaa ttt gca caa aaa tta ctg aag 441
Lys Gln Phe Ile Glu Asn Gly Ser Glu Phe Ala Gln Lys Leu Leu Lys
      100      105      110
aaa ttc agt cta tta aaa cca tgg gca tgagaagctg aataatggga 488
Lys Phe Ser Leu Leu Lys Pro Trp Ala
      115      120

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tcatgtgacct taaagccctta aatacccttg tagcccagag ctattaaaac gaaagcatcc	548
aaaaaaaaaa aaaaaaa	565

<210> 12
 <211> 1663
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 152..475

<220>
 <221> sig_peptide
 <222> 152..244
 <223> Von Heijne matrix
 score 10.0910253445132
 seq LVLLLVTRSPVNA/CL

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gtgccttgga cctccccctt cgtctctcgt tctactgccc caggagcccg gcgggtcccg	120
gactcccgct cgtgcgcgtg cgggcgccgg c atg tgg ctg tgg gag gac cag	172
Met Trp Leu Trp Glu Asp Gln	
-30 -25	
ggc ggc ctc ctg ggc cct ttc tcc ttc ctg ctg cta gtg ctg ctg ctg	220
Gly Gly Leu Leu Gly Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Leu	
-20 -15 -10	
gtg acg cgg agc ccg gtc aat gcc tgc ctc ctc acc ggc agc ctc ttc	268
Val Thr Arg Ser Pro Val Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe	
-5 1 5	
gtt cta ctg cgc gtc ttc agc ttt gag ccg gtg ccc tct tgc agg gcc	316
Val Leu Leu Arg Val Phe Ser Phe Glu Pro Val Pro Ser Cys Arg Ala	
10 15 20	
ctg cag gtg ctc aag ccc ccg gac cgc att tct gcc atc gcc cac cgt	364
Leu Gln Val Leu Lys Pro Arg Asp Arg Ile Ser Ala Ile Ala His Arg	
25 30 35 40	
ggc ggc agc aam sag gcg ccc gag aac acg ctg gcg gcc att cgg cag	412
Gly Gly Ser Xaa Xaa Ala Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln	
45 50 55	
cta aga atg gag caa cag gcg tgg agt tgg aca ttg agt tta ctt ctg	460
Leu Arg Met Glu Gln Gln Ala Trp Ser Trp Thr Leu Ser Leu Leu Leu	
60 65 70	
acg gga ttc ctg tct taatgcacga taacacagta gataggacga ctgattgggac	515
Thr Gly Phe Leu Ser	
75	
tgggcgattg tgtgattga catttgaaca aattaggaag ctgaatccctg cagcaaaacca	575
cagactcagg aatgatttcc ctgatgaaaa gatccctacc ctaaggggaag ctgttgcaga	635
gtgcctaaac cataacctca caatcttctt tgatgtcaaa ggccatgcac acaaggctac	695
tgaggctcta aagaaaatgt atatggaatt tcctcaactg tataataata gtgtggtctg	755
ttctttcttg ccagaagtta tctacaaggt aacattcggg atttttcttg tacatattag	815
atgagacaaa cagatccggga tgtataaaca gcattaaact acagaccttg gagcctaagc	875
catacaggag atgggaaacc acgctatgat accttctgga aacattttat attgtttatg	935
atggacattt tgctcgattg gagcatgcac aatatcttgt ggtacctgtg tgggaattca	995
gctttctctca tgcaaaaagga ttttgatacc ccggcctact tgaagaagtg gtcagctaaa	1055
ggaatccagg ttgttggttg gactgttaat acctttgatg aaaagagtta ctacgaatcc	1115
catcttggtt ccagctatat cactgacagc atggtagaag actgcgaacc tcactcttag	1175
actttcacgg tgggacgaaa cgggttcaga aactgccagg ggcctcatag agggatatca	1235

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aaataccctt tgtgtagcc caggccctgg ggaatcaggt gactcacaca aatgcaatag 1295
ttgtgctactg catttttacc tgaaccaaaag ctaaaccctgg tgttgccacc atgcaccatg 1355
gcatgccaga gttcaacact gttgctcttgg aaaatctctgg tctgaaaaaa cgcacaagag 1415
cccttgccct gccctagctg aggcacacag ggagaccag tgaggataag cacagattga 1475
attgtacaat ttgcagatgc agatgtaaat gcatgggaca tgcagtataa ctcagagttg 1535
acattttaaa accttgccaca cttatttcaa atattgttac tcagctatgt taacatgtac 1595
tgtagacatc aaacttgtgg ccatactaata aaaattatta aaaggagcac taaaaaaaaa 1655
aaaaaaaaa 1663

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<210> 13
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<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 112..552

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<220>
<221> sig_peptide
<222> 112..183
<223> Von Heijne matrix
      score 11.7298925418815
      seq FVLGLGLTPPTLA/QD

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actgccagat ttttgaaga ttcttctctc tgggagcctg tgttggaaga g atg gtg 117
                                     Met Val
atg ggc ctg ggc gtt ttg ttg ttg gtc ttc gtg ctg ggt ctg ggt ctg 165
Met Gly Leu Gly Val Leu Leu Leu Val Phe Val Leu Gly Leu Gly Leu
-20 -15 -10
acc cca ccg acc ctg gct cag gat aac tcc agg tac aca cac ttc ctg 213
Thr Pro Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His Phe Leu
-5 1 5 10
acc cag cac tat gat gcc aaa cca cag ggc cgg gat gac aga tac tgt 261
Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg Tyr Cys
15 20 25
gaa agc atc atg agg aga cgg ggc ctg acc tca ccc tgc aaa gac atc 309
Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys Asp Ile
30 35 40
aac aca ttt att cat ggc aac aag cgc acg atc aag gcc atc tgt gaa 357
Asn Thr Phe Ile His Gly Asn Lys Arg Thr Ile Lys Ala Ile Cys Glu
45 50 55
aac aag aat gga aac cct cac aga gaa aac cta aga ata agc aag tct 405
Asn Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile Ser Lys Ser
60 65 70
tct ttc cag gtc acc act tgc aag cta cat gga ggt tcc ccc tgg cct 453
Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro Trp Pro
75 80 85 90
cca tgc cag tac cga gcc aca gcg ggg ttc aga aac gtt gtt gtt gct 501
Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn Val Val Val Ala
95 100 105
tgt gaa aat ggc tta cct gtc cac ttg gat cag tca att ttc cgt cgt 549
Cys Glu Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile Phe Arg Arg
110 115 120
ccg taaccagcgg gccctggctc aagtgtctggc tctgtctgtcc ttgccttcca 602
Pro

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tttccccctct gcacccagaa cagtgggtggc aacattcatt gccaaagggcc caaagaaaga 662
gtacactgga ccttttgttt tctgtttgac aacatgttta ataaataaaa atgtcttgat 722
atcagcaaaa aaaaaaaaaa aa 744

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<210> 14
<211> 1759
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 101..1243

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<220>
<221> sig_peptide
<222> 101..199
<223> Von Heijne matrix
      score 3.57142340200611
      seq FLCLGMALCPRQA/TR

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ttttttccat tctctctctc cacttcttca gtgagcagcc atg agt tgg act gtg 115
                                     Met Ser Trp Thr Val
                                     -30
cct gtt gtg cgg gcc agc cag aga gtg agc tcg gtg gga gcg aat ttc 163
Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser Val Gly Ala Asn Phe
                                     -25
                                     -20
                                     -15
cta tgc ctg ggg atg gcc ctg tgt ccg cgt caa gca acg cgc atc ccg 211
Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln Ala Thr Arg Ile Pro
                                     -10
                                     -5
                                     1
ctc aac ggc acc tgg ctc ttc acc ccc gtg agc aag atg gcg act gtg 259
Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser Lys Met Ala Thr val
5 10 15 20
aag agt gag ctt att gag cgt ttc act tcc gag aag ccc gtt cat cac 307
Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu Lys Pro Val His His
25 30 35
agt aag gtc tcc atc ata gga act gga tcg gtg ggc atg gcc tgc gct 355
Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val Gly Met Ala Cys Ala
40 45 50
atc agc atc tta tta aaa ggc ttg agt gat gaa ctt gcc ctt gtg gat 403
Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu Leu Ala Leu Val Asp
55 60 65
ctt gat gaa gac aaa ctg aag ggt gag acg atg gat ctt caa cat ggc 451
Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met Asp Leu Gln His Gly
70 75 80
agc cct ttc acg aaa atg cca aat att gtt tgt agc aaa gat tac ttt 499
Ser Pro Phe Thr Lys Met Pro Asn Ile Val Cys Ser Lys Asp Tyr Phe
85 90 95 100
gtc aca gca aac tcc aac cta gtg att atc aca gca ggt gca cgc caa 547
Val Thr Ala Asn Ser Asn Leu Val Ile Ile Thr Ala Gly Ala Arg Gln
105 110 115
gaa aag gga gaa acg cgc ctt aat tta gtc cag cga aat gtg gcc atc 595
Glu Lys Gly Glu Thr Arg Leu Asn Leu Val Gln Arg Asn Val Ala Ile
120 125 130
ttc aag tta atg att tcc agt att gtc cag tac agc ccc cac tgc aaa 643
Phe Lys Leu Met Ile Ser Ser Ile Val Gln Tyr Ser Pro His Cys Lys
135 140 145

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ctg att att gtt tcc aat cca gtg gat atc tta act tat gta gct tgg	691
Leu Ile Ile Val Ser Asn Pro Val Asp Ile Leu Thr Tyr Val Ala Trp	
150 155 160	
aag ttg agt gca ttt ccc aaa aac cgt att att gga agc ggc tgt aat	739
Lys Leu Ser Ala Phe Pro Lys Asn Arg Ile Ile Gly Ser Gly Cys Asn	
165 170 175 180	
ctg gat act gct cgt ttt cgt ttc ttg att gga caa aag ctt ggt atc	787
Leu Asp Thr Ala Arg Phe Arg Phe Leu Ile Gly Gln Lys Leu Gly Ile	
185 190 195	
cat tct gaa agc tgc cat gga tgg atc ctc gga gag cat gga gac tca	835
His Ser Glu Ser Cys His Gly Trp Ile Leu Gly Glu His Gly Asp Ser	
200 205 210	
agt gtt cct gtg tgg agt gga gtg aac ata gct ggt gtc cct ttg aag	883
Ser Val Pro Val Trp Ser Gly Val Asn Ile Ala Gly Val Pro Leu Lys	
215 220 225	
gat ctg aac tct gat ata gga act gat aaa gat cct gag caa tgg aaa	931
Asp Leu Asn Ser Asp Ile Gly Thr Asp Lys Asp Pro Glu Gln Trp Lys	
230 235 240	
aat gtc cac aaa gaa gtg act gca act gcc tat gag att att aaa atg	979
Asn Val His Lys Glu Val Thr Ala Thr Ala Tyr Glu Ile Ile Lys Met	
245 250 255 260	
aaa ggt tat act tct tgg gcc att ggc cta tct gtg gcc gat tta aca	1027
Lys Gly Tyr Thr Ser Trp Ala Ile Gly Leu Ser Val Ala Asp Leu Thr	
265 270 275	
gaa agt att ttg aag aat ctt agg aga ata cat cca gtt tcc acc ata	1075
Glu Ser Ile Leu Lys Asn Leu Arg Arg Ile His Pro Val Ser Thr Ile	
280 285 290	
att aag ggc ctc tat gga ata gat gaa gaa gta ttc ctc agt att cct	1123
Ile Lys Gly Leu Tyr Gly Ile Asp Glu Glu Val Phe Leu Ser Ile Pro	
295 300 305	
tgt atc ctg gga gag aac ggt att acc aac ctt ata aag ata aag ctg	1171
Cys Ile Leu Gly Glu Asn Gly Ile Thr Asn Leu Ile Lys Ile Lys Leu	
310 315 320	
acc cct gaa gaa gag gcc cat ctg aaa aaa agt gca aaa aca ctc tgg	1219
Thr Pro Glu Glu Glu Ala His Leu Lys Lys Ser Ala Lys Thr Leu Trp	
325 330 335 340	
gaa att cag aat aag ctt aag ctt taaagtgc taaaactacc attccgaaat	1273
Glu Ile Gln Asn Lys Leu Lys Leu	
345	
tattgaagag atcatagata caggattata taacgaaatt ttgaataaac ttgaattcct	1333
aaaagatgga aacaggaag taggtagagt gattttccta tttatttagt cctccagctc	1393
ttttattgag catccacgtg ctggacgata cttatttaca attcctaagt atttttggtta	1453
ctctgatgt agcagcactt gccatgttat atatatgtag ttggcatttg gttcccaaaa	1513
agtaggatgt aggtatttat tgtgttctag aaattccgac tcttttcatt agatatatgc	1573
tattttcttc attcttgcgt gttttatacct atgttcatatt atatgctgta aaaaagtagt	1633
agcttcttct acaattgtaaa aataaatgta catacaaaaa aatgcagtag tatatacaat	1693
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aaaaaa	1759

<210> 15
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 101..517

<220>
 <221> sig_peptide
 <222> 101..199
 <223> Von Heijne matrix
 score 3.57613483592743
 seq FLCLGMALCLRQA/TR

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ttttttccat tctctctctc cacttcttca gtgagcagcc atg agt tgg act gtg 115
Met Ser Trp Thr Val
-30
cct gtt gtg cgg gcc agc cag aga atg agc tcg gtg gga gcg aat ttc 163
Pro Val Val Arg Ala Ser Gln Arg Met Ser Ser Val Gly Ala Asn Phe
-25 -20
cta tgc ctg ggg atg gcc ctg tgt ctg cgt caa gca acg cgc atc ccg 211
Leu Cys Leu Gly Met Ala Leu Cys Leu Arg Gln Ala Thr Arg Ile Pro
-10 -5 1
ctc aac ggc acc tgg ctc ttc aca ccc gtg agc aag atg gcg act gtg 259
Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser Lys Met Ala Thr Val
5 10 15 20
aag agt gag ctt att gag cgt ttc act tcc gag aag ccc gtt cat cac 307
Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu Lys Pro Val His His
25 30 35
agt aag gtc tcc atc ata gga act gga tcg gtg ggc atg gcc tgc gct 355
Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val Gly Met Ala Cys Ala
40 45 50
atc agc atc ttg tta aaa ggc ttg agt gat gaa ctt gcc ctt gtg gat 403
Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu Leu Ala Leu Val Asp
55 60 65
ctt gat gaa gac aaa ctg aag ggt gag acg atg gat ctt caa cat ggc 451
Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met Asp Leu Thr His Gly
70 75 80
agc cct ttc acg aaa atg cca ata ttg ttt gta gca aag att act ttg 499
Ser Pro Phe Thr Lys Met Pro Ile Leu Phe Val Ala Lys Ile Thr Leu
85 90 95 100
tca cag caa act cca acc tagtgattat cacagcaggt gcacgccaaag 547
Ser Gln Gln Thr Pro Thr
105
aaaaaggaga aacgcgcctt aatttagtcc agcgaaatgt ggccatcttc aagtaatgat 607
ttccagtatt gtccagtaca gcccccactg caaactgatt attgtttcca atccagtgga 667
tatcttaact tatgtagcct ggaagttgag tgcatttccc aaaaaccgta ttattggaag 727
cggctgtaat ctggatactg ctgcgttttcg tttcttgatt ggacaaaagc ttggtatcca 787
ttctgaaagc tgccatggat ggatccctcg agagcatgga gactcaagtg ttccgtgtgtg 847
gagtggagtg aacatagctg gtgtcccttt gaaggatctg aactctgata taggaactga 907
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gaatagatga agaagtatcc ctcagtatcc ctgttatcct gggagagaaac ggtattacca 1147
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gctatttctt ctattctctg tggtttatac ctatgttcat ttatatgctg taaaaaagta 1627
gtagcttctt ctacaatgta aaaataaatg tacatacaaa aaaaatgcagt agtatatata 1687

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atcttttgggt ttgcttcctt tgatagttaa taaattccgt ttgttgaatc aataaaaaaa 1747
 aaaaaaaa 1755

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 <211> 936
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 59..853

<220>
 <221> sig_peptide
 <222> 59..100
 <223> Von Heijne matrix
 score 5.2402423806254
 seq NFILFIFIPGVFS/LK

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 atg aat ttt ata ttg ttt att ttt ata cct gga gtt ttt tcc tta aaa 106
 Met Asn Phe Ile Leu Phe Ile Phe Ile Pro Gly Val Phe Ser Leu Lys
 -10 -5 1
 agt agc act ttg aag cct act att gaa gca ttg cct aat gtg cta cct 154
 Ser Ser Thr Leu Lys Pro Thr Ile Glu Ala Leu Pro Asn Val Leu Pro
 5 10 15
 tta aat gaa gat gtt aat aag cag gaa gaa aag aat gaa gat cat act 202
 Leu Asn Glu Asp Val Asn Lys Gln Glu Glu Lys Asn Glu Asp His Thr
 20 25 30
 ccc aat tat gct cct gct aat gag aaa aat ggc aat tat tat aaa gat 250
 Pro Asn Tyr Ala Pro Ala Asn Glu Lys Asn Gly Asn Tyr Tyr Lys Asp
 35 40 45 50
 ata aaa caa tat gtg ttc aca aca caa aat cca aat ggc act gag tct 298
 Ile Lys Gln Tyr Val Phe Thr Thr Gln Asn Pro Asn Gly Thr Glu Ser
 55 60 65
 gaa ata tct gtg aga gcc aca act gac ctg aat ttt gct cta aaa aac 346
 Glu Ile Ser Val Arg Ala Thr Thr Asp Leu Asn Phe Ala Leu Lys Asn
 70 75 80
 gga tca acc cca aac gtg cct gca ttt tgg aca atg tta gct aaa gct 394
 Gly Ser Thr Pro Asn Val Pro Ala Phe Trp Thr Met Leu Ala Lys Ala
 85 90 95
 ata aat gga aca gca gtg gtc atg gat gat aaa gat caa tta ttt cac 442
 Ile Asn Gly Thr Ala Val Met Asp Lys Asp Gln Leu Phe His
 100 105 110
 cca att cca gag tct gat gtg aat gct aca cag gga gaa aat cag cca 490
 Pro Ile Pro Glu Ser Asp Val Asn Ala Thr Gln Gly Glu Asn Gln Pro
 115 120 125
 gat cta gag gat ctg aag atc aaa ata atg ctg gga atc tcg ttg atg 538
 Asp Leu Glu Asp Leu Lys Ile Lys Ile Met Leu Gly Ile Ser Leu Met
 135 140 145
 acc ctc ctc ctc ttt gtg gtc ctc ttg gca ttc tgt agt gct aca ctg 586
 Thr Leu Leu Leu Phe Val Val Leu Leu Ala Phe Cys Ser Ala Thr Leu
 150 155 160
 tac aaa ctg agg cat ctg agt tat aaa agt tgt gag agt cag tac tct 634
 Tyr Lys Leu Arg His Leu Ser Tyr Lys Ser Cys Glu Ser Gln Tyr Ser
 165 170 175
 gtc aac cca gag ctg gcc acg atg tct tac ttt cat cca tca gaa ggt 682

Val	Asn	Pro	Glu	Leu	Ala	Thr	Met	Ser	Tyr	Phe	His	Pro	Ser	Glu	Gly		
	180					185				190							
ggt	tca	gat	aca	tcc	ttt	tcc	aag	agt	gca	gag	agc	agc	aca	ttt	ttg	730	
Val	Ser	Asp	Thr	Ser	Phe	Ser	Lys	Ser	Ala	Glu	Ser	Ser	Thr	Phe	Leu		
	195				200					205				210			
ggg	acc	act	tct	tca	gat	atg	aga	aga	tca	ggc	aca	aga	aca	tca	gaa	778	
Gly	Thr	Thr	Ser	Ser	Asp	Met	Arg	Arg	Ser	Gly	Thr	Arg	Thr	Ser	Glu		
				215					220					225			
tct	aag	ata	atg	acg	gat	atc	att	tcc	ata	ggc	tca	gat	aat	gag	atg	826	
Ser	Lys	Ile	Met	Thr	Asp	Ile	Ile	Ser	Ile	Gly	Ser	Asp	Asn	Glu	Met		
			230					235					240				
cat	gaa	aac	gat	gag	tcg	gtt	acc	cgg	tgaagaaatc	aaggaacccc						873	
His	Glu	Asn	Asp	Glu	Ser	Val	Thr	Arg									
	245					250											
gtgaagaaat	cttattgatg	aataaataac	tttaattatt	ttgtcatcaa	aaaaaaaaaa											933	
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<220>
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 seq SPVFLVPPEITA/SE

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	Met Asp	Ser Ser	Thr Ala	His Ser	Pro Val	Phe Leu	Val										
	-20		-15		-10												
ttt cct cca	gaa atc	act gct tca	gaa tat	gag tcc	aca gaa	ctt tca										159	
Phe Pro Pro	Glu Ile	Thr Ala	Ser Glu	Tyr Glu	Ser Thr	Glu Leu	Ser										
	-5		1		5												
gcc acg acc	ttt tca	act caa	agc ccc	ttg caa	aaa tta	ttt gct	aga									207	
Ala Thr Thr	Phe Ser	Thr Gln	Ser Pro	Leu Gln	Lys Leu	Phe Ala	Arg										
	10		15		20		25										
aaa atg aaa	atc tta	ggg act	atc cag	atc ctg	ttt gga	att atg	acc									255	
Lys Met Lys	Ile Leu	Gly Thr	Ile Gln	Ile Leu	Phe Gly	Ile Met	Thr										
	30		35		40												
ttt tct ttt	gga gtt	atc ttc	ctt ttc	act ttg	tta aaa	cca tat	cca									303	
Phe Ser Phe	Gly Val	Ile Phe	Leu Phe	Thr Leu	Leu Lys	Pro Tyr	Pro										
	45		50		55												
agg ttt ccc	ttt ata	ttt ctt	tca gga	tat cca	tto tgg	ggc tct	ggt									351	
Arg Phe Pro	Phe Ile	Phe Leu	Ser Gly	Tyr Pro	Phe Trp	Gly Ser	Val										
	60		65		70												
ttg ttc att	aat tct	gga gcc	ttc cta	att gca	gtg aaa	aga aaa	acc									399	
Leu Phe Ile	Asn Ser	Gly Ala	Phe Leu	Ile Ala	Val Lys	Arg Lys	Thr										
	75		80		85												
aca gaa act	ctg ata	ata ttg	agc cga	ata atg	aat ttt	ctt agt	gcc									447	
Thr Glu Thr	Leu Ile	Ile Leu	Ser Arg	Ile Met	Asn Phe	Leu Ser	Ala										

90	ctg gga gca ata gct	95	gga atc att ctc ctc	100	aca ttt ggt ttc atc cta	105	
	Leu Gly Ala Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu						495
		110		115		120	
	gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag						543
	Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys	125		130		135	
	gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc						591
	Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe	140		145		150	
	agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc						639
	Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys	155		160		165	
	cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tgtgagaata						692
	His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys	170		175		180	
	aagatgtgtt aaaatatttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa						747

<210> 18
 <211> 1884
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 94..1275

<220>
 <221> sig_peptide
 <222> 94..210
 <223> Von Heijne matrix
 score 4.55778392992629
 seq LVLVKRLLAIVSVS/CI

<400> 18	acagcgctg cagcctctgtg cagctcttct ggtctccggc gcccgccct cagacgtaat	60
	gttgaattaa agaaaatact ttatcagaag aag atg gcc act gcc cag ttg cag	114
	Met Ala Thr Ala Gln Leu Gln	
	-35	
	agg act ccc atg agt gca ctg gta ttt ccc aat aag ata tca act gaa	162
	Arg Thr Pro Met Ser Ala Leu Val Phe Pro Asn Lys Ile Ser Thr Glu	
	-30 -25 -20	
	cac cag tct ttg gtg tta gtg aag agg ctt cta gca gtt tca gta tcc	210
	His Gln Ser Leu Val Leu Val Lys Arg Leu Leu Ala Val Ser Val Ser	
	-15 -10 -5	
	tgt atc acg tat ttg agg gga ata ttc cca gaa tgc gct tat gga aca	258
	Cys Ile Thr Tyr Leu Arg Gly Ile Phe Pro Glu Cys Ala Tyr Gly Thr	
	1 5 10 15	
	aga tat cta gat gat ctt tgt gtc aaa ata ctg aga gaa gat aaa aat	306
	Arg Tyr Leu Asp Asp Leu Cys Val Lys Ile Leu Arg Glu Asp Lys Asn	
	20 25 30	
	tgc cca gga tct aca cag tta gtg aaa tgg att cta gga tgt tat gat	354
	Cys Pro Gly Ser Thr Gln Leu Val Lys Trp Ile Leu Gly Cys Tyr Asp	
	35 40 45	
	gct tta cag aaa aaa tat cta agg atg gtt gtt cta gct gta tac aca	402
	Ala Leu Gln Lys Lys Tyr Leu Arg Met Val Val Leu Ala Val Tyr Thr	
	50 55 60	
	aac cca gaa gat cct cag aca att tca gaa tgt tac caa ttc aaa ttc	450


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atcttgagat aaatccaata gaacttttga ataaaagcaa aagtacaaat gtcataattg 1495
attcggttaat aagtaaaatt tcaaaattga ttttggatcat tacctactta atatttcctt 1555
taaataatata ctaactgtta aggcctctcta atgccatttt tctaaacagt aatgtttact 1615
ttggattataa aatttggat tgattcaatt tttacttatg ttaaaattat accatttaac 1675
tggctcttttt gtcattgtgc tgtattataa acaatgttct tcaatatttt gacataatgt 1735
attaacattt taatatataa tgtacaattt aagaattggg gctttaccct tactatgctt 1795
tttttacag acaaaaagac tgatttttaa agtatggcat tttttgcagc ataaataaaa 1855
tattgttcag tacgaaaaaa aaaaaaaaaa 1884

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<210> 19
<211> 691
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 42..515

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<220>
<221> sig_peptide
<222> 42..92
<223> Von Heijne matrix
      score 10.7019149919754
      seq VLMLLAVLIWTGA/EN

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<400> 19
gagttgtcct gtgctggagg tctgctcaga cgaaggctctc c atg gcg tta gaa gtc 56
Met Ala Leu Glu Val
-15
ttg atg ctc ctc gct gtc ttg att tgg acc ggt gct gag aac ctc cat 104
Leu Met Leu Leu Ala Val Leu Ile Trp Thr Gly Ala Glu Asn Leu His
-10 -5 1
gtg aaa ata agt tgc tct ctg gac tgg ttg atg gtc tca gtt atc cca 152
Val Lys Ile Ser Cys Ser Leu Asp Trp Leu Met Val Ser Val Ile Pro
5 10 15 20
ggt gca gaa agc aga aat ctg tat ata ttt gcg gat gaa tta cat ctg 200
Val Ala Glu Ser Arg Asn Leu Tyr Ile Phe Ala Asp Glu Leu His Leu
25 30 35
gga atg ggc tgc cct gca aat cgg ata cat aca tat gta tat gag ttt 248
Gly Met Gly Cys Pro Ala Asn Arg Ile His Thr Tyr Val Tyr Glu Phe
40 45
ata tat ctt gtt cgt gat tgt ggc atc agg aca agg gta gtt tct gag 296
Ile Tyr Leu Val Arg Asp Cys Gly Ile Arg Thr Arg Val Val Ser Glu
55 60 65
gaa act ctc ctt ttt caa acc gag ctg tac ttt acc cca agg aat ata 344
Glu Thr Leu Leu Phe Gln Thr Glu Leu Tyr Phe Thr Pro Arg Asn Ile
70 75 80
gat cat gat cct cag gaa atc cat ttg gag tgt tcc acc tct agg aaa 392
Asp His Asp Pro Gln Glu Ile His Leu Glu Cys Ser Thr Ser Arg Lys
85 90 95 100
tca gtg tgg ctt aca cca gtt tct act gag aat gaa ata aaa ttg gat 440
Ser Val Trp Leu Thr Pro Val Ser Thr Glu Asn Glu Ile Lys Leu Asp
105 110 115
cct agt cct ttt att gct gac ttt cag aca aca gca gaa gag tta gga 488
Pro Ser Pro Phe Ile Ala Asp Phe Gln Thr Thr Ala Glu Glu Leu Gly
120 125 130
tta tta tct tct agt cca aac ttg ctc tgagctaaag gagaaatgga 535
Leu Leu Ser Ser Ser Pro Asn Leu Leu

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	135	140	
aacttgaagc	tggtgttatg	tattttgcag	gaaaacagtt
tatatgttgt	gtatatctct	ccttaagtct	ctggtttcta
gtcctgatta	gttgattagc	gaaaaaaaaa	aaaaaa

595
655
691

<210> 20
<211> 1138
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 271..969

<220>
<221> sig_peptide
<222> 271..366
<223> Von Heijne matrix
score 5.6680378526706
seq WMGLACFRSLAAS/SP

<220>
<221> misc_feature
<222> 989
<223> n=a, g, c or t

<400> 20	
aaaaaccttt	caagtcccc
ctcctttcct	taaagtcttt
tataggggtc	cccttcttgg
ccatctccat	cctgtgagtc
aggactgaaa	gggcacagac
aggctcactgc	cagcattgtt
ggggcaagcc	tgcaagcacg
catcactggg	gatctgacat
gacaaatggcc	gctgtcccc
tctgagggct	acaggactta
ccccagtggg	aagcagctaa
gcaggtctga	ccagccgacc
tggaacctggc	caagggtcct
gtcatccctc	atg gcc acc
ccg cca ttc	cgg ctg

60
120
180
240
294

Met Ala Thr Pro Pro Phe Arg Leu	
-30	
ata agg aag atg ttt tcc ttc aag gtg agc aga tgg atg ggg ctt gcc	
Ile Arg Lys Met Phe Ser Phe Lys Val Ser Arg Trp Met Gly Leu Ala	
-20	
tgcc ttc cgg tcc ctg gcg gca tcc tct ccc agt att cgc cag aag aaa	
Cys Phe Arg Ser Leu Ala Ala Ser Ser Pro Ser Ile Arg Gln Lys Lys	
-5	

390

cta atg cac aag ctg cag gag gaa aag gct ttt cgc gaa gag atg aaa	
Leu Met His Lys Leu Gln Glu Glu Lys Ala Phe Arg Glu Glu Met Lys	
10	
15	
20	

438

att ttt cgt gaa aaa ata gag gac ttc agg gaa gag atg tgg act ttc	
Ile Phe Arg Glu Lys Ile Glu Asp Phe Arg Glu Glu Met Trp Thr Phe	
25	
30	
35	
40	

486

cga ggc aag atc cat gct ttc cgg ggc cag atc ctg ggt ttt tgg gaa	
Arg Gly Lys Ile His Ala Phe Arg Gly Gln Ile Leu Gly Phe Trp Glu	
45	
50	
55	

534

gag gag aga cct ttc tgg gaa gag gag aaa acc ttc tgg aaa gag gaa	
Glu Glu Arg Pro Phe Trp Glu Glu Lys Thr Phe Trp Lys Glu Glu	
60	
65	
70	

582

aaa tcc ttc tgg gaa atg gaa aag tct ttc agg gag gaa gag aaa act	
Lys Ser Phe Trp Glu Met Glu Lys Ser Phe Arg Glu Glu Glu Lys Thr	
75	
80	
85	

630

ttc tgg aaa aag tac cgc act ttc tgg aag gag gat aag gcc ttc tgg	
Phe Trp Lys Lys Tyr Arg Thr Phe Trp Lys Glu Asp Lys Ala Phe Trp	
90	
95	
100	

678


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aaa gag gac aat gcc tta tgg gaa aga gac cgg aac ctt ctt cag gag      726
Lys Glu Asp Asn Ala Leu Trp Glu Arg Asp Arg Asn Leu Leu Gln Glu
105                               110                               115                               120
gac aag gcc ctg tgg gag gaa gaa aag gcc ctg tgg gta gag gaa aga      774
Asp Lys Ala Leu Trp Glu Glu Glu Lys Ala Leu Trp Val Glu Glu Arg
125                               130                               135
gcc ctg ctt gag ggg gag aaa gcc ctg tgg gaa gat aaa acg tcc ctg      822
Ala Leu Leu Glu Gly Glu Lys Ala Leu Trp Glu Asp Lys Thr Ser Leu
140                               145                               150
tgg gag gaa gag aat gcc ctg tgg gag gaa gag agg gcc ttc tgg atg      870
Trp Glu Glu Glu Asn Ala Leu Trp Glu Glu Glu Arg Ala Phe Trp Met
155                               160                               165
gag aac aat ggc cac att gcc gga gag cag atg ctg gaa gat ggg ccc      918
Glu Asn Asn Gly His Ile Ala Gly Glu Gln Met Leu Glu Asp Gly Pro
170                               175                               180
cac aac gcc aac aga ggg cag cgc ttg ctg gcc ttc tcc cga ggc agg      966
His Asn Ala Asn Arg Gly Gln Arg Leu Leu Ala Phe Ser Arg Gly Arg
185                               190                               195                               200
gcg tagccagcat cgaggtgcan gggccctgtg gtccagactc ccctggggtg      1019
Ala
ggattcaagt ccagggtgag cccatgtgct ggagaaaata cacactcatt ggtctccttg      1079
ctttgaaaga tccaataaag tcttgaggca aggtttggaa aacacaaaaa aaaaaaaaa      1138

<210> 21
<211> 468
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 76..276

<220>
<221> sig_peptide
<222> 76..135
<223> Von Heijne matrix
      score 5.21332530399231
      seq SPVFLVFPPEITA/SE

<400> 21
agcacagaag aagaacatgg tctagactga agtaccacat aaatcatctc ctttcaaatt      60
atcacgcaga ccatc atg gat tca agc acc gca cac agt ccg gtg ttt ctg      111
      Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu
      -20                               -15                               -10
gta ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt      159
Val Phe Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu
      -5                               1                               5
tca gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct      207
Ser Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala
10                               15                               20
aga aaa atg aaa atc tta ggg gat atc cat tct ggg gct ctg ttt tgt      255
Arg Lys Met Lys Ile Leu Gly Asp Ile His Ser Gly Ala Leu Phe Cys
25                               30                               35                               40
tca tta att ctg gag cct tcc taattgcagt gaaaagaaaa accacagaaa      306
Ser Leu Ile Leu Glu Pro Ser
45
ctctgggaat ttgattaca ttgatgactt tcagcattat tgaattattc atttctctgc      366
ctttctcaat ttgggggtgc cactcagagg attgtgattg tgaacaatgt tgttgactag      426

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cactgtgaga ataaagatgt gttaaaaataa aaaaaaaaaa aa

468

<210> 22
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 6..287

<220>
<221> sig_peptide
<222> 6..80
<223> Von Heijne matrix
score 4.17710408129886
seq ISLSHLFLDLRS/LW

<400> 22
atttg atg tgc ttc tta gtc tcg ttt aac ttg ccg att cat ata tcc ctg 50
Met Cys Phe Leu Val Ser Phe Asn Leu Pro Ile His Ile Ser Leu
-25 -20 -15
tct cat ttg ttc tta gat ttg tca cga agc ctc tgg ttt ttg gct tgt 98
Ser His Leu Phe Leu Asp Leu Ser Arg Ser Leu Trp Phe Leu Ala Cys
-10 -5 1 5
cct ggt ttg aac ttg gtg tat ctg gct ctt gac tca ttt tct gac ctc 146
Pro Gly Leu Asn Leu Val Tyr Leu Ala Leu Asp Ser Phe Ser Asp Leu
10 15 20
aga cca tcc tta aat ctg ctt ttc tac ttt gta cca ggc ttt ggc gtc 194
Arg Pro Ser Leu Asn Leu Leu Phe Tyr Phe Val Pro Gly Phe Gly Val
25 30 35
tcc aag tac ctg acc tca gct caa cct gtc ttg ggt ttt ctt ctc ctc 242
Ser Lys Tyr Leu Thr Ser Ala Gln Pro Val Leu Gly Phe Leu Leu Leu
40 45 50
cct gac att gac aac cca gcc ctc cta ggc aca gag aga tgg agc 287
Pro Asp Ile Asp Asn Pro Ala Leu Leu Gly Thr Glu Arg Trp Ser
55 60 65
tgagtgtggt tttcctgaaa taaagcttgc attatgagag ggaataaaca gaagaaaaaa 347
atagtaagta aaatcttgct tgcctctcag taaaataaag ctctattttt cgtttttttt 407
ttttccaact tctgtacaaa aaaagggaaa actttagcct ttgggggaaa ttgggagcta 467
gcctgttggt actgttgagc ttagtgtatc tataactata tattattcca caatatctta 527
aatactttat aaagatatatt tcataaatta cagcaatcct ggctttagat gattgatggc 587
catttttaaa caattaaagc taatttctag ctttttatga gtttggtatt aagcacagta 647
gtttcttaga aagttccag ggaatgcatt ttgcaaaata aaaatcagct aatgacccaa 707
aaaaaaaaa aaa 720

<210> 23
<211> 727
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 171..692

<220>
<221> sig_peptide
<222> 171..227

<223> Von Heijne matrix
score 4.17573075349936
seq LLLGGQRCSLKVSG/QE

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<400> 23
attgtgacat caccgtgcac tagccaatgg ctgcctgcct aagctgggct cctgggtctcc      60
tgggactact agccctttgt tgataggagg aagccaacat ctccgcagag accccctaata      120
cttcagggca gctcccagag catggatccc tctgtattcc actcagcccg atg ttc      176
                                     Met Phe
ctc aca gtc aag ctg ctc ctg ggc cag aga tgc agt ctg aag gtg tca      224
Leu Thr Val Lys Leu Leu Leu Gly Gln Arg Cys Ser Leu Lys Val Ser
      -15                                     -10      -5
ggg caa gag agt gta gcc acg ctg aag aga ctg gtg tcc agg cgg ctg      272
Gly Gln Glu Ser Val Ala Thr Leu Lys Arg Leu Val Ser Arg Arg Leu
      1           5           10           15
aag gtg cct gag gag cag cag cac ctg ctt ttc cgt ggc cag ctc ctg      320
Lys Val Pro Glu Glu Gln Gln His Leu Leu Phe Arg Gly Gln Leu Leu
      20           25           30
gag gat gac aag cac ctc tct gac tac tgc att ggg ccc aat gcc tct      368
Glu Asp Asp Lys His Leu Ser Asp Tyr Cys Ile Gly Pro Asn Ala Ser
      35           40           45
atc aat gtc atc atg cag ccc ttg gag aag atg gcg cta aag gag gcc      416
Ile Asn Val Ile Met Gln Pro Leu Glu Lys Met Ala Leu Lys Glu Ala
      50           55           60
cac cag ccg cag acc cag ccc ctg tgg cac cag ctg gga ctg gtc cta      464
His Gln Pro Gln Thr Gln Pro Leu Trp His Gln Leu Gly Leu Val Leu
      65           70           75
gct aaa cac ttt gaa cca cag gat gcc aag gcc gtg ctg cag ctg cta      512
Ala Lys His Phe Glu Pro Gln Asp Ala Lys Ala Val Leu Gln Leu Leu
      80           85           90           95
agg cag gag cac gag gag cgc ctg cag aag ata agc ctg gag cac ctg      560
Arg Gln Glu His Glu Glu Arg Leu Leu Gln Lys Ile Ser Leu Glu His Leu
      100           105           110
gag cag ctg gcc cag tac ctc ctg gca gag gag cct cac gtg gag cca      608
Glu Gln Leu Ala Gln Tyr Leu Leu Ala Glu Glu Pro His Val Glu Pro
      115           120           125
gct gga gag agg gag ctt gag gcg aag gca cgg cct cag agc tcc tgt      656
Ala Gly Glu Arg Glu Leu Glu Ala Lys Ala Arg Pro Gln Ser Ser Cys
      130           135           140
gac atg gag gag aag gag gag gca gca gct gat cag taaacggggcc      702
Asp Met Glu Glu Lys Glu Glu Ala Ala Ala Asp Gln
      145           150           155
atcctaccgg aaaaaaaaaa aaaaaa      727

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<210> 24
<211> 470
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 137..454

<220>
<221> sig_peptide
<222> 137..187
<223> Von Heijne matrix
score 10.7019149919754

seq VLMLLAVLIWIGA/EN

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<400> 24
atcctgtgaa ctacccaaaa ggaggaaaaac gaacgcagct gagcatggga tgccatataa      60
aaatcactta aaccagtcgc cactccttgt ttccctgagtt gtccctgtgct ggagggtctgc      120
tcacaggaag gtctcc atg gcg tta gaa gtc ttg atg ctg ctc gct gtc ttg      172
          Met Ala Leu Glu Val Leu Met Leu Leu Ala Val Leu
          -15                      -10

att tgg acc ggt gct gag aac ctc cat gtg aaa ata agt tgc tct ctg      220
Ile Trp Thr Gly Ala Glu Asn Leu His Val Lys Ile Ser Cys Ser Leu
-5                      1                      5                      10
gac tgg ttg atg gtc tca gtt atc cca gtt gca gaa agc aga aat ctg      268
Asp Trp Leu Met Val Ser Val Ile Pro Val Ala Glu Ser Arg Asn Leu
          15                      20                      25

tat ata ttt gcg gat gaa tta cat ctg gga atg ggc tgc cct gca aat      316
Tyr Ile Phe Ala Asp Glu Leu His Leu Gly Met Gly Cys Pro Ala Asn
          30                      35                      40

cgg ata cat aca tat gta tat gag ttt ata tat ctt gtt cgt gat tgt      364
Arg Ile His Thr Tyr Val Tyr Glu Phe Ile Tyr Leu Val Arg Asp Cys
          45                      50                      55

ggc atc agg aca agg gta aga aca gtg att gtc tgt aaa aaa tac tgc      412
Gly Ile Arg Thr Arg Val Arg Thr Val Ile Val Cys Lys Lys Tyr Cys
          60                      65                      70                      75

atg ttt tgt cag act ttt atg cct agt att aaa att gtc ttt      454
Met Phe Cys Gln Thr Phe Met Pro Ser Ile Lys Ile Val Phe
          80                      85

taaaaaaaaa aaaaaa      470

<210> 25
<211> 987
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 238..609

<220>
<221> sig_peptide
<222> 238..291
<223> Von Heijne matrix
      score 10.0374888212272
      seq LLLLVMALPPGTT/GV

<400> 25
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agaggggacgc agggcggttg gaacagagga cactccaggc gctgacctg ggaggccagg      120
accagggccca aagtccccgtg ggcaagagga gtccctcagag gtcccttcatt cagcgggtcc      180
gggagggtctg ggaagccccc ggcctggctg gggcagggtc aacgcgcgcca ggccgccc      237
atg gtc ctg tgc tgg ctg ctg ctt ctg gtg atg gct ctg ccc cca ggc      285
Met Val Leu Cys Trp Leu Leu Leu Leu Val Met Ala Leu Pro Pro Gly
          -15                      -10                      -5

acg acg ggc gtc aag gac tgc gtc ttc tgt gag ctg acc gac tcc atg      333
Thr Thr Gly Val Lys Asp Cys Val Phe Cys Glu Leu Thr Asp Ser Met
          1                      5                      10

cag tgt cct ggt acc tac atg cac tgt ggc gat gac gag gac tgc ttc      381
Gln Cys Pro Gly Thr Tyr Met His Cys Gly Asp Asp Glu Asp Cys Phe
          15                      20                      25                      30

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aca ggc cac ggg gtc gcc ccg ggc act ggt ccg gtc atc aac aaa ggc      429
Thr Gly His Gly Val Ala Pro Gly Thr Gly Pro Val Ile Asn Lys Gly
      35      40      45
tgc ctg cga gcc acc agc tgc ggc ctt gag gaa ccc gtc agc tac agg      477
Cys Leu Arg Ala Thr Ser Cys Gly Leu Glu Glu Pro Val Ser Tyr Arg
      50      55      60
ggc gtc acc tac agc ctc acc acc aac tgc tgc acc ggc cgc ctg tgt      525
Gly Val Thr Tyr Ser Leu Thr Thr Asn Cys Cys Thr Gly Arg Leu Cys
      65      70      75
aac aga gcc ccg agc agc cag aca gtg ggg gcc acc acc agc ctg gca      573
Asn Arg Ala Pro Ser Ser Gln Thr Val Gly Ala Thr Thr Ser Leu Ala
      80      85      90
ctg ggg ctg ggt atg ctg ctt cct cca cgt ttg ctg tgaccaacag      619
Leu Gly Leu Gly Met Leu Leu Pro Pro Arg Leu Leu
      95      100      105
ggaggacagg gcctgggact gttctccagc atccgccact ccccatgtcc ccatgtcctt      679
cccccaactaa atggccagag agggccctgga caacctcttg cggccctggc ttcacccctt      739
ctaaggctgt ccaccaggag cccgggtgcta ggggaagcat cccaggcct gactgagcgg      799
caggggagca cggcccgtgg gtttgattgt attactctgt tccactggtt ctaagacgca      859
gagcttctca catctcaatc aggatgcttc tctccattgg tagcacttta gagtccatga      919
aatatggtaa aaaatatata tatatcataa taaatgacag ctgatgttca tggaaaaaaa      979
aaaaaaaaa
      987

<210> 26
<211> 908
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..862

<220>
<221> sig_peptide
<222> 80..127
<223> Von Heijne matrix
      score 3.66725851505537
      seq FSLLSISGFPPISS/SA

<400> 26
gaatgtttat cctctggaca aaccagccag cctctccaga gcaggcgtgt gatctctgta      60
ccccgcagtg ggtcagaat atg gag aac ttc tca ctc ctc agc atc tct gga      112
      Met Glu Asn Phe Ser Leu Leu Ser Ile Ser Gly
      -15      -10
cct cca atc tct tcc tcc gcc ctg agt gct ttt ccc gac att atg ttc      160
Pro Pro Ile Ser Ser Ser Ala Leu Ser Ala Phe Pro Asp Ile Met Phe
      -5      1      5      10
tct cgt gcc acc agc ctg cca gac att gca aag aca gca gta ccc act      208
Ser Arg Ala Thr Ser Leu Pro Asp Ile Ala Lys Thr Ala Val Pro Thr
      15      20      25
gag gca tcc agc cca gct cag gcc ctg cca ccc cag tac caa agc atc      256
Glu Ala Ser Ser Pro Ala Gln Ala Leu Pro Pro Gln Tyr Gln Ser Ile
      30      35      40
att gtc agg caa ggg ata cag aac aca gtg ctc tca cca gac tgc agc      304
Ile Val Arg Gln Gly Ile Gln Asn Thr Val Leu Ser Pro Asp Cys Ser
      45      50      55
ttg ggg gac acc cag cac gga gag aag ctg agg cgg aac tgc act atc      352
Leu Gly Asp Thr Gln His Gly Glu Lys Leu Arg Arg Asn Cys Thr Ile

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09721872-1207100

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60          65          70          75
tac cgg ccc tgg ttc tcc ccc tac agc tac ttc gtg tgt gca gac aaa      400
Tyr Arg Pro Trp Phe Ser Pro Tyr Ser Tyr Phe Val Cys Ala Asp Lys
80          85          90
gag agc cag ctg gag gcc tat gac ttc cca gag gtg cag cag gat gag      448
Glu Ser Gln Leu Glu Ala Tyr Asp Phe Pro Glu Val Gln Gln Asp Glu
95          100          105
ggc aag tgg gac aac tgc ctt tct gag gac atg gct gag aac atc tgt      496
Gly Lys Trp Asp Asn Cys Leu Ser Glu Asp Met Ala Glu Asn Ile Cys
110          115          120
tcg tcc tct tcc tcc cca gag aac act tgc cct cga gaa gcc acc aag      544
Ser Ser Ser Ser Ser Pro Glu Asn Thr Cys Pro Arg Glu Ala Thr Lys
125          130          135
aaa tcc agg cat ggc ctg gac tcc atc aca tcc cag gac atc cta atg      592
Lys Ser Arg His Gly Leu Asp Ser Ile Thr Ser Gln Asp Ile Leu Met
140          145          150
gct tcc aga tgg cac cca gca cag cag aat ggc tac aag tgc gtg gcc      640
Ala Ser Arg Trp His Pro Ala Gln Gln Asn Gly Tyr Lys Cys Val Ala
155          160          165
tgc tgc cgc atg tac ccc acc ctg gac ttc ctc aag agc cac atc aag      688
Cys Cys Arg Met Tyr Pro Thr Leu Asp Phe Leu Lys Ser His Ile Lys
170          175          180
agg ggc ttc agg gag ggc ttc agc tgc aag gtg tac tac cgc aag ctc      736
Arg Gly Phe Arg Glu Gly Phe Ser Cys Lys Val Tyr Tyr Arg Lys Leu
185          190          195
aaa gcc ctg tgg agc aag gag cag aag gcc cgg ctg gga gac agg ctg      784
Lys Ala Leu Trp Ser Lys Glu Gln Lys Ala Arg Leu Gly Asp Arg Leu
200          205          210
tcc tcc ggc agc tgc cag gcc ttc aat agt cct gct gaa cac ctt agg      832
Ser Ser Gly Ser Cys Gln Ala Phe Asn Ser Pro Ala Glu His Leu Arg
215          220          225
caa att ggc ggt gaa gcc tac tta tgt ctc tagagagatg ccaataaagt      882
Gln Ile Gly Gly Glu Ala Tyr Leu Cys Leu
230          235          240
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245

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seq LCALLSNFCPSTT/VK

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gccctgaaaa gtccctggct ca atg tgc atg tcc ctt tct atg aaa gtt cct      112
Met Cys Met Ser Leu Ser Met Lys Val Pro
-25          -20
tgc tgc cta tgc gcc ttg ctc tct aac ttc tgt ccc tcc aca act gtg      160

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Cys Cys Leu Cys Ala Leu Leu Ser Asn Phe Cys Pro Ser Thr Thr Val
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Lys Gly Asp Val Val Thr Ser Phe Phe Arg Ala Asp Tyr Asp Leu Ala
5 10 15
agt agg tct gca gat cag tcc tcc cag aaa gtg aag ttg cgc atg ttc 256
Ser Arg Ser Ala Asp Gln Ser Ser Gln Lys Val Lys Leu Arg Met Phe
20 25 30
act ggg cgt ctt ccc atc ggc ccc ttc gcc agt gtg ggg aac gcg gcg 304
Thr Gly Arg Leu Pro Ile Gly Pro Phe Ala Ser Val Gly Asn Ala Ala
35 40 45
gag ctg tgagccggcg actcgggtcc ctgaggtctg gattctttct ccgctactga 360
Glu Leu
50
gacacggcgg acacacacaa acacagaacc acacagccag tcccaggagc ccagtaatgg 420
agagccccc aaagaagaac cagcagctga aagtcgggat cctacacctg ggcagcagac 480
agaagaagat caggatacac ctgagatccc agtcgcgcac atggaagggt atctgcaaga 540
gctgcctcag tcaaacaccg gggataaatc tggatttggg ttccggcgctc aaggtgaaga 600
taatacctaa agaggaacac tgtaaaatgc cagaagcagg tgaagagcaa ccacaagttt 660
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seq FPLLLSLGLVLA/EA

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tgtcaaaaga gaaggtgcac ttacgctagt tgtagctct gtcttttgta accatcaagt 180
tccatgcgat tgatcagatt taggaggggg cgttggggga taatcaattt tgggtgtcac 240
caggtaaaca gagccctcag catctgaata gaaactgaac aggaacagaa gagattcact 300
acatctgag atg gag acc ttt cct ctg ctg ctg ctc agc ctg ggc ctg gtt 351
Met Glu Thr Phe Pro Leu Leu Leu Leu Ser Leu Gly Leu Val
-15 -10 -5
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Leu Ala Glu Ala Ser Glu Ser Thr Met Lys Ile Ile Lys Glu Glu Phe
1 5 10
aca gac gaa gag atg caa tat gac atg gca aaa agt ggc caa gaa aaa 447
Thr Asp Glu Glu Met Gln Tyr Asp Met Ala Lys Ser Gly Gln Glu Lys
15 20 25 30
cag acc att gag ata tta atg aac ccg atc ctg tta gtt aaa aat acc 495
Gln Thr Ile Glu Ile Leu Met Asn Pro Ile Leu Leu Val Lys Asn Thr
35 40 45
agc ctc agc atg tcc aag gat gat atg tct tcc aca tta ctg aca ttc 543
Ser Leu Ser Met Ser Lys Asp Asp Met Ser Ser Thr Leu Leu Thr Phe

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	50								55							60						
aga agt tta cat tat aat gac ccc aag gga aac agt tcg ggt aat gac																						591
Arg Ser Leu His Tyr Asn Asp Pro Lys Gly Asn Ser Ser Gly Asn Asp																						
65									70							75						
aaa gag tgt tgc aat gac atg acg ttc tgg aga aaa gtt tca gaa gca																						639
Lys Glu Cys Cys Asn Asp Met Thr Val Trp Arg Lys Val Ser Glu Ala																						
80									85							90						
aac gga tcg tgc aag tgg agc aat aac ttc atc cgx agc tcc aca gaa																						687
Asn Gly Ser Cys Lys Trp Ser Asn Asn Phe Ile Arg Ser Ser Thr Glu																						
95									100							105						110
gtg atg cgc agg gtc cac agg gcc ccc agc tgc aag ttt gta cag aat																						735
Val Met Arg Arg Val His Arg Ala Pro Ser Cys Lys Phe Val Gln Asn																						
115									120							125						
cct ggc ata agc tgc tgt gag agc cta gaa ctg gaa aat aca gtg tgc																						783
Pro Gly Ile Ser Cys Cys Glu Ser Leu Glu Leu Glu Asn Thr Val Cys																						
130									135							140						
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Gln Phe Thr Thr Thr Gly Lys Lys Phe Pro Arg Cys Gln Tyr His Ser Val																						
145									150							155						
acc tca tta gag aag ata ttg acca gtg ctg aca ggt cat tct ctg atg																						879
Thr Ser Leu Glu Lys Ile Leu Thr Val Leu Thr Gly His Ser Leu Met																						
160									165							170						
agc tgg tta gtt tgt ggc tct aag ttg taaatcccac agagtcttag																						926
Ser Trp Leu Val Cys Gly Ser Lys Leu																						
175									180													
gactagggtc ttactaagga aggacctctt cttgttcatt cttgtttaaa cctttcctta																						986
atatctactc tttagcacta tagtgaaetc ctgtattatt attctaactc gaggagttaa																						1046
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seq ILMRDFSPSGIFG/AF
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Ser	Cys	Ser	Ser	Asp	Ile	Ala	Asp	Val	Glu	Val	Asp	Met	Ser	Gly	Asp		
			135				140				145						
ttg	ggg	tgg	ctg	ttg	aac	ctc	ttc	cac	aac	cag	att	gag	tcc	aag	ttc		698
Leu	Gly	Trp	Leu	Leu	Asn	Leu	Phe	His	Asn	Gln	Ile	Glu	Ser	Lys	Phe		
			150				155				160						
cag	aaa	gta	ctg	gag	agc	agg	att	tg	gaa	atg	atc	cag	aaa	tcg	gtg		746
Gln	Lys	Val	Leu	Glu	Ser	Arg	Ile	Cys	Glu	Met	Ile	Gln	Lys	Ser	Val		
			165				170				175				180		
tcc	tcc	gat	cta	cag	cct	tat	ctc	caa	act	ctg	aca	gtt	aca	aca	gag		794
Ser	Ser	Asp	Leu	Gln	Pro	Tyr	Leu	Gln	Thr	Leu	Thr	Val	Thr	Thr	Glu		
			185							190					195		
att	gac	agt	ttc	gcc	gac	att	gat	tat	agc	tta	gtg	gaa	gcc	cct	cgg		842
Ile	Asp	Ser	Phe	Ala	Asp	Ile	Asp	Tyr	Ser	Leu	Val	Glu	Ala	Pro	Arg		
			200							205				210			
gca	aca	gcc	cag	atg	ctg	gag	gtg	atg	ttt	aag	ggt	gaa	atc	ttt	cat		890
Ala	Thr	Ala	Gln	Met	Leu	Glu	Val	Met	Phe	Lys	Gly	Glu	Ile	Phe	His		
			215				220				225						
cgt	aac	cac	cgt	tct	cca	gtt	acc	ctc	ctt	gct	gca	gtc	atg	agc	ctt		938
Arg	Asn	His	Arg	Ser	Pro	Val	Thr	Leu	Leu	Ala	Ala	Val	Met	Ser	Leu		
			230				235				240						
cct	gag	gaa	cac	aac	aaa	atg	gtc	tac	ttt	gcc	atc	tcg	gat	tat	gtc		986
Pro	Glu	Glu	His	Asn	Lys	Met	Val	Tyr	Phe	Ala	Ile	Ser	Asp	Tyr	Val		
			245			250				255					260		
ttc	aac	acg	gcc	agc	ctg	gtt	tat	cat	gag	gaa	gga	tat	ctg	aac	ttc		1034
Phe	Asn	Thr	Ala	Ser	Leu	Val	Tyr	His	Glu	Gly	Tyr	Leu	Asn	Phe			
			265						270					275			
tcc	atc	aca	gat	gac	atg	ata	cog	cct	gac	tct	aat	atc	cga	ctg	acc		1082
Ser	Ile	Thr	Asp	Asp	Met	Ile	Pro	Pro	Asp	Ser	Asn	Ile	Arg	Leu	Thr		
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acc	aag	tcc	ttc	cga	ccc	ttc	gtc	cca	cgg	tta	gcc	agg	ctc	tac	ccc		1130
Thr	Lys	Ser	Phe	Arg	Pro	Phe	Val	Pro	Arg	Leu	Ala	Arg	Leu	Tyr	Pro		
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aac	atg	aac	ctg	gaa	ctc	cag	gga	tca	gtg	ccc	tct	gct	cgc	ctc	ctg		1178
Asn	Met	Asn	Leu	Glu	Leu	Gln	Gly	Ser	Val	Pro	Ser	Ala	Pro	Leu	Leu		
			310			315					320						
aac	ttc	agc	cct	ggg	aat	ctg	tct	gtg	gac	ccc	tat	atg	gag	ata	gat		1226
Asn	Phe	Ser	Pro	Gly	Asn	Leu	Ser	Val	Asp	Pro	Tyr	Met	Glu	Ile	Asp		
			325			330				335				340			
gcc	ttt	gtg	ctc	ctg	ccc	agc	tcc	agc	aag	gag	cct	gtc	ttc	cgc	ctc		1274
Ala	Phe	Val	Leu	Leu	Pro	Ser	Ser	Ser	Lys	Glu	Pro	Val	Phe	Arg	Leu		
			345						350					355			
agt	gtg	gcc	act	aat	gtg	tcc	gcc	acc	ttg	acc	ttc	aat	acc	agc	aag		1322
Ser	Val	Ala	Thr	Asn	Val	Ser	Ala	Thr	Leu	Thr	Phe	Asn	Thr	Ser	Lys		
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atc	act	ggg	ttc	ctg	aag	cca	gga	aag	gta	aaa	gtg	gaa	ctg	aaa	gaa		1370
Ile	Thr	Gly	Phe	Leu	Lys	Pro	Gly	Lys	Val	Lys	Val	Glu	Leu	Lys	Glu		
			375			380					385						
tcc	aaa	gtt	gga	cta	ttc	aat	gca	gag	ctg	ttg	gaa	gcg	ctc	ctc	aac		1418
Ser	Lys	Val	Gly	Leu	Phe	Asn	Ala	Glu	Leu	Leu	Glu	Ala	Leu	Leu	Asn		
			390			395				400							
tat	tac	atc	ctt	aac	acc	ttc	tac	ccc	aag	ttc	aat	gat	aag	ttg	gcc		1466
Tyr	Tyr	Ile	Leu	Asn	Thr	Phe	Tyr	Pro	Lys	Phe	Asn	Asp	Lys	Leu	Ala		
			405			410				415				420			
gaa	ggc	ttc	ccc	ctt	cct	ctg	ctg	aag	cgt	gtt	cag	ctc	tac	gac	ctt		1514
Glu	Gly	Phe	Pro	Leu	Pro	Leu	Leu	Lys	Arg	Val	Gln	Leu	Tyr	Asp	Leu		
			425					430						435			

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ggg ctg cag atc cat aag gac ttc ctg ttc ttg ggt gcc aat gtc caa      1562
Gly Leu Gln Ile His Lys Asp Phe Leu Phe Leu Gly Ala Asn Val Gln
      440      445      450
tac atg aga gtt tgaggacaag aaagatgaag cttaggaggtc acagctggat      1614
Tyr Met Arg Val
      455
ctgcttgttg catttcacgc tgtgcagcac gtctcagaga ttcttgaaga atgaagacat      1674
ttctgtctctc agctccgggg gtgaggtgtg cctggcctct gctccacacc tctctctctt      1734
caccaggtgc atgcatgccc tctctgagtc tggactttgc ttccctccca ggagggacca      1794
ccctccctga ctggcctggg atatctttac aagcaggcac tgtatttttt tattcgccat      1854
ctgatcccca tgcctagcag agtgctggca cttagtaggt cctcaataaa tattttattaa      1914
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tgtcctctgt cgccgggaac tggcgaggtg gttccttcgc ggtggagaga cctgga atg      119
      Met
gcc aaa tat caa ggt gaa gtt caa agt ttg aaa ctg gat gat gat tca      167
Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp Ser
      -40      -35      -30
gtt ata gaa gga gta agc gac caa gta ctt gtg gca gtt gtg gtc agt      215
Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val Ser
      -25      -20      -15
ttc gct ttg att gct acc ctg gta tat gca ctt ttc aga aat gta cat      263
Phe Ala Leu Ile Ala Thr Leu Val Tyr Ala Leu Phe Arg Asn Val His
      -10      -5      1      5
caa aac att cac cca gaa aac cag gag cta gta agg gta ctt cga gaa      311
Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg Glu
      10      15      20
cag ctt caa aca gaa cag gat gca cct gct gcc act cga cag cag ttc      359
Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Ala Thr Arg Gln Gln Phe
      25      30      35
tac act gac atg tac tgt ccc atc tgc ctg cac caa gcc tcc ttc ccg      407
Tyr Thr Asp Met Tyr Cys Pro Ile Cys Leu His Gln Ala Ser Phe Pro
      40      45      50
gtg gag acc aac tgt gga cat ctt ttt tgt ggt gcc tgc att att gct      455
Val Glu Thr Asn Cys Gly His Leu Phe Cys Gly Ala Cys Ile Ile Ala
      55      60      65
tac tgg cga tat ggt tca tgg ctt ggg gca atc agt tgt cca atc tgt      503
Tyr Trp Arg Tyr Gly Ser Trp Leu Gly Ala Ile Ser Cys Pro Ile Cys
      75      80      85
aga caa acg aga cat ggc cac att gca ttg tcc aga aca gct      545

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00724973-120700

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gaaaccccat	ctctagaaaa	aacacacaaa	aattggacaa	gagtgttggc	acatgcctgt									965
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Met	
1	
gcc aaa tat caa ggt gaa gtt caa agt ttg aaa ctg gat gat gat tca	167
Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp Ser	
5 10 15	
ggt ata gaa gga gta agc gac caa gta ctt gtg gca gtt gtg gtc agt	215
Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val Ser	
20 25 30	
ttc gct ttg att gct acc ctg gta tat gca ctt ttc aga aat gta cat	263
Phe Ala Leu Ile Ala Thr Leu Val Tyr Ala Leu Phe Arg Asn Val His	
35 40 45	
caa aac att cac cca gaa aac cag gag cta gta agg gta ctt cga gaa	311
Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg Glu	
50 55 60 65	
cag ctt caa aca gaa cag gat gca cct gct gac tcg aca gca gtt cta	359
Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Asp Ser Thr Ala Val Leu	
70 75 80	
cac tgacatgtac tgtcccatct gcctgcacca agcctccttc ccggtggaga	412
His	
ccaactgtgg acatcttttt tgtggtgcct gcattattgc ttactggcga tatggttcat	472
ggcttggggc aatcagttgt ccaatctgta gacaaacgag acatggccac attgcattgt	532
ccagaaacagc ttagaccatg acagttagca tcgaagccac ctgaggaggg aggcagtaac	592
cttactccta acagtatattg gtgaagatga tcagctctcag gatgttctga gattgcatca	652
ggatattaat gattataaac ggagattctc agggcaaccc agatctgttaa gtaatgctaa	712
agcattgtca aagtttagagg aagacacatt tcttctcttt tgtaaaagtga ggtttaccaa	772
caagtattct ttgactatga gaaatcttgg ccaggcacag tagctaacgc ctataatcct	832
agcacttttg gaggccaagg caggtggatc acttgagccc aggagtttga gaccagcctt	892
ggaacaatga tgaaccacca tctctagaaa aaacacccaa aaattggaca agagtgttgg	952
cacatgcctg tagtccctgc ttcttggggg gctgaaatgg gaggatcacc tgagcccagg	1012
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 <223> Von Heijne matrix
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 ctg agg acc cgg aca gcc gtt aca tcc ttg cta agc ccc act ccg gct 103
 Leu Arg Thr Arg Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro Ala
 -15 -10 -5
 aca gct ctt gct gtc aga tac gca tcc aag aag tcg ggt ggt agc tcc 151
 Thr Ala Leu Ala Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser Ser
 1 5 10
 aaa aac ctc ggt gga aag tca tca gcc aga cgc caa gcc att aag aaa 199
 Lys Asn Leu Gly Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys Lys
 15 20 25 30
 atg gaa ggt cac tat gtt cat gct ggg aac atc att gca aca cag cgc 247
 Met Glu Gly His Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln Arg
 35 40 45
 cat ttc cgc tgg cac cca ggt gcc cat gtg agt tgc tcc gtt gct gcc 295
 His Phe Arg Trp His Pro Gly Ala His Val Ser Cys Ser Val Ala Ala
 50 55 60
 ccc ctt ttt cct ttt cta ggt tgacctctcc ttgccccctaa gcatggtaat 346
 Pro Leu Phe Pro Phe Leu Gly
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 <222> 177..767

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 score 6.51720597568932
 seq LAVILTLGLAIL/AI

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 ctctctgaca aagaaatcca gatgatgcga gacctgatga agacaataca tggaaa atg 179
 Met
 -20
 aca gtc ttg gaa ata act ttg gct gtc atc ctg act cta ctg gga ctt 227
 Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly Leu
 -15 -10 -5
 gcc atc ctg gct att ttg tta aca aga tgg gca cga cgt aag caa agt 275
 Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln Ser
 1 5 10

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gac tat gag gat ggt aga gga tcc cga cat gca tat tca aca caa agt      371
Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln Ser
30                                35                                40                                45
gag aga tcc aaa aga gat tac aca cca tca acc aac tct cta gca ctg      419
Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala Leu
50                                55                                60
tct cga tca agt att gct tta cct caa gga tcc atg agt agt ata aaa      467
Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile Lys
65                                70                                75
tgt tta caa aca act gaa gaa cct cct tcc aga act gca gga gcc atg      515
Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala Met
80                                85                                90
atg caa ttc aca gcc cct att ccc gga gct aca gga cct atc aag ctc      563
Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys Leu
95                                100                                105
tct caa aaa acc att gtg caa act cta gga cct att gta caa tat cct      611
Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr Pro
110                                115                                120                                125
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Gly Ser Asn Gln Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp Leu
130                                135                                140
act ggg gct aaa gga agg gtc aca tct ggt cca cag ttc cct aat agc      707
Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn Ser
145                                150                                155
cac cat gtg cca gag aat cta cat gga tac atg aat tcc ctt tcc ctt      755
His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser Leu
160                                165                                170
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gctgctgttt gaattatctg tgaatgttgg gaagaggaat gccagagctg ccggctgaaa      180
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Met Asp Phe Leu Val Leu Phe Leu Phe
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Tyr	Leu	Ala	Ser	Val	Leu	Met	Gly	Leu	Val	Leu	Ile	Cys	Val	Cys	Ser	
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Lys	Thr	His	Ser	Leu	Lys	Gly	Leu	Ala	Arg	Gly	Gly	Ala	Gln	Ile	Phe	
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Ser	Cys	Ile	Ile	Pro	Glu	Cys	Leu	Gln	Arg	Ala	Val	His	Gly	Leu	Leu	
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His	Tyr	Leu	Phe	His	Thr	Arg	Asn	His	Thr	Phe	Ile	Val	Leu	His	Leu	
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Val	Leu	Gln	Gly	Met	Val	Tyr	Thr	Glu	Tyr	Thr	Trp	Glu	Val	Phe	Gly	
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Tyr	Cys	Gln	Glu	Leu	Glu	Leu	Ser	Leu	His	Tyr	Leu	Leu	Leu	Pro	Tyr	
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Asn	Pro	Gly	Ile	Ile	Thr	Lys	Ala	Asn	Glu	Leu	Leu	Phe	Leu	His	Val	
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Tyr	Glu	Phe	Asp	Glu	Val	Met	Phe	Pro	Lys	Asn	Val	Arg	Cys	Ser	Thr	
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Cys	Asp	Leu	Arg	Lys	Pro	Ala	Arg	Ser	Lys	His	Cys	Ser	Val	Cys	Asn	
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Trp	Cys	Val	His	Arg	Phe	Asp	His	His	Cys	Val	Trp	Val	Asn	Asn	Cys	
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Thr	Ala	Ser	Ala	Ala	Thr	Val	Ala	Ile	Val	Ser	Thr	Thr	Phe	Leu	Val	
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His	Leu	Val	Val	Met	Ser	Asp	Leu	Tyr	Gln	Glu	Thr	Tyr	Ile	Asp	Asp	
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Leu	Gly	His	Leu	His	Val	Met	Asp	Thr	Val	Phe	Leu	Ile	Gln	Tyr	Leu	
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Phe	Leu	Thr	Phe	Pro	Arg	Ile	Val	Phe	Met	Leu	Gly	Phe	Val	Val	Val	
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Leu	Ser	Phe	Leu	Leu	Gly	Gly	Tyr	Leu	Leu	Phe	Val	Leu	Tyr	Leu	Ala	
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Ala	Thr	Asn	Gln	Thr	Thr	Asn	Glu	Trp	Tyr	Arg	Gly	Asp	Trp	Ala	Trp	
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tgc	cag	cgt	tgt	ccc	ctt	gtg	gcc	tgg	ect	cgg	tca	gca	gag	ccc	caa	1146
Cys	Gln	Arg	Cys	Pro	Leu	Val	Ala	Trp	Pro	Pro	Ser	Ala	Glu	Pro	Gln	
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gtc	cac	cgg	aac	att	cac	tcc	cat	ggg	ctt	cgg	agc	aac	ctt	caa	gag	1194

Val His Arg Asn Ile His Ser His Gly Leu Arg Ser Asn Leu Gln Glu
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 atc ttt cta cct gcc ttt cca tgt cat gag agg aag aaa caa gaa 1239
 Ile Phe Leu Pro Ala Phe Pro Cys His Glu Arg Lys Lys Gln Glu
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 seq SGLLLQVLFRLLIT/FV

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 Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ser Ser Ser
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 Gly Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn
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 Ala Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn
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 Val Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu
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 Ala Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser
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 Gln Thr Leu Asn Leu Leu Trp Leu Thr Val Pro Leu Gly Val Phe Trp
 55 60 65
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 Ser Leu Phe Leu Gly Trp Ile Trp Leu Gln Leu Leu Glu Val Pro Asp
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 Pro Asn Val Val Pro His Tyr Ala Thr Gly Val Val Leu Phe Gly Leu
 85 90 95 100
 tcg gca gtg gtg gag ctt cta gga gag ccc ttt tgg gtc ttg gca caa 491
 Ser Ala Val Val Glu Leu Leu Gly Glu Pro Phe Trp Val Leu Ala Gln
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 gca cat atg ttt gtg aag ctc aag gtg att gca gag agc ctg tgc gta 539
 Ala His Met Phe Val Lys Leu Lys Val Ile Ala Glu Ser Leu Ser Val
 120 125 130
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 Ile Leu Lys Thr Val Leu Thr Ala Phe Leu Val Leu Trp Leu Pro His

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155												160												683												
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440																																				
445												450																								

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gcc aga ctg gca cac att gct gtg ggg gcc ttc tgt ctg gga gca act 1595
Ala Arg Leu Ala His Ile Ala Val Gly Ala Phe Cys Leu Gly Ala Thr
470 475 480
ctc ggg aca gca ttc ctc aca gag acc aag ctg atc cat ttc ctc agg 1643
Leu Gly Thr Ala Phe Leu Thr Glu Thr Lys Leu Ile His Phe Leu Arg
485 490 495 500
act cag tta ggt gtg ccc aga cgc act gac aaa atg aca tgacttcagg 1692
Thr Gln Leu Gly Val Pro Arg Arg Thr Asp Lys Met Thr
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cgaacagcgt caactcc atg gcg cgg ttc ctg aca ctt tgc act tgg ctg 230
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Gln Asp Cys Ala Thr Cys Ser Tyr Arg Leu Val Arg Pro Ala Asp Ile
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aac ttc ctg gct tgc gta atg gaa tgt gaa ggt aaa ctg cct tct ctg 374
Asn Phe Leu Ala Cys Val Met Glu Cys Glu Gly Lys Leu Pro Ser Leu
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Lys Ile Trp Glu Thr Cys Lys Glu Leu Leu Gln Leu Ser Lys Pro Asp
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Leu Pro Gln Asp Gly Thr Ser Thr Leu Arg Glu Asn Ser Lys Pro Glu
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Glu Glu Ala Asn Gly Ser Glu Ile Leu Ala Lys Arg Tyr Gly Gly Phe
      100      105      110      115
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Leu Leu Lys Glu Leu Leu Glu Thr Gly Asp Asn Arg Glu Arg Ser His
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His Gln Asp Gly Ser Asp Asn Glu Glu Val Ser Lys Arg Tyr Gly
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Lys Glu Leu Gln Lys Arg Tyr Gly Gly Phe Met Arg Arg Val Gly Arg
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Pro Glu Trp Trp Met Asp Tyr Gln Lys Arg Tyr Gly Gly Phe Leu Lys
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Arg Phe Ala Glu Ala Leu Pro Ser Asp Glu Glu Gly Glu Ser Tyr Ser
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aaa gaa gtt cct gaa atg gaa aaa aga tac gga gga ttt atg aga ttt 998
Lys Glu Val Pro Glu Met Glu Lys Arg Tyr Gly Gly Phe Met Arg Phe
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score 8.5056444915604
seq VVMLMLLTLLVLG/MV

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Glu Thr Val Val Met Leu Met Leu Leu Thr Leu Leu Val Leu Gly Met						
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Val Trp Val Val Ala Ser Ala Ile Val Asp Lys Asn Lys Ala Asn Arg Glu						
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Ile Ser Phe Leu Gly Val Leu Leu Leu Val Cys Thr Pro Leu Gly						
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Leu Ala Arg Met Phe Ser Val Thr Gly Lys Leu Leu Val Lys Pro Arg						
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70	75					
gca gcc ctg acc cgc agg atc tgt aat cct act tcc tgc tgg ctg cct						915
Ala Ala Leu Thr Arg Arg Ile Cys Asn Pro Thr Ser Cys Trp Leu Pro						
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Arg Val Leu Leu Glu Lys Arg Arg Lys Ala Ser Ala Trp Gln Arg Asn						
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Leu Gly Tyr Pro Leu Ala Met Leu Cys Leu Leu Val Leu Thr Gly Leu						
130	135					
tct gtg ctc att gtg gcc atc cac atc ctg gag ctg ctc atc gat gag						1107
Ser Val Leu Ile Val Ala Ile His Ile Leu Glu Leu Leu Ile Asp Glu						
150	155					
gct gcc atg ccc cga gcc atg cag ggt acc tcc tta gcc cag gtc tcc						1155
Ala Ala Met Pro Arg Gly Met Gln Gly Thr Ser Leu Gly Gln Val Ser						
165	170					
ttc tcc aag ctg gcc tcc ttt ggt gcc gtc att cag gtt gta ctc atc						1203
Phe Ser Lys Leu Gly Ser Phe Gly Ala Val Ile Gln Val Val Leu Ile						
180	185					
ttt tac cta atg gtg tcc tca gtt gtg gcc ttc tat agc tct cca ctc						1251
Phe Tyr Leu Met Val Ser Ser Val Val Gly Phe Tyr Ser Ser Pro Leu						
195	200					
ttc cgg agc ctg cgg ccc aga tgg cac gac act gcc atg acg cag ata						1299
Phe Arg Ser Leu Arg Pro Arg Trp His Asp Thr Ala Met Thr Gln Ile						
210	215					
att ggg aac tgt gtc tgt ctc ctg gtc cta agc tca gca ctt cct gtc						1347
Ile Gly Asn Cys Val Cys Leu Leu Val Leu Ser Ser Ala Leu Pro Val						

	230	235	240	
ttc tct cga acc ctg ggg ctc act cgc ttt gac ctg ctg ggt gac ttt				1395
Phe Ser Arg Thr Leu Gly Leu Thr Arg Phe Asp Leu Leu Gly Asp Phe				
	245	250	255	
gga cgc ttc aac tgg ctg ggc aat ttc tac att gtg ttc ctc tac aac				1443
Gly Arg Phe Asn Trp Leu Gly Asn Phe Tyr Ile Val Phe Leu Tyr Asn				
	260	265	270	
gca gcc ttt gca ggc ctc acc aca ctc tat ctg gtg aag acc ttc act				1491
Ala Ala Phe Ala Gly Leu Thr Thr Leu Tyr Leu Val Lys Thr Phe Thr				
	275	280	285	
gca gct gtg cgg gca gag ctg atc cgg gcc ttt ggg ctg gac aga ctg				1539
Ala Ala Val Arg Ala Glu Leu Ile Arg Ala Phe Gly Leu Asp Arg Leu				
	290	295	300	305
ccg ctg ccc gtc tcc ggt ttc ccc cag gca tct agg aag acc cag cac				1587
Pro Leu Pro Val Ser Gly Phe Pro Gln Ala Ser Arg Lys Thr Gln His				
	310	315	320	
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Gln				
gcctaggcct ggagggaagc ccaaggctac ttggacctca ggacctggaa tctgagaggg				1700
tggggtggcag aggggagcag agccatctgc actattgcat aatctgagcc agagtgtggg				1760
accaggacct cctgcttttc catacttaac tgtggcctca gcattgggta gggctgggtg				1820
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cagagcctaa gcactgtgct atcctggagg ggccttggac cacctgaaag accaagggga				2060
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aaaa				2124

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aggccgcggc cgccagcgtg ggg atg tct agg agc tgc aag gtg gtg ctg ggc		113
Met Ser Arg Ser Ser Lys Val Val Leu Gly		
	-20	-15
ctc tgc gtg ctg ctg acg gcg gcc aca gtg gcc ggc gta cat gtg aag		161
Leu Ser Val Leu Leu Thr Ala Ala Thr Val Ala Gly Val His Val Lys		
	-10	-5
cag cag tgg gac cag cag agg ctt cgt gac gga gtt atc aga gac att		209
Gln Gln Trp Asp Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile		
	10	15
gag agg caa att cgg aaa aaa gaa aac att cgt ctt ttg gga gaa cag		257
Glu Arg Gln Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln		
	25	30
		35

att att ttg act gag caa ctt gaa gca gaa aga gag aag atg tta ttg 305
 Ile Ile Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu
 40 45 50
 gca aaa gga tct caa aaa tca tgacttgaat gtgaaatc tgttggacag 356
 Ala Lys Gly Ser Gln Lys Ser
 55 60
 acaacacgag ttgtgtgtg ttgtgtgatg gagagtagct tagtagtacc ttcatctttt 416
 tttttgttca ctgtctcttt aaacttgatc aaataaagga cagtgggtca tataagtacc 476
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 agttgatcac ctataaatatt atataaaaca taggcatggt tgtactaatg aaacgtactg 1076
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 seq SGLLLQVLFRLIT/FV

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 Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser Gly
 -25 -20 -15
 ctc ctc ctg cag gtg ttg ttt cgg ttg atc acc ttt gtc ttg aat gca 154
 Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn Ala
 -10 -5 1 5
 ttt att ctt cgc ttc ctg tca aag gaa atc gtt gcc gta gta aat gta 202
 Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn Val
 10 15 20
 aga cta acg ctg ctt tac tca acc acc ctc ttc ctg gcc aga gag gcc 250
 Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu Ala
 25 30 35
 ttc cgc aga gca tgt ctc agt ggg gcc acc cag cga gac tgg agc cag 298
 Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser Gln
 40 45 50
 acc ctc aac ctg ctg tgg cta aca gtc ccc ctg ggt gtg ttt tgg tcc 346
 Thr Leu Asn Leu Leu Trp Leu Thr Val Pro Leu Gly Val Phe Trp Ser
 55 60 65


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Asp Arg Tyr Asn Phe Val Met Leu Ala Leu Ser Ser Ser Phe Leu Val
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Leu Ser Tyr Leu Leu Thr Arg Trp Cys Gly Ser Val Gly Phe Ile Leu
  390                               395                               400                               405
gcc aac tgc ttt aac atg ggc att cgg atc acg cag agc ctt tgc ttc      1402
Ala Asn Cys Phe Asn Met Gly Ile Arg Ile Thr Gln Ser Leu Cys Phe
  410                               415                               420
atc cac cgc tac tac cga agg agc ccc cac agg ccc ctg gct ggc ctg      1450
Ile His Arg Tyr Tyr Arg Arg Ser Pro His Arg Pro Leu Ala Gly Leu
  425                               430                               435
cac cta tgc cca gtc ctg ctc ggg aca ttt gcc ctc agt ggt ggg gtt      1498
His Leu Ser Pro Val Leu Leu Gly Thr Phe Ala Leu Ser Gly Gly Val
  440                               445                               450
act gct gtt tgc gag gta ttc ctc tgc tgt gag cag ggc tgg cca gcc      1546
Thr Ala Val Ser Glu Val Phe Leu Cys Cys Glu Gln Gly Trp Pro Ala
  455                               460                               465
aga ctg gca cac att gct gtg ggg gcc ttc tgt ctg gga gca act ctc      1594
Arg Leu Ala His Ile Ala Val Gly Ala Phe Cys Leu Gly Ala Thr Leu
  470                               475                               480                               485
ggg aca gca ttc ctc aca gag acc aag ctg atc cat ttc ctc agg act      1642
Gly Thr Ala Phe Leu Thr Glu Thr Lys Leu Ile His Phe Leu Arg Thr
  490                               495                               500
cag tta ggt gtg ccc aga cgc act gac aaa atg acg tgacttcagg      1688
Gln Leu Gly Val Pro Arg Arg Thr Asp Lys Met Thr
  505                               510
gaagcctgga caccgaggc acctggacca gctatgggta gttctgtggg tggaaacacat      1748
tctgtgtaag agccccactg agggctctgc agcggagtgga cagcaacccc agagatgagg      1808
caccagagag tgccactgca tgagacacct gtgaccattc gaagtctgaa atgcgggggg      1868
ggagtttcat ttttaagtga agaccaaaag ccctttaaaa ataatagttt tttatcattt      1928
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gcagcgtagg actgtggaga agggcgggtgg gcaaggagggg aactcgagag cagcctcc      118
atg ggc aca cag gag ggc tgg tgc ctg ctg ctc tgc ctg gct cta tct      166
Met Gly Thr Gln Glu Gly Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser
  -20                               -15                               -10
gga gca gca gaa acc aag ccc cac cca gca gag ggg cag tgg cgg gca      214
Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Trp Arg Ala
  -5                               1                               5                               10
gtg gac gtg gtc cta gac tgt ttc ctg gtg aag gac ggt gcg cac cgt      262

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Val Asp Val	Val Leu Asp Cys Phe	Leu Val Lys Asp Gly Ala His Arg	
	15	20	25
gga gct ctc gcc agc agt gag gac agg gca agg gcc tcc ctt gtg ctg			310
Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala Arg Ala Ser Leu Val Leu			
	30	35	40
aag cag gtg cca gtg ctg gac gat ggc tcc ctg gag gac ttc acc gat			358
Lys Gln Val Pro Val Leu Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp			
	45	50	55
ttc caa ggg ggc aca ctg gcc caa gat gac cca cct att atc ttt gag			406
Phe Gln Gly Gly Thr Leu Ala Gln Asp Asp Pro Pro Ile Ile Phe Glu			
	60	65	70
gcc tca gtg gac ctg gtc cag att ccc cag gcc gag gcc ttg ctc cat			454
Ala Ser Val Asp Leu Val Gln Ile Pro Gln Ala Glu Ala Leu Leu His			
	80	85	90
gct gac tgc agt ggg aag gag gtg acc tgt gag atc tcc cgc tac ttt			502
Ala Asp Cys Ser Ser Gly Lys Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe			
	95	100	105
ctc cag atg aca gag acc act gtt aag aca gca gct tgg ttc atg gcc			550
Leu Gln Met Thr Glu Thr Thr Val Lys Thr Ala Ala Trp Phe Met Ala			
	110	115	120
aac gtg cag gtc tct gga ggg gga cct agc atc tcc ttg gtg atg aag			598
Asn Val Gln Val Ser Gly Gly Gly Pro Ser Ile Ser Leu Val Met Lys			
	125	130	135
act ccc agg gtc gcc aag aat gag gtg ctc tgg cac cca acg ctg aac			646
Thr Pro Arg Val Ala Lys Asn Glu Val Leu Trp His Pro Thr Leu Asn			
	140	145	150
ttg cca ctg agc ccc cag ggg act gtg cga act gca gtg gag ttc cag			694
Leu Pro Leu Ser Pro Gln Gly Thr Val Arg Thr Ala Val Glu Phe Gln			
	160	165	170
gtg atg aca cag acc caa tcc ctg agc ttc ctg ctg ggg tcc tca gcc			742
Val Met Thr Gln Thr Gln Ser Leu Ser Phe Leu Leu Gly Ser Ser Ala			
	175	180	185
tcc ttg gac tgt ggc ttc tcc atg gca ccg ggc ttg gac ctc atc agt			790
Ser Leu Asp Cys Gly Phe Ser Met Ala Pro Gly Leu Asp Leu Ile Ser			
	190	195	200
gtg gag tgg cga ctg cag cac aag ggc agg ggt cag ttg gtg tac agc			838
Val Glu Trp Arg Leu Gln His Lys Gly Arg Gly Gln Leu Val Tyr Ser			
	205	210	215
tgg acc gca ggg cag ggg cag gct gtg cgg aag ggc gct acc ctg gag			886
Trp Thr Ala Gly Gln Gly Gln Ala Val Arg Lys Gly Ala Thr Leu Glu			
	220	225	230
cct gca caa ctg ggc atg gcc agg gat gcc tcc ctc acc ctg ccc ggc			934
Pro Ala Gln Leu Gly Met Ala Arg Asp Ala Ser Leu Thr Leu Pro Gly			
	240	245	250
ctc act ata cag gac gag ggg acc tac att tgc cag atc acc acc tct			982
Leu Thr Ile Gln Asp Glu Gly Thr Tyr Ile Cys Gln Ile Thr Thr Ser			
	255	260	265
ctg tac cga gct cag cag atc atc cag ctc aac atc caa gct tcc cct			1030
Leu Tyr Arg Ala Gln Gln Ile Ile Gln Leu Asn Ile Gln Ala Ser Pro			
	270	275	280
aaa gta cga ctg agc ttg gca aac gaa gct ctg ctg ccc acc ctc atc			1078
Lys Val Arg Leu Ser Leu Ala Asn Glu Ala Leu Leu Pro Thr Leu Ile			
	285	290	295
tgc gac att gct ggc tat tac cct ctg gat gtg gtg acg tgg acc			1126
Cys Asp Ile Ala Gly Tyr Tyr Pro Leu Asp Val Val Val Thr Trp Thr			
	300	305	310
cga gag gag ctg ggt gga tcc cca gcc caa gtc tct ggt gcc tcc ttc			1174
Arg Glu Glu Leu Gly Gly Ser Pro Ala Gln Val Ser Gly Ala Ser Phe			

Val Thr Leu Gln Ala Leu Asp Thr	Val Glu Asn Leu Met Lys Val Thr	
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ggc cct ccc cag gga gtt aca gac tcc atg caa tgc ttc aat gat cag	498	
Gly Pro Pro Gln Gly Val Thr Asp Ser Met Gln Cys Phe Asn Asp Gln		
10	20	
tgg cct tta tct aac acc agg agc agc gag cac ata aaa gag gtc atg	546	
Trp Pro Leu Ser Asn Thr Arg Ser Ser Glu His Ile Lys Glu Val Met		
25	35	40
gtt gag ctg ggg aag ttt gaa agg aag gag ttt aaa agt tcc agt ttg	594	
Val Glu Leu Gly Lys Phe Glu Arg Lys Glu Phe Lys Ser Ser Ser Leu		
45	50	55
caa gat gga cat aca aaa atg gag gaa gca cct acg cat ctt aat tca	642	
Gln Asp Gly His Thr Lys Met Glu Glu Ala Pro Thr His Leu Asn Ser		
60	65	70
ttt ctt aag aaa gaa gga ttg acc ttc aac agg aaa aga aaa tgg gaa	690	
Phe Leu Lys Lys Glu Gly Leu Thr Phe Asn Arg Lys Arg Lys Trp Glu		
75	80	85
ttg gac agc tac ccc att atg ctc tgg tgg tcc ccg ctg acg ggg gag	738	
Leu Asp Ser Tyr Pro Ile Met Leu Trp Trp Ser Pro Leu Thr Gly Glu		
90	95	100
act ggg agg tta ggc caa tgt gga gca gat gct tgt ttc ttc acc atc	786	
Thr Gly Arg Leu Gly Gln Cys Gly Ala Asp Ala Cys Phe Phe Thr Ile		
105	110	115
aac cgg acc tac ctc cat cat cac atg acc aaa gca ttc ctc ttc tat	834	
Asn Arg Thr Thr Leu His His His Met Thr Lys Ala Phe Leu Phe Tyr		
125	130	135
ggg act gac ttt aac ata gat agc tta cct ctg cct cgg aaa gcc cat	882	
Gly Thr Asp Phe Asn Ile Asp Ser Leu Pro Leu Pro Arg Lys Ala His		
140	145	150
cat gac tgg gct gtt ttt cat gaa gag tcc ccg aaa aac aat tat aag	930	
His Asp Trp Ala Val Phe His Glu Glu Ser Pro Lys Asn Asn Tyr Lys		
155	160	165
ctc ttt cat aaa cca gtg atc acc ttg ttc aac tac act gcc acg ttc	978	
Leu Phe His Lys Pro Val Ile Thr Leu Phe Asn Tyr Thr Ala Thr Phe		
170	175	180
agc agg cat tcc cac ttg cca cta act acc caa tac ttg gag agc att	1026	
Ser Arg His Ser His Leu Pro Leu Thr Thr Gln Tyr Leu Glu Ser Ile		
185	190	195
gaa gtc ctg aag tca ctc cga tac cta gtt cct ttg cag tcc aaa aac	1074	
Glu Val Leu Lys Ser Leu Arg Tyr Leu Val Pro Leu Gln Ser Lys Asn		
205	210	215
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Lys Leu Arg Lys Arg Leu Ala Pro Leu Val Tyr Val Gln Ser Tyr Cys		
220	225	230
gac cca cca tca gac agg gac agc tat gtt cgc gag ctg atg act tac	1170	
Asp Pro Pro Ser Asp Arg Asp Ser Tyr Val Arg Glu Leu Met Thr Tyr		
235	240	245
atc gag gtc gat tcc tat ggt gaa tgt tta cga aac aaa gac ctc cct	1218	
Ile Glu Val Asp Ser Tyr Gly Glu Cys Leu Arg Asn Lys Asp Leu Pro		
250	255	260
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Gln Gln Leu Lys Asn Pro Ala Ser Met Asp Ala Asp Gly Phe Tyr Arg		
265	270	275
atc att gca cag tat aag ttt atc cta gct ttt gag aat gca gtt tgt	1314	
Ile Ile Ala Gln Tyr Lys Phe Ile Leu Ala Phe Glu Asn Ala Val Cys		
285	290	295
gat gac tac atc act gag aag ttc tgg agg cca ctg aaa ctg ggg gta	1362	
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Val Pro Val Tyr Tyr Gly Ser Pro Ser Ile Thr Asp Trp Leu Pro Ser
          315          320          325
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Asn Lys Ser Ala Ile Leu Val Ser Glu Phe Ser His Pro Arg Glu Leu
          330          335          340
gca agt tac atc aga cga ctg gat tct gat gac aga ttg tat gag gcc   1506
Ala Ser Tyr Ile Arg Arg Leu Asp Ser Asp Asp Arg Leu Tyr Glu Ala
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tat gta gaa tgg aag ctg aag ggt aga tct cta acc agc gac ttc   1551
Tyr Val Glu Trp Lys Leu Lys Gly Arg Ser Leu Thr Ser Asp Phe
          365          370          375
tgacagctct cagggaaacgg aaatggggag tgcaagacgt caaccaggac aattacatcg   1611
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ccagcttttga acaatccaag aaagaagccc aggcactaag gtggctggtt gataggaatc   1851
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          -25          -20          -15
ggg gtg ggg ctg gtc act ctg ctc ggc ctg gct gtg ggc tcc tac ttg   158
Gly Val Gly Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu
          -10          -5          1
gtt cgg agg tcc cgc cgg cct cag gtc act ctc ctg gac ccc aat gaa   206
Val Arg Arg Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu
          5          10          15
aag tac ctg cta cga ctg cta gac aag acg act gtg agc cac aac acc   254
Lys Tyr Leu Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr
          20          25          30          35
aag agg ttc cgc ttt gcc ctg ccc acc gcc cac cac act ctg ggg ctg   302
Lys Arg Phe Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu
          40          45          50
cct gtg ggc aaa cat atc tac ctc tcc acc cga att gat ggc agc ctg   350
Pro Val Gly Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu
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 ggcggtgggg aaggagggaa ctccagagca gcctcc atg ggc aca cag gag ggc 174
 Met Gly Thr Gln Glu Gly
 -20
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 Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser Gly Ala Ala Glu Thr Lys
 -15 -10 -5 1
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 Pro His Pro Ala Glu Gly Gln Leu Arg Ala Val Asp Val Val Leu Asp
 5 10 15
 tgc ttc ctg gcg aag gac ggt gcg cac cgt gga gct ctc gcc agc agt 318
 Cys Phe Leu Ala Lys Asp Gly Ala His Arg Gly Ala Leu Ala Ser Ser
 20 25 30
 gag gac agg gca agg gcc tcc ctt gtg ctg aag cag gtg cca gtg ctg 366
 Glu Asp Arg Ala Arg Ala Ser Leu Val Leu Lys Gln Val Pro Val Leu
 35 40 45
 gac gat ggc tcc ctg gag gac ttc acc gat ttc caa ggg ggc aca ctg 414
 Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp Phe Gln Gly Gly Thr Leu
 50 55 60 65
 gcc caa gat gac cca cct att atc ttt gag gcc tca gtg gac ctg gtc 462
 Ala Gln Asp Asp Pro Pro Ile Ile Phe Glu Ala Ser Val Asp Leu Val
 70 75 80
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 Gln Ile Pro Gln Ala Glu Ala Leu His Ala Asp Cys Ser Gly Lys
 85 90 95
 gag gtg acc tgt gag atc tcc cgc tac ttt ctc cag atg aca gag acc 558
 Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe Leu Gln Met Thr Glu Thr
 100 105 110
 act gtt aag aca gca gct tgg ttc atg gcc aac atg cag gtc tct gga 606
 Thr Val Lys Thr Ala Ala Trp Phe Met Ala Asn Met Gln Val Ser Gly
 115 120 125
 ggg gga cst agc atc tcc ttg gtg atg aag act ccc agg gtc acc aag 654
 Gly Gly Xaa Ser Ile Ser Leu Val Met Lys Thr Pro Arg Val Thr Lys
 130 135 140 145
 aat gag gcg ctc tgg cac ccg acg ctg aac ttg cca ctg agc ccc cag 702
 Asn Glu Ala Leu Trp His Pro Thr Leu Asn Leu Pro Leu Ser Pro Gln
 150 155 160
 ggg act gtg cga act gca gtg gag ttc cag gtg atg aca cag acc caa 750
 Gly Thr Val Arg Thr Ala Val Glu Phe Gln Val Met Thr Gln Thr Gln
 165 170 175
 tcc ctg agc ttc ctg ctg ggg tcc tca gcc tcc ttg gac tgt ggc ttc 798
 Ser Leu Ser Phe Leu Leu Gly Ser Ser Ala Ser Leu Asp Cys Gly Phe
 180 185 190
 tcc atg gca ccg ggc ttg gac ctc atc agt gtg gag tgg cga ctg cag 846
 Ser Met Ala Pro Gly Leu Asp Leu Ile Ser Val Glu Trp Arg Leu Gln
 195 200 205

00731972-120700

cac aag ggc agg ggt cag ttg gtg tac agc tgg acc gca ggg cag ggg 894
 His Lys Gly Arg Gly Gln Leu Val Tyr Ser Trp Thr Ala Gly Gln Gly
 210 215 220 225
 cag gct gtg cgg aag ggc gct acc ctg gag cct gca caa ctg ggc atg 942
 Gln Ala Val Arg Lys Gly Ala Thr Leu Glu Pro Ala Gln Leu Gly Met
 230 235 240
 gcc agg gat gcc tcc ctc acc ctg ccc ggc ctc act ata cag gac gag 990
 Ala Arg Asp Ala Ser Leu Thr Leu Pro Gly Leu Thr Ile Gln Asp Glu
 245 250 255
 ggg acc tac att tgc cag atc acc acc tct ctg tac cga gct cag cag 1038
 Gly Thr Tyr Ile Cys Gln Ile Thr Thr Ser Leu Tyr Arg Ala Gln Gln
 260 265 270
 atc atc cag ctc aac atc caa gct tcc cct aaa gta cga ctg agc ttg 1086
 Ile Ile Gln Leu Asn Ile Gln Ala Ser Pro Lys Val Arg Leu Ser Leu
 275 280 285
 gca aac gaa gct ctg ctg ccc acc ctc atc tgc gac att gct ggc tat 1134
 Ala Asn Glu Ala Leu Leu Pro Thr Leu Ile Cys Asp Ile Ala Gly Tyr
 290 295 300 305
 tac cct ctg gat gtg gtg gtg acg tgg acc cga gag gag ctg ggt gga 1182
 Tyr Pro Leu Asp Val Val Val Thr Trp Thr Arg Glu Glu Leu Gly Gly
 310 315 320
 tcc cca gcc caa gtc tct ggt gcc tcc ttc tcc agc ctc agg caa agc 1230
 Ser Pro Ala Gln Val Ser Gly Ala Ser Phe Ser Ser Leu Arg Gln Ser
 325 330 335
 gtg gca ggc acc tac agc atc tcc tcc tct ctc acc gca gaa cct ggc 1278
 Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser Leu Thr Ala Glu Pro Gly
 340 345 350
 tct gca ggt gcc act tac acc tgc cag gtc aca cac atc tct ctg gag 1326
 Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val Thr His Ile Ser Leu Glu
 355 360 365
 gag ccc ctt ggg gcc agc acc cag gtt gtc cca cca gag cgg aga aca 1374
 Glu Pro Leu Gly Ala Ser Thr Gln Val Val Pro Pro Glu Arg Arg Thr
 370 375 380 385
 gcc ttg gga gtc atc ttt gcc agc agt ctc ttc ctt ctt gca ctg atg 1422
 Ala Leu Gly Val Ile Phe Ala Ser Ser Leu Phe Leu Leu Ala Leu Met
 390 395 400
 ttc ctg ggg ctt cag aga cgg caa gca cct aca gga ctt ggg ctg ctt 1470
 Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro Thr Gly Leu Gly Leu Leu
 405 410 415
 cag gct gaa cgc taggagacca cttcctgtgc tgacacacag agctcccatc 1522
 Gln Ala Glu Arg
 420
 tccatgaaga ccgcacacgc cgtgtaagcc agcccagctg acctaaagcg acatgagact 1582
 actagaaaga aacgacaccc ttccccaagc cccacagct actccaacc aaacaacaac 1642
 caagccagtt taatggtagg aattgtatt ttttgccttt gttcagaata catgacattg 1702
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<211> 1871

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 195..1052

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<221> sig_peptide

<222> 195..338
 <223> Von Heijne matrix
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 seq LGVFFVCHQLSSS/LN

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 tggcagccca gattgaagat ggatacgtga caatcccagg gaccgctgca ctgacttcat 120
 ttcccttagac aagacacagt gtagggcccg gcccggtgtt gccccaggac tcctttggaa 180
 tatagctgtg gaca atg aat cct gcg agc gat ggg ggc aca tca gag agc 230
 Met Asn Pro Ala Ser Asp Gly Gly Thr Ser Glu Ser
 -45 -40
 att ttt gac ctg gac tat gca tcc tgg ggg atc cgc tcc acg ctg atg 278
 Ile Phe Asp Leu Asp Tyr Ala Ser Trp Gly Ile Arg Ser Thr Leu Met
 -35 -30 -25
 gtc gct ggc ttt gtc ttc tac ttg ggc gtc ttt gtg gtc tgc cac cag 326
 Val Ala Gly Phe Val Phe Tyr Leu Gly Val Phe Val Val Cys His Gln
 -20 -15 -10 -5
 ctg tcc tct tcc ctg aat gcc act tac cgt tct ttg gtg gcc aga gag 374
 Leu Ser Ser Ser Leu Asn Ala Thr Tyr Arg Ser Leu Val Ala Arg Glu
 1 5 10
 aag gtc ttc tgg gac ctg gcg gcc acg cgt gca gtc ttt ggt gtt cag 422
 Lys Val Phe Trp Asp Leu Ala Ala Thr Arg Ala Val Phe Gly Val Gln
 15 20 25
 agc aca gcc gca ggc ctg tgg gct ctg ctg ggg gac cct gtg ctg cat 470
 Ser Thr Ala Ala Gly Leu Trp Ala Leu Leu Gly Asp Pro Val Leu His
 30 35 40
 gcc gac aag gcg cgt ggc cag cag aac tgg tgc tgg ttt cac atc acg 518
 Ala Asp Lys Ala Arg Gly Gln Gln Asn Trp Cys Trp Phe His Ile Thr
 45 50 55 60
 aca gca acg gga ttc ttt tgc ttt gaa aat gtt gca gtc cac ctg tcc 566
 Thr Ala Thr Gly Phe Phe Cys Phe Glu Asn Val Ala Val His Leu Ser
 65 70 75
 aac ttg atc ttc cgg aca ttt gac ttg ttt ctg gtt atc cac cat ctc 614
 Asn Leu Ile Phe Arg Thr Phe Asp Leu Phe Leu Val Ile His His Leu
 80 85 90
 ttt gcc ttt ctt ggg ttt ctt ggc tgc ttg gtc aat ctc caa gct ggc 662
 Phe Ala Phe Leu Gly Phe Leu Gly Cys Leu Val Asn Leu Gln Ala Gly
 95 100 105
 cac tat cta gct atg acc acg ttg ctc ctg gag atg agc acg ccc ttt 710
 His Tyr Leu Ala Met Thr Thr Leu Leu Leu Glu Met Ser Thr Pro Phe
 110 115 120
 acc tgc gtt tcc tgg atg ctc tta aag gcg ggc tgg tcc gag tct ctg 758
 Thr Cys Val Ser Trp Met Leu Lys Ala Gly Trp Ser Glu Ser Leu
 125 130 135 140
 ttt tgg aag ctc aac cag tgg ctg atg att cac atg ttt cac tgc cgc 806
 Phe Trp Lys Leu Asn Gln Trp Leu Met Ile His Met Phe His Cys Arg
 145 150 155
 atg gtt cta acc tac cac atg tgg tgg gtg tgt ttc tgg cac tgg gac 854
 Met Val Leu Thr Tyr His Met Trp Trp Val Cys Phe Trp His Trp Asp
 160 165 170
 ggc ctg gtc agc agc ctg tat ctg cct cat ttg aca ctg ttc ctt gtc 902
 Gly Leu Val Ser Ser Leu Tyr Leu Pro His Leu Thr Leu Phe Leu Val
 175 180 185
 gga ctg gct ctg ctt acg cta atc att aat cca tat tgg acc cat aag 950
 Gly Leu Ala Leu Leu Thr Leu Ile Ile Asn Pro Tyr Trp Thr His Lys
 190 195 200
 aag act cag cag ctt ctc aat ccg gtg gac tgg aac ttc gca leu cca 998

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Lys Thr Gln Gln Leu Leu Asn Pro Val Asp Trp Asn Phe Ala Gln Pro
205          210          215          220
gaa gcc aag agc agg cca gaa ggc aac ggg cag ctg ctg cgg aag aag      1046
Glu Ala Lys Ser Arg Pro Glu Gly Asn Gly Gln Leu Leu Arg Lys Lys
          225          230          235
agg cca tagctgtcc agccgggggct cgggggcggc agcagagctg gcacaccgat      1102
Arg Pro
tctgggaagc cccgcgaatg atggcttttg aattaatgag gcagtgaatg ttttgtgttt      1162
acttctaagg gaaataactaa ctttctttcg cattagttat aattttgaag tagctacaaa      1222
gtatttttaa gaaattataa ttttatgact gtctggcagg ctctgtcagt ttagccgcgc      1282
cggaccgtgt caagcatcta ggagaggagt ccatgggtgc caggcatcgg ggcgtcacac      1342
ctgttgagga gtgggtgggc tttgaatgct ggaaatggct tcatagttaa gtgcctccca      1402
caggggcggg gggtcagcgt tgactctttc cagctgcaca ctcatatgcc gtgtgttetta      1462
ttcagaagtc acattctttt cagttggaga gaattgggct aagatagaaa ataacatgat      1522
ttgttcctta ttaaagtttc ccagcgtatg aaattctaag ctggggtggg tggctcacac      1582
ccgacgtaat cccagcacgt tgggaggccg aggcagggtg atcacttgag gccaggagtt      1642
cgagaccagc ctggtcaaga tggtgaaacc ccatctctac taaaattaca aaaattagcc      1702
gggtgtctg gacacacact gtaatccag ctatttgga ggccaaggca ggagaattgc      1762
ctgaaccggg gaggcggagg ttgcagttag ctgagatgc accactgcac tccagcactc      1822
cagcctgggt gacggagcaa cactctctcg caaaaaaaaa aaaaaaaaaa      1871

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<211> 1523
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> 217..1410

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<221> sig_peptide
<222> 217..279
<223> Von Heijne matrix
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      seq ALLWAAQEVGVLA/GR

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agtcggcagc cctgtggcag ccggcgggct ggtttccatg gttgcacgat taggaaccac      120
cagctgtctg atcccatggc caggggtggc gtccagggtg cagagcagct aggaacgcaa      180
ggcctgaacc tggggccaga caccctctc ccggcc atg gtc aac gac cct cca      234
                                Met Val Asn Asp Pro Pro
                                -20
gta cct gcc tta ctg tgg gcc cag gag gtg ggc caa gtc ttg gca ggc      282
Val Pro Ala Leu Leu Trp Ala Gln Glu Val Gly Gln Val Leu Ala Gly
-15          -10          -5          1
cgt gcc cgc agg ctg ctg ctg cag ttt ggg gtg ctg ttc tgc acc atc      330
Arg Ala Arg Arg Leu Leu Leu Gln Phe Gly Val Leu Phe Cys Thr Ile
          5          10          15
ctc ctt ttg ctg tgg gtg tct gtc ttc ctg tat ggc tcc ttc tac tat      378
Leu Leu Leu Leu Trp Val Ser Val Phe Leu Tyr Gly Ser Phe Tyr Tyr
          20          25          30
tcc tat atg ccg aca gtc agc cac ctg agc cct gtg cat ttc tac tac      426
Ser Tyr Met Pro Thr Val Ser His Leu Ser Pro Val His Phe Tyr Tyr
          35          40          45
agg acc gac tgt gat tcc tcc acc acc tca ctg tgc tcc ttc cct gtt      474
Arg Thr Asp Cys Asp Ser Ser Thr Thr Ser Leu Cys Ser Phe Pro Val

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cag cgc ccc acc tgc tct agt tcc tgaagaaaag gggcagactc ctcacattcc 1440
Gln Arg Pro Thr Cys Ser Ser Ser
370 375
agcactttcc cacctgactc ctctccctc gtttttctt caataaacta ttttgtgtca 1500
gcttcgaaaa aaaaaaaaaa aaa 1523

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<211> 832
<212> DNA
<213> Homo sapiens

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<222> 103..492

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<221> sig_peptide
<222> 103..162
<223> Von Heijne matrix
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      seq LFPCYLLFLTCSG/VE

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ctcctccaag gtctagtgac ggagcccgcg cgcggcgcca cc atg cgg cag aag 114
                               Met Arg Gln Lys
                               -20
gcg gta tgc ctt ttc ttc tgc tac ctg ctg ctc ttc act tgc agt ggg 162
Ala Val Ser Leu Phe Phe Cys Tyr Leu Leu Leu Phe Thr Cys Ser Gly
-15 -10 -5
gtg gag gca ggt aag aaa aag tgc tgc gag agc tgc gac agc ggc tcc 210
Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser Asp Ser Gly Ser
1 5 10 15
ggg ttc tgg aag gcc ctg acc ttc atg gcc gtc gga gga gga ctc gca 258
Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly Gly Gly Leu Ala
20 25 30
gtc gcc ggg ctg ccc gcg ctg ggc ttc acc gcc gcc ggc atc gcg gcc 306
Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala Gly Ile Ala Ala
35 40 45
aac tgc gtg gct gcc tgc ctg atg agc tgg tct gcg atc ctg aat ggg 354
Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala Ile Leu Asn Gly
50 55 60
ggc ggc gtg ccc gcc ggg ggg cta gtg gcc acg ctg cag agc ctc ggg 402
Gly Gly Val Pro Ala Gly Gly Leu Val Ala Thr Leu Gln Ser Leu Gly
65 70 75 80
gct ggt ggc agc agc gtc gtc ata ggt aat att ggt gcc ctg atg gcc 450
Ala Gly Gly Ser Ser Val Val Ile Gly Asn Ile Gly Ala Leu Met Gly
85 90 95
tac gcc acc cac aag tat ctc gat agt gag gag gat gag gag 492
Tyr Ala Thr His Lys Tyr Leu Asp Ser Glu Glu Asp Glu Glu
100 105 110
tagccagcag ctcccagaaac ctcttcttcc ttcttggcct aactcttcca gttaggatct 552
agaactttgc cttttttttt tttttttttt tttttttgag atgggtcttc actatattgt 612
ccaggctaga gtgcagtggc tattcacaga tgcgaacata gtacactgca gcctccaact 672
cctagctcca agtgcctctc ctgtctcaac ctcccagata ggattacaag catgcgccga 732
cgatgccagc aatccagaaac tttgtctatc actctcccca acaacctaga tgtgaaaaca 792
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 <211> 831
 <212> DNA
 <213> Homo sapiens

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 <222> 234..293
 <223> Von Heijne matrix
 score 4.85037394589162
 seq AVAGLPALGPTGA/GI

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 ctctcccaag gtctagtgac ggagcccgcg cgcggcgcca ccatgcggca gaaggcggta 120
 tcgcttttct ctgctacctg ctgctcttca cttgcagtgg ggtggaggca ggtaagaaaa 180
 agtgctcgga gagctcggac agcggctccg ggttctggaa ggccttgacc ttc atg 236
 Met
 -20
 gcc gtc gga gga gga ctc gca gtc gcc ggg ctg ccc gcg ctg ggc ttc 284
 Ala Val Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe
 -15 -10 -5
 acc ggc gcc ggc atc gcg gcc aac tcg gtg gct gcc tcg ctg atg agc 332
 Thr Gly Ala Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser
 1 5 10
 tgg tct gcg atc ctg aat ggg ggc gcc gtg ccc gcc ggg ggg cta gtg 380
 Trp Ser Ala Ile Leu Asn Gly Gly Val Pro Ala Gly Gly Leu Val
 15 20 25
 gcc acg ctg cag agc ctc ggg gct ggt ggc agc agc gtc gtc ata ggt 428
 Ala Thr Leu Gln Ser Leu Gly Ala Gly Gly Ser Val Val Ile Gly
 30 35 40 45
 aat att ggt gcc ctg atg ggc tac gcc acc cac aag tat ctc gat agt 476
 Asn Ile Gly Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp Ser
 50 55 60
 gag gag gat gag gag tagccagcag ctcccagaac ctcttcttcc ttcttgccct 531
 Glu Glu Asp Glu Glu
 65
 aactcttcca gttaggatct agaactttgc cttttttttt tttttttttt tttttttgag 591
 atgggtttctc actatattgt ccaggctaga gtgcagtgcc tattcacaga tgcgaacata 651
 gtacactgca gcctccaact cctagcctca agtgatcctc ctgtctcaac ctcccaagta 711
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 <211> 917
 <212> DNA
 <213> Homo sapiens

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 <222> 180..800

<220>
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<222> 180..248
 <223> Von Heijne matrix
 score 14.6828672385356
 seq ILLLLLWLIAPSRA/CT

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tcaggccctcg ccgccatcgc cgcagatcca gcgcccagag agacaccaga gaaccacc 179
atg gcc ccc ttt gag ccc ctg gct tct ggc atc ctg ttg ttg ctg tgg 227
Met Ala Pro Phe Glu Pro Leu Ala Ser Gly Ile Leu Leu Leu Leu Trp
-20 -15 -10
ctg ata gcc ccc agc agg gcc tgc acc tgt gtc cca ccc cac cca cag 275
Leu Ile Ala Pro Ser Arg Ala Cys Thr Cys Val Pro Pro His Pro Gln
-5 1 5
acg gcc ttc tgc aat tcc gac ctc gtc atc agg gcc aag ttc gtg ggg 323
Thr Ala Phe Cys Asn Ser Asp Leu Val Ile Arg Ala Lys Phe Val Gly
10 15 20 25
aca cca gaa gtc aac cag acc acc tta tac cag cgt tat gag atc aag 371
Thr Pro Glu Val Asn Gln Thr Thr Leu Tyr Gln Arg Tyr Glu Ile Lys
30 35 40
atg acc aag atg tat aaa ggg ttc caa gcc tta ggg gat gcc gct gac 419
Met Thr Lys Met Tyr Lys Gly Phe Gln Ala Leu Gly Asp Ala Ala Asp
45 50 55
atc cgg ttc gtc tac acc ccc gcc atg gag agt gtc tgc gga tac ttc 467
Ile Arg Phe Val Tyr Thr Pro Ala Met Glu Ser Val Cys Gly Tyr Phe
60 65 70
cac agg tcc cac aac cgc agc gag gag ttt ctc att gct gga aaa ctg 515
His Arg Ser His Asn Arg Ser Glu Glu Phe Leu Ile Ala Gly Lys Leu
75 80 85
cag gat gga ctc ttg cac atc act acc tgc agt ttt gtg gct ccc tgg 563
Gln Asp Gly Leu Leu His Ile Thr Thr Cys Ser Phe Val Ala Pro Trp
90 95 100 105
aac agc ctg agc tta gct cag cgc cgg gcc ttc acc aag acc tac act 611
Asn Ser Leu Ser Leu Ala Gln Arg Arg Gly Phe Thr Lys Thr Tyr Thr
110 115 120
gtt ggc tgt gag gaa tgc aca gtg ttt ccc tgt tta tcc ttc ccc tgc 659
Val Gly Cys Glu Glu Cys Thr Val Phe Pro Cys Leu Ser Phe Pro Cys
125 130 135
aaa ctg cag agt gcc act cat tgc ttg tgg acg gac cag ctc ctc caa 707
Lys Leu Gln Ser Gly Thr His Cys Leu Trp Thr Asp Gln Leu Leu Gln
140 145 150
ggc tct gaa aag gcc ttc cag tcc cgt cac ctt gcc tgc ctg cct cgg 755
Gly Ser Glu Lys Gly Phe Gln Ser Arg His Leu Ala Cys Leu Pro Arg
155 160 165
gag cca ggg ctg tgc acc tgg cag tcc ctg cgg tcc cag ata gcc 800
Glu Pro Gly Leu Cys Thr Trp Gln Ser Leu Arg Ser Gln Ile Ala
170 175 180
tgaatcctcgc ccggagtgga agctgaagcc tgcacagtgt ccacctgttt cccactccca 860
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<222> 140..472

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<222> 140..211

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aagtggctca taggagaaa atg aaa tat gat tgt ccc ttc agt ggg aca tca 172
Met Lys Tyr Asp Cys Pro Phe Ser Gly Thr Ser
-20

ttt gtg gtc ttc tct ctc ttt ttg atc tgt gca atg gct gga gat gta 220
Phe Val Val Phe Ser Leu Phe Leu Ile Cys Ala Met Ala Gly Asp Val
-10

gtc tac gct gac atc aaa act gtt cgg act tcc ccg tta gaa ctc gcg 268
Val Tyr Ala Asp Ile Lys Thr Val Arg Thr Ser Pro Leu Glu Leu Ala
5
-5 1
10 15

ttt cca ctt cag aga tct gtt tct ttc aac ttt tct act gtc cat aaa 316
Phe Pro Leu Gln Arg Ser Val Ser Phe Asn Phe Ser Thr Val His Lys
20 25 30 35

tca tgt cct gcc aaa gac tgg aag gtg cat aag gga aaa tgt tac tgg 364
Ser Cys Pro Ala Lys Asp Trp Lys Val His Lys Gly Lys Cys Tyr Trp
40 45 50

att gct gaa act aag aaa tct tgg aac aaa agt caa aat gac tgt gcc 412
Ile Ala Glu Thr Lys Lys Ser Trp Asn Lys Ser Gln Asn Asp Cys Ala
55 60 65

ata aac aat tca tat ctc atg gtg att caa gac att act gct atg gtg 460
Ile Asn Asn Ser Tyr Leu Met Val Ile Gln Asp Ile Thr Ala Met Val
70 75 80

aga ttt aac att tagaggtgac agcatccccc acatggcag ttaatttttt 512
Arg Phe Asn Ile
85

gtctacaaac ttggcaaaag tctgtgaaaa gaagtttcaa cttcatgtgt tattaactat 572
acaaatatta gttgaatgaa ttgttgaaatt aaaaaaaaaa aaaaaaaaaa 621

<210> 52

<211> 673

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 68..484

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<221> sig_peptide

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<223> Von Heijne matrix

score 4.93618539864455

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      15              20              25
act tta gaa gaa ctg gaa gtg gtc tcg gaa agt tgt gtg gaa gtt cag      247
Thr Leu Glu Glu Leu Glu Val Ser Glu Ser Cys Val Glu Val Gln
      30              35              40
gag ata aat gaa gaa gaa tat ctg gtt att atc agg ttc acg cca aca      295
Glu Ile Asn Glu Glu Glu Tyr Leu Val Ile Ile Arg Phe Thr Pro Thr
      45              50              55
gta cct cat tgc tct ttg gcg act ctt att ggg ctg tgc tta aga gta      343
Val Pro His Cys Ser Leu Ala Thr Leu Ile Gly Leu Cys Leu Arg Val
      60              65              70              75
aaa ctt cag cga tgt tta cca ttt aaa cat aag ttg gaa atc tac att      391
Lys Leu Gln Arg Cys Leu Pro Phe Lys His Lys Leu Glu Ile Tyr Ile
      80              85              90
tct gaa gga acc cac tca aca gaa gaa gac atc aat aag cag ata aat      439
Ser Glu Gly Thr His Ser Thr Glu Glu Asp Ile Asn Lys Gln Ile Asn
      95              100              105
gac aaa gag cga gtg gca gct gca atg gaa aac ccc aac tta cgg gaa      487
Asp Lys Glu Arg Val Ala Ala Ala Met Glu Asn Pro Asn Leu Arg Glu
      110              115              120
att gtg gaa cag tgt gtc ctt gaa cct gac tgatagctgt ttttaagagcc      537
Ile Val Glu Gln Cys Val Leu Glu Pro Asp
      125              130
actggcctgt aattgtttga tatatttgta actctttgta taatgtcaga gactcatggt      597
taatacatag gtgattttgta cctcagagca ttttttaaag gattctttcc aagcgagatt      657
taattataag gtagtaccta atttgttcaa tgtataacat tctcaggatt tgtaacactt      717
aaatgatcag acagaataat attttctagt tattatgtgt aagatgagtt gctatttttc      777
tgatgctcat tctgatacaa ctatttttcg tgtcaaatat ctactgtgcc caaatgtact      837
caattttaat cattactctg taaaataaat aagcagatga ttcttataaa aaaaaaaaaa      897

<210> 54
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<212> DNA
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<222> 92..634

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<221> sig_peptide
<222> 92..139
<223> Von Heijne matrix
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      seq FLLLTCLFITGTS/VS

<400> 54
cttaaaaaaa aaagtgtctg aaagagaagg ggacaaaagga acaccagtat taagaggatt      60
ttccagtgtt tctggcagtt ggtccagaag g atg cct cca ttc ctg ctt ctc      112
                        Met Pro Pro Phe Leu Leu Leu
                        -15                        -10
acc tgc ctc ttc atc aca ggc acc tcc gtg tca ccc gtg gcc cta gat      160
Thr Cys Leu Phe Ile Thr Gly Thr Ser Val Ser Pro Val Ala Leu Asp
                        -5                        1                        5
cct tgt tct gct tac atc agc ctg aat gag ccc tgg agg aac act gac      208
Pro Cys Ser Ala Tyr Ile Ser Leu Asn Glu Pro Trp Arg Asn Thr Asp
                        10                        15                        20
cac cag ttg gat gag tct caa ggt cct cct cta tgt gac aac cat gtg      256
His Gln Leu Asp Glu Ser Gln Gly Pro Pro Leu Cys Asp Asn His Val

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<222> 4..126
 <223> Von Heijne matrix
 score 4.34454795165846
 seq RVVSWLFSIVVFG/SI

<400> 56
 acg atg gaa ggg ggt gcg tac gga gcg ggc aaa gcc ggg ggc gcc ttc 48
 Met Glu Gly Gly Ala Tyr Gly Ala Gly Lys Ala Gly Gly Ala Phe
 -40 -35 -30
 gac ccc tac acc ctg gtc cgg cag ccg cac acc atc ctg cgc gtc gtg 96
 Asp Pro Tyr Thr Leu Val Arg Gln Pro His Thr Ile Leu Arg Val Val
 -25 -20 -15
 tct tgg ctg ttc tcc ata gtg gtg ttc ggc tcc atc gtg aac gag ggc 144
 Ser Trp Leu Phe Ser Ile Val Val Phe Gly Ser Ile Val Asn Glu Gly
 -10 -5 1 5
 tac ctc aac agc gcc tcc gag ggg gag cag ttc tgc atc tac aac cgc 192
 Tyr Leu Asn Ser Ala Ser Glu Gly Glu Gln Phe Cys Ile Tyr Asn Arg
 10 15 20
 aac ccc aac gcc tgc agc tat ggc gtg gcc gtg ggc gtg ctc gcc ttc 240
 Asn Pro Asn Ala Cys Ser Tyr Gly Val Ala Val Gly Val Leu Ala Phe
 25 30 35
 ctc acc tgc ctg ctg tac ctg gcc ctg gac gtg tac ttc ccg cag atc 288
 Leu Thr Cys Leu Leu Tyr Leu Ala Leu Asp Val Tyr Phe Pro Gln Ile
 40 45 50
 agc agc gtc aag gac cgc aag aaa gcc gtc ctg tcc gac atc ggt gtc 336
 Ser Ser Val Lys Asp Arg Lys Lys Ala Val Leu Ser Asp Ile Gly Val
 55 60 65 70
 tcg ggt gag ccc cac cca gca ggt acc ccc tgc aca gag tct aca gag 384
 Ser Gly Glu Pro His Pro Ala Gly Thr Pro Cys Thr Glu Ser Thr Glu
 75 80 85
 ggc tgt ccc ggg cca taggaggcgg ctgccaccct tcttcccatg ttccagatga 439
 Gly Cys Pro Gly Pro
 90
 gggaaatgag ccttctgggc ttctctctgg ttcgtgggat tctgetacct ggccaaccag 499
 tggcaggctc ccaagcccaa ggacaaccca ctgaacgaag ggacggacgc agcccggggcc 559
 gccatcgccct tctccttttt ctccatcttc acctggagcc tgaccgcagc cctggccggtg 619
 cggagattca aggacctaag cttccaggag gagtacagca cactgttccc tgcttcggca 679
 cagccgtagg cctccccggc ttgcagaggc cggcagccct gtatcacccc tggcagtgag 739
 gtggcaggag cagcctagtg ccagaaatgt ccaagatgcc agggcagtgga gggcagtgga 799
 aggcctggctt gaggaaccaa ttcaggttct ccactgactc attcattctc tcaccgcctc 859
 cttcattgat tcttcatgcy ttcattcatt cagtaaacat ttattgagta aaaaaaaaaa 919
 aaaaaa 925

<210> 57
 <211> 1240
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 127..879

<220>
 <221> sig_peptide
 <222> 127..198
 <223> Von Heijne matrix
 score 5.38660866264012
 seq ALCVSCSMSVLRA/YP

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<400> 57
agtctaggat cctcacacca gctacttgca agggagaagg aaaaggccag taaggcctgg      60
gccaggagag tcccgcacagg agtgtcaggt ttcaatctca gcaccagcca ctcagagcag      120
ggcacg atg ttg ggg gcc cgc ctc agg ctc tgg gtc tgt gcc ttg tgc      168
      Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys
      -20                                -15
agc gtc tgc agc atg agc gtc ctc aga gcc tat ccc aat gcc tcc cca      216
Ser Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
-10                                -5                                1                                5
ctg ctc ggc tcc agc tgg ggt ggc ctg atc cac ctg tac aca gcc aca      264
Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr
      10                                15                                20
gcc agg aac agc tac cac ctg cag atc cac aag aat ggc cat gtg gat      312
Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp
      25                                30                                35
ggc gca ccc cat cag acc atc tac agt gcc ctg atg atc aga tca gag      360
Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu
      40                                45                                50
gat gct ggc ttt gtg gtg att aca ggt gtg atg agc aga aga tac ctc      408
Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu
      55                                60                                65                                70
tgc atg gat ttc aga ggc aac att ttt gga tca cac tat ttc gac ccg      456
Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro
      75                                80                                85
gag aac tgc agg ttc caa cac cag acg ctg gaa aac ggg tac gac gtc      504
Glu Asn Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val
      90                                95                                100
tac cac tct cct cag tat cac ttc ctg gtc agt ctg ggc cgg gcg aag      552
Tyr His Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys
      105                                110                                115
aga gcc ttc ctg cca ggc atg aac cca ccc ccg tac tcc cag ttc ctg      600
Arg Ala Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu
      120                                125                                130
tcc cgg agg aac gag atc ccc cta att cac ttc aac acc ccc ata cca      648
Ser Arg Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro
      135                                140                                145                                150
cgg cgg cac acc cgg agc gcc gag gac gac tcg gag cgg gac ccc ctg      696
Arg Arg His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu
      155                                160                                165
aac gtg ctg aag ccc cgg gcc cgg atg acc ccg gcc ccg gcc tcc tgt      744
Asn Val Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys
      170                                175                                180
tca cag gag ctc ccg agc gcc gag gac aac agc ccg atg gcc agt gac      792
Ser Gln Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp
      185                                190                                195
cca tta ggg gtg gtc agg ggc ggt cga gtg aac acg cac gct ggg gga      840
Pro Leu Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly
      200                                205                                210
acg ggc ccg gaa ggc tgc cgc ccc ttc gcc aag ttc atc tagggctgct      889
Thr Gly Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
      215                                220                                225
ggaagggcac cctctttaac ccatccctca gcaaacgcag ctcttcccaa ggaccaggtc      949
ccttgacgtt ccgaggatgg gaaaggtgac aggggcatgt atggaatttg ctgcttctct      1009
ggggctccct ccacaggagg tctgtgaga accaaccttt gagggccaa gtcattctct      1069
tcaccgcctt cctcaactcca tatagaacac ctttcccaat aggaaaccoc aacaggtaaa      1129
ctagaaattt cccttcatg aaggttagaga gaagggtct ctcccaaat atttctcttc      1189
cttgtgcctc tcctctttat cacttttaag catgaaaaaa aaaaaaaaaa a      1240

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<210> 58
 <211> 902
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 156..566

<220>
 <221> sig_peptide
 <222> 156..221
 <223> Von Heijne matrix
 score 5.67458379966095
 seq LVSMAGRVCLCQG/SA

<400> 58
 atttccagc gtgcctcagg aagggcgcca ggactgcatt ttgctccgga gcgtccagag 60
 tcctggccct gagcggaat cgcagtgccc gaggctgagc ggcaggcgga tcgccccgac 120
 cctcactcct ggcgctcgag tctctggcgt agccc atg ctg agt ggg cgg ctg 173
 Met Leu Ser Gly Arg Leu
 -20
 gtc ctg ggt ctg gtc tcc atg gct ggc cgc gtt tgt ttg tgc cag ggc 221
 Val Leu Gly Leu Val Ser Met Ala Gly Arg Val Cys Leu Cys Gln Gly
 -15 -10 -5
 agc gcg gga tcc ggg gcc atc ggt ccg gtg gag gcc gcc att cgc acg 269
 Ser Ala Gly Ser Gly Ala Ile Gly Pro Val Glu Ala Ala Ile Arg Thr
 1 5 10 15
 aag ttg gag gag gcc ctg agc ccc gag gtg cta gag ctt cgc aac gag 317
 Lys Leu Glu Glu Ala Leu Ser Pro Glu Val Leu Glu Leu Arg Asn Glu
 20 25 30
 agc ggt ggc cac gcg gtc ccg cca ggc agt gag act cac ttc cgc gtg 365
 Ser Gly Gly His Ala Val Pro Pro Gly Ser Glu Thr His Phe Arg Val
 35 40 45
 gct gtg gtg agc tct cgt ttc gag gga ctg agc ccc cta caa cga cac 413
 Ala Val Val Ser Ser Arg Phe Glu Gly Leu Ser Pro Leu Gln Arg His
 50 55 60
 cgg ctg gtc cac gca gcg ctg gcc gag gag ctg gga ggt ccg gtc cat 461
 Arg Leu Val His Ala Ala Leu Ala Glu Glu Leu Gly Gly Pro Val His
 65 70 75 80
 gcg ctg gcc atc cag gca cgg acc ccc gcc cag tgg aga gag aac tct 509
 Ala Leu Ala Ile Gln Ala Arg Thr Pro Ala Gln Trp Arg Glu Asn Ser
 85 90 95
 cag ctg gac act agc ccc cca tgc ctg ggt ggg aac aag aaa act cta 557
 Gln Leu Asp Thr Ser Pro Pro Cys Leu Gly Gly Asn Lys Lys Thr Leu
 100 105 110
 gga acc ccc tgaaccccaa gagagggagg accaggatcc gaatgggctg 606
 Gly Thr Pro
 115
 ggtgagcag aattaccgag gccttccttt tgatacagtc caggatttgt aagggatgaa 666
 gacctctggg ccccatctgt ttgggggtcca tacatactct ccgaagatag caacttgctt 726
 caggtcaaa tgaaaccgag aaaaagagaag aatcactcac tactgtcttt gccttggaact 786
 attcaggaag gccagcccg atgttccatg ttaaatcgtg acagaattgc accagacctg 846
 atgagttgga aacaatccta tacattaaaa gaaattacac taaaaaaaaa aaaaaa 902

<210> 59
 <211> 1969

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 35..1657

<220>
<221> sig_peptide
<222> 35..118
<223> Von Heijne matrix
score 3.75144398608723
seq SGLLLQVLFRLLT/FV

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<400> 59
atttttctgt gtgtctgagc ctggcgcgga ggct atg ggc agc cag gag gtg ctg      55
                                     Met Gly Ser Gln Glu Val Leu
                                     -25
ggc cac gcg gcc cgg ctg gcc tcc tcc ggt ctc ctc ctg cag gtg ttg      103
Gly His Ala Ala Arg Leu Ala Ser Ser Gly Leu Leu Leu Gln Val Leu
-20                               -15                               -10
ttt cgg ttg atc acc ttt gtc ttg aat gca ttt att ctt cgc ttc ctg      151
Phe Arg Leu Ile Thr Phe Val Leu Asn Ala Phe Ile Leu Arg Phe Leu
-5                               1                               5                               10
tca aag gaa atc gtt ggc gta gta aat gta aga cta acg ctg ctt tac      199
Ser Lys Glu Ile Val Gly Val Val Asn Val Arg Leu Thr Leu Leu Tyr
15                               20
tca acc acc ctc ttc ctg gcc aga gag gcc ttc cgc aga gca tgt ctc      247
Ser Thr Thr Leu Phe Leu Ala Arg Glu Ala Phe Arg Arg Ala Cys Leu
30                               35                               40
agt ggg ggc acc cag cga gac tgg agc cag acc ctc aac ctg ctg tgg      295
Ser Gly Gly Thr Gln Arg Asp Trp Ser Gln Thr Leu Asn Leu Leu Trp
45                               50                               55
cta aca gtc ccc ctg ggt gtg ttt tgg tcc tta ttc ctg ggc tgg atc      343
Leu Thr Val Pro Leu Gly Val Phe Trp Ser Leu Phe Leu Gly Trp Ile
60                               65                               70                               75
tgg ttg cag ctg ctt gaa gtg cct gat cct aat gtt gtc cct cac tat      391
Trp Leu Gln Leu Leu Glu Val Pro Asp Pro Asn Val Val Pro His Tyr
80                               85                               90
gca act gga gtg gtg ctg ttt ggt ctc tcg gca gtg gtg gag ctt cta      439
Ala Thr Gly Val Val Leu Phe Gly Leu Ser Ala Val Val Glu Leu Leu
95                               100                               105
gga gag ccc ttt tgg gtc ttg gca caa gca cat atg ttt gtg aag ctc      487
Gly Glu Pro Phe Trp Val Leu Ala Gln Ala His Met Phe Val Lys Leu
110                               115                               120
aag gtg att gca gag agc ctg tcg gta att ctt aag agc gtt ctg aca      535
Lys Val Ile Ala Glu Ser Leu Ser Val Ile Leu Lys Ser Val Leu Thr
125                               130                               135
gct ttt ctc gtg ctg tgg ttg cct cac tgg gga ttg tac att ttc tct      583
Ala Phe Leu Val Leu Trp Leu Pro His Trp Gly Leu Tyr Ile Phe Ser
140                               145                               150                               155
ttg gcc cag ctt ttc tat acc aca gtt ctg gtg ctc tgc tat gtt att      631
Leu Ala Gln Leu Phe Tyr Thr Thr Val Leu Val Leu Cys Tyr Val Ile
160                               165                               170
tat ttc aca aag tta ctg ggt tcc cca gaa tca acc aag ctt caa act      679
Tyr Thr Thr Lys Leu Leu Gly Ser Pro Glu Ser Thr Lys Leu Gln Thr
175                               180                               185
ctt cct gtc tcc aga ata aca gat ctg tta ccc aat att aca aga aat      727

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Leu Pro Val Ser Arg Ile Thr Asp Leu Leu Pro Asn Ile Thr Arg Asn
 190 195 200
 gga gcg ttt ata aac tgg aaa gag gct aaa ctg act tgg agt ttt ttc 775
 Gly Ala Phe Ile Asn Trp Lys Glu Ala Lys Leu Thr Trp Ser Phe Phe
 205 210 215
 aaa cag tct ttc ttg aaa cag att ttg aca gaa ggc gag cga tat gtg 823
 Lys Gln Ser Phe Leu Lys Gln Ile Leu Thr Glu Gly Glu Arg Tyr Val
 220 225 230 235
 atg aca ttt ttg aat gta ttg aac ttt ggt gat cag ggt gtg tat gat 871
 Met Thr Phe Leu Asn Val Leu Asn Phe Gly Asp Gln Gly Val Tyr Asp
 240 245 250
 ata gtg aat aat ctt ggc tcc ctt gtg gcc aga tta att ttc cag cca 919
 Ile Val Asn Asn Leu Gly Ser Leu Val Ala Arg Leu Ile Phe Gln Pro
 255 260 265
 ata gag gaa agt ttt tat ata ttt ttt gct aag gtg ctg gag agg gga 967
 Ile Glu Glu Ser Phe Tyr Ile Phe Phe Ala Lys Val Leu Glu Arg Gly
 270 275 280
 aag gat gcc aca ctt cag aag cag gag gac gtt gct gtg gct gct gca 1015
 Lys Asp Ala Thr Leu Gln Lys Gln Glu Asp Val Ala Val Ala Ala Ala
 285 290 295
 gtc ttg gag tcc ctg ctc aag ctg gcc ctg ctg gcc ggc ctg acc atc 1063
 Val Leu Glu Ser Leu Leu Lys Leu Ala Leu Leu Ala Gly Leu Thr Ile
 300 305 310 315
 act gtt ttt ggc ttt gcc tat tct cag ctg gct ctg gat atc tac gga 1111
 Thr Val Phe Gly Phe Ala Tyr Ser Gln Leu Ala Leu Asp Ile Tyr Gly
 320 325 330
 ggg acc atg ctt agc tca gga tcc ggt cct gtt ttg ctg cgt tcc tac 1159
 Gly Thr Met Leu Ser Ser Gly Ser Gly Pro Val Leu Leu Arg Ser Tyr
 335 340 345
 tgt ctc tat gtt ctc ctg ctt gcc atc aat gga gtg aca gag tgt tta 1207
 Cys Leu Tyr Val Leu Leu Leu Ala Ile Asn Gly Val Thr Glu Cys Leu
 350 355 360
 aca ttt gct gcc atg agc aaa gag gag gtc gac agg tac aat ttt gtg 1255
 Thr Phe Ala Ala Met Ser Lys Glu Glu Val Asp Arg Tyr Asn Phe Val
 365 370 375
 atg ctg gcc ctg tcc tcc tca ttc ctg gtg tta tcc tat ctc ttg acc 1303
 Met Leu Ala Leu Ser Ser Ser Phe Leu Val Leu Ser Tyr Leu Leu Thr
 380 385 390 395
 cgt tgg tgt ggc agc gtg ggc ttc atc ttg gcc aac tgc ttt aac atg 1351
 Arg Trp Cys Gly Ser Val Gly Phe Ile Leu Ala Asn Cys Phe Asn Met
 400 405 410
 ggc att cgg atc acg cag agc ctt tgc ttc atc cac cgc tac tac cga 1399
 Gly Ile Arg Ile Thr Gln Ser Leu Cys Phe Ile His Arg Tyr Tyr Arg
 415 420 425
 agg agc ccc cac agg ccc ctg gct ggc ctg cac cta tgc cca gtc ctg 1447
 Arg Ser Pro His Arg Pro Leu Ala Gly Leu His Leu Ser Pro Val Leu
 430 435 440
 ctc ggg aca ttt gcc ctc agt ggt ggg gtt act gct gtt tgc gag gta 1495
 Leu Gly Thr Phe Ala Leu Ser Gly Gly Val Thr Ala Val Ser Glu Val
 445 450 455
 ttc ctc tgc tgt gat cag ggc tgg cca gcc aga ctg gca cac att gct 1543
 Phe Leu Cys Cys Asp Gln Gly Trp Pro Ala Arg Leu Ala His Ile Ala
 460 465 470 475
 gtg ggg gcc ttc tgt ctg gga gca act ctc ggg aca gca ttc ctc aca 1591
 Val Gly Ala Phe Cys Leu Gly Ala Thr Leu Gly Thr Ala Phe Leu Thr
 480 485 490
 gag acc aag ctg atc cat ttc ctc agg act cag tta ggt gtg ccc aga 1639
 Glu Thr Lys Leu Ile His Phe Leu Arg Thr Leu Leu Gly Val Pro Arg

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          495              500              505
cgc act gac aaa atg aca tgacttcagg gaagcctgga caccgcaggc      1687
Arg Thr Asp Lys Met Thr
      510
accotgaacca gctatgggta gttctgtggg tggaacacat tctgtgtaag agccccactg      1747
agggctctgc agcggagtga cagcaacccc agagatgagg caccagagag tgccactgca      1807
tgagacacct gtgaccattc gaagtctgaa atgcgggggg ggagtttcat ttttaagtga      1867
agacccaaaag ccccttaaaa ataatagttt tttatcattt tatagtaate agcattttct      1927
cttttactaa tatactcatt ccttttgaaa aaaaaaaaaa aa      1969

<210> 60
<211> 1132
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 77..937

<220>
<221> sig_peptide
<222> 77..127
<223> Von Heijne matrix
      score 3.74817238048175
      seq RIVSAALLAFVQT/HL

<400> 60
gttgggtgggg cgtgggggatg agagctgcac cgcgcggggac aagtcgccgg cggccccgagc      60
gagcagaaga gagagc atg gag ctg gag agg atc gtc agt gca gcc ctc ctt      112
      Met Glu Leu Glu Arg Ile Val Ser Ala Ala Leu Leu
      -15 -10
gcc ttt gtc cag aca cac ctc ccg gag gcc gac ctc agt ggc ttg gat      160
Ala Phe Val Gln Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu Asp
-5 1 5 10
gag gtc atc ttc tcc tat gtg ctt ggg gtc ctg gag gac ctg ggc ccc      208
Glu Val Ile Phe Ser Tyr Val Leu Gly Val Leu Glu Asp Leu Gly Pro
15 20 25
tcg ggc cca tca gag gag aac ttc gat atg gag gct ttc act gag atg      256
Ser Gly Pro Ser Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu Met
30 35 40
atg gag gcc tat gtg cct ggc ttc gcc cac atc ccc agg ggc aca ata      304
Met Glu Ala Tyr Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr Ile
45 50 55
ggg gac atg atg cag aag ctc tca ggg cag ctg agc gat gcc agg aac      352
Gly Asp Met Met Gln Lys Leu Ser Gly Gln Leu Ser Asp Ala Arg Asn
60 65 70 75
aaa gag aac ctg caa ccg cag agc tct ggt gtc caa ggt cag gtg ccc      400
Lys Glu Asn Leu Gln Pro Gln Ser Ser Gly Val Gln Gly Gln Val Pro
80 85 90
atc tcc cca gag ccc ctg cag cgg ccc gaa atg ctc aaa gaa gag act      448
Ile Ser Pro Glu Pro Leu Gln Arg Pro Glu Met Leu Lys Glu Glu Thr
95 100 105
agg tct tcg gct gct gct gct gca gac acc caa gat gag gca act ggc      496
Arg Ser Ser Ala Ala Ala Ala Ala Asp Thr Gln Asp Glu Ala Thr Gly
110 115 120
gct gag gag gag ctt ctg cca ggg gtg gat gta ctc ctg gag gtg ttc      544
Ala Glu Glu Glu Leu Leu Pro Gly Val Asp Val Leu Leu Glu Val Phe
125 130 135

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cct acc tgt tgc gtg gag cag gcc cag tgg gtg ctg gcc aaa gct cgg      592
Pro Thr Cys Ser Val Glu Gln Ala Gln Trp Val Leu Ala Lys Ala Arg
140                               145                               150                               155
ggg gac ttg gaa gaa gct gtg cag atg ctg gta gag gga aag gaa gag      640
Gly Asp Leu Glu Glu Ala Val Gln Met Leu Val Glu Gly Lys Glu Glu
160                               165                               170
ggg cct gca gcc tgg gag ggc ccc aac cag gac ctg ccc aga cgc ctc      688
Gly Pro Ala Ala Trp Glu Gly Pro Asn Gln Asp Leu Pro Arg Arg Leu
175                               180                               185
aga ggc ccc caa aag gat gag ctg aag tcc ttc atc ctg cag aag tac      736
Arg Gly Pro Gln Lys Asp Glu Leu Lys Ser Phe Ile Leu Gln Lys Tyr
190                               195                               200
atg atg gtg gat agc gca gag gat cag aag att cac cgg ccc atg gct      784
Met Met Val Asp Ser Ala Glu Asp Gln Lys Ile His Arg Pro Met Ala
205                               210                               215
ccc aag gag gcc ccc aag aag ctg atc cga tac atc gac aac cag gta      832
Pro Lys Glu Ala Pro Lys Lys Leu Ile Arg Tyr Ile Asp Asn Gln Val
220                               225                               230                               235
gtg agc acc aaa ggg gag cga ttc aaa gat gtg cgg aac cct gag gcc      880
Val Ser Thr Lys Gly Glu Arg Phe Lys Asp Val Arg Asn Pro Glu Ala
240                               245                               250
gag gag atg aag gcc aca tac atc aac ctc aag cca gcc aga aag tac      928
Glu Glu Met Lys Ala Thr Tyr Ile Asn Leu Lys Pro Ala Arg Lys Tyr
255                               260                               265
cgc ttc cat tgaggcactc gccggactct gcccgagcct tctaggctca      977
Arg Phe His
270
gatccacagag ggaatgcagga gccctataacc cctacacagg gggccccctaa ctcctgtccc      1037
cctctctcac tcctttgtctc catagtgtta acctactctc ggagctgcct ccatggggcac      1097
agtaaaaggtg gcccagaagaa aaaaaaaaaa aaaaaa      1132

<210> 61
<211> 631
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 9..503

<220>
<221> sig_peptide
<222> 9..113
<223> Von Heijne matrix
score 10.2506494380376
seq LLPLVLLPPLAAA/AA

<400> 61
tgccaggg atg atg cgc tgc tgc cgc cgc cgc tgc tgc tgc cgg caa cca      50
Met Met Arg Cys Cys Arg Arg Arg Cys Cys Cys Arg Gln Pro
-35                               -30                               -25
ccc cat gcc ctg agg cgg ttg ctg ttg ctg ccc ctc gtc ctt tta cct      98
Pro His Ala Leu Arg Pro Leu Leu Leu Leu Pro Leu Val Leu Leu Pro
-20                               -15                               -10
ccc ctg gca gca gct gca gcg ggc cca aac cga tgt gac acc ata tac      146
Pro Leu Ala Ala Ala Ala Ala Gly Pro Asn Arg Cys Asp Thr Ile Tyr
-5                               1                               5                               10
cag ggc ttc gcc gag tgt ctc atc cgc ttg ggg gac agc atg ggc cgc      194

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Gln Gly Phe Ala Glu Cys Leu Ile Arg Leu Gly Asp Ser Met Gly Arg
15 20 25
gga ggc gag ctg gag acc atc tgc agg tct tgg aat tac ttc cat gcc 242
Gly Gly Glu Leu Glu Thr Ile Cys Arg Ser Trp Asn Tyr Phe His Ala
30 35 40
tgt gcc tct cag gtc ctg tca ggc tgt ccg gag gag gca gct gca gtg 290
Cys Ala Ser Gln Val Leu Ser Gly Cys Pro Glu Glu Ala Ala Ala Val
45 50 55
tgg gaa tca cta cag caa gaa gct cgc cag gcc ccc cgt ccg aat aac 338
Trp Glu Ser Leu Gln Gln Glu Ala Arg Gln Ala Pro Arg Pro Asn Asn
60 65 70 75
ttg cac act ctg tgc ggt gcc ccg gtg cat gtt cgg gag cgc ggc aca 386
Leu His Thr Leu Cys Gly Ala Pro Val His Val Arg Glu Arg Gly Thr
80 85 90
ggc tcc gaa acc aac cag gag acg ctg cgg gct aca gcg cct gca ctc 434
Gly Ser Glu Thr Asn Gln Glu Thr Leu Arg Ala Thr Ala Pro Ala Leu
95 100 105
ccc atg gcc cct cgc gcc cca ctg ctg gcg gct gct ctg gct ctg gcc 482
Pro Met Ala Pro Ala Pro Pro Leu Leu Ala Ala Ala Leu Ala Leu Ala
110 115 120
tac ctc ctg agg cct ctg gcc tagcttgttg ggtgggtag cagcgcgccgt 533
Tyr Leu Leu Arg Pro Leu Ala
125 130
acctcagcc ctgctctggc ggtggtgtgc caggctctgc agagcgcagc agggccttttc 593
attaaggta tttatatattg caaaaaaaaa aaaaaaaaa 631

<210> 62
<211> 722
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..464

<220>
<221> sig_peptide
<222> 21..95
<223> Von Heijne matrix
score 5.38058532480537
seq AVTSLLSPTPATA/LA

<400> 62
ggaagtgtgt gatcgaaagc atg gcg tcg gtg gtg ttg gcg ctg agg acc cgg 53
Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg
-25 -20 -15
aca gcc gtt aca tcc ttg cta agc ccc act ccg gct aca gct ctt gct 101
Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala
-10 -5 1
gtc aga tac gca tcc aag aag tcg ggt ggt agc tcc aaa aac ctc ggt 149
Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly
5 10 15
gga aag tca tca ggc aga cgc caa ggc att aag aaa atg gaa ggt cac 197
Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His
20 25 30
tat gtt cat gct ggg aac atc att gca aca cag cgc cat ttc cgc tgg 245
Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp
35 40 45 50

cac cca ggt gcc cat gtg ggt gtt ggg aag aat aaa tgt ctg tat gcc	293
His Pro Gly Ala His Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala	
55 60 65	
ctg gaa gag ggg ata gtc cgc tac act aag gag gtc tac gtg cct cat	341
Leu Glu Glu Gly Ile Val Arg Tyr Thr Lys Glu Val Tyr Val Pro His	
70 75 80	
ccc aga aac acg gag gct gtg gat ctg atc acc agg ctg ccc aag ggt	389
Pro Arg Asn Thr Glu Ala Val Asp Leu Ile Thr Arg Leu Pro Lys Gly	
85 90 95	
gct gtg ctc tac aag act ttt gtc cac gtg gtt cct gcc aag cct gag	437
Ala Val Leu Tyr Lys Thr Phe Val His Val Val Pro Ala Lys Pro Glu	
100 105 110	
ggc acc ttc aaa ctg gta gct atg ctt tgaatgtcctg ttgaggccat	484
Gly Thr Phe Lys Leu Val Ala Met Leu	
115 120	
cggacagaga ctggagccca ggtgacagga gatggtgata ccagaagtca aggggtgggg	544
tggcgacacg gcctcccag gaagaggtct gcttgatggt gactctgcag gagactctga	604
agtgaactgct gggaaaccct ttgggagacc tgacctgggg ccaaaaaataa agtgagccag	664
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<210> 63
 <211> 1442
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 178..1050

<220>
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 <222> 178..279
 <223> Von Heijne matrix
 score 10.0571391689271
 seq FLCLLSALLLTG/KK

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gcagagatac agaggcagag gaaaagggca ctccatgtg acctgttctt agagcaagac	120
aatcaccatc tgaattccag aagccctgtt catggttggg gatattttct cgactgc	177
atg gaa tca gaa aga agc aaa agg atg gga aat gcc tgc att ccc ctg	225
Met Glu Ser Glu Arg Ser Lys Arg Met Gly Asn Ala Cys Ile Pro Leu	
-30 -25 -20	
aaa aga att gct tat ttc cta tgt ctc tta tct gcg ctt ttg ctg act	273
Lys Arg Ile Ala Tyr Phe Leu Cys Leu Leu Ser Ala Leu Leu Leu Thr	
-15 -10 -5	
gag ggg aag aaa cca gcg aag cca aaa tgc cct gcc gtg tgt act tgt	321
Glu Gly Lys Lys Pro Ala Lys Pro Lys Cys Pro Ala Val Cys Thr Cys	
1 5 10	
acc aaa gat aat gct tta tgt gag aat gcc aga tcc att cca cgc acc	369
Thr Lys Asp Asn Ala Leu Cys Glu Asn Ala Arg Ser Ile Pro Arg Thr	
15 20 25 30	
ggt cct cct gat gtt atc tca tta tcc ttt gtg aga tct ggt ttt act	417
Val Pro Pro Asp Val Ile Ser Leu Ser Phe Val Arg Ser Gly Phe Thr	
35 40 45	
gaa atc tca gaa ggg agt ttt tta ttc acg cca tcg ctg cag ctc ttg	465
Glu Ile Ser Glu Gly Ser Phe Leu Phe Thr Pro Ser Leu Glu Leu Leu	
50 55 60	

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tta ttc aca tcg aac tcc ttt gat gtg atc agt gat gat gct ttt att      513
Leu Phe Thr Ser Asn Ser Phe Asp Val Ile Ser Asp Asp Ala Phe Ile
65 70 75
ggg ctt cca cat cta gag tat tta ttc ata gaa aac aac atc aag      561
Gly Leu Pro His Leu Glu Tyr Leu Phe Ile Glu Asn Asn Asn Ile Lys
80 85 90
tca att tca aga cat act ttc cgg gga cta aag tca tta att cac ttg      609
Ser Ile Ser Arg His Thr Phe Arg Gly Leu Lys Ser Leu Ile His Leu
95 100 105 110
agc ctt gca aac aac aat ctc cag aca ctc cca aaa gat att ttc aaa      657
Ser Leu Ala Asn Asn Asn Leu Gln Thr Leu Pro Lys Asp Ile Phe Lys
115 120 125
ggc ctg gat tct tta aca aat gtg gac ctg agg ggt aat tca ttt aat      705
Gly Leu Asp Ser Leu Thr Asn Val Asp Leu Arg Gly Asn Ser Phe Asn
130 135 140
tgt gac tgt aaa ctg aaa tgg cta gtg gaa tgg ctt ggc cac acc aat      753
Cys Asp Cys Lys Leu Lys Trp Leu Val Glu Trp Leu Gly His Thr Asn
145 150 155
gca act gtt gaa gac atc tac tgc gaa ggc ccc cca gaa tac aag aag      801
Ala Thr Val Glu Asp Ile Tyr Cys Glu Gly Pro Glu Tyr Lys Lys
160 165 170 175
cgc aaa atc aat agt ctc tcc tcg aag gat ttc gat tgc atc att aca      849
Arg Lys Ile Asn Ser Leu Ser Ser Lys Asp Phe Asp Cys Ile Ile Thr
180 185 190
gaa ttt gca aag tct caa gac ctg cct tat caa tta ttc ata gac      897
Glu Phe Ala Lys Ser Gln Asp Leu Pro Tyr Gln Ser Leu Ser Ile Asp
195 200 205
act ttt tct tat ttg aat gat gag tat gta gtc atc gct cag cct ttt      945
Thr Phe Ser Tyr Leu Asn Asp Glu Tyr Val Val Ile Ala Gln Pro Phe
210 215 220
act gga aaa tgc att ttc ctt gaa tgg gac cat gtg gaa aag acc ttc      993
Thr Gly Lys Cys Ile Phe Leu Glu Trp Asp His Val Glu Lys Thr Phe
225 230 235
cgg aat tat gac aac att aca gtt tta agg gaa ata cac aga ttt aca      1041
Arg Asn Tyr Asp Asn Ile Thr Val Leu Arg Glu Ile His Arg Phe Thr
240 245 250
aac atg tca tagttgacctt aagcgcatga gacaccaaatt tctgtggctg      1090
Asn Met Ser
255
ccatcagaaa tttttctacag tacatgaccc ggatgaactc aatgcatgat gactcttctt      1150
atcacacttg caaatgaatg cetttcaaac attgagactg ctagaaccaa gcactaccag      1210
tatctccatc ctttaactgtc cagtccagtg atgtgggaag ttacctttta taagacaaaa      1270
tttaattgtg taactgttct ttgcagttaa gatgtgtaaa taagcgttta atggatatctg      1330
ttactccaaa aagaaatatt aatatgtact ttccatttta ttattcatg tgtacagaaa      1390
caactgccaa ataaaatggtt tacattttctt ttcagaaaaa aaaaaaaaaa aa      1442

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<210> 64
<211> 795
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 32..274

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<220>
<221> sig_peptide
<222> 32..178

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<223> Von Heijne matrix
score 4.30837886795471
seq LMVELLKVFVVEA/AV

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Met Glu Gly Ala Gly Ala Gly
-45
tcc ggc ttc cgg aag gag ctg gtg agc agg ctg ctg cac ctg cac ttc 100
Ser Gly Phe Arg Lys Glu Leu Val Ser Arg Leu Leu His Leu His Phe
-40 -35 -30
aag gat gac aag acc aaa gtg agc ggg gac gcg ctg cag ctc atg gtg 148
Lys Asp Asp Lys Thr Lys Val Ser Gly Asp Ala Leu Gln Leu Met Val
-25 -20 -15
gag ttg ctg aag gtc ttc gtt gtg gaa gca gca gtc cgc ggc gtg cgg 196
Glu Leu Leu Lys Phe Val Val Glu Ala Ala Val Arg Gly Val Arg
-10 -5 1 5
cag gcc cag gca gaa gac gcg ctc cgt gtg gac gtg gac cag ctg gag 244
Gln Ala Gln Ala Glu Asp Ala Leu Arg Val Asp Val Asp Gln Leu Glu
10 15 20
aag gtg ctt ccg cag ctg ctc ctg gac ttc tagggatctc agccgtggct 294
Lys Val Leu Pro Gln Leu Leu Leu Asp Phe
25 30
gaggccacc ccagaggagc ccttggtcca cagaagcagg ctttgtgttt ccagcggcct 354
ctgataagag gcaggggaagg acctgaagga ttggagttg attcaaacaa gatctctggg 414
agtctccagc ctgtgcagaa ggggcaggac tgcagtgcac tgcgggcctt ggagtgtcca 474
gtgggggacac tgggttgagg aggggcagca cctggggagt cctctctct cctccctggg 534
acaatagtgt gcatgccacc cggggtccta caggcagggt ctgggaaagg cctggccagc 594
aggtagcctg tgtgtttgac aaacagcagc tggcagcgct gcctctgcg cacattcctg 654
ccaccgcaca tcaaaactgg cgtgtgacct ttccagccat gcgatatcc ccttggaaga 714
tgcttcccca ggctataaat ttgttctcac aaagcaacat caataaatca aaactgtctc 774
tctcaaaaaa aaaaaaaaaa a 795

<210> 65
<211> 1236
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 222..920

<220>
<221> sig_peptide
<222> 222..311
<223> Von Heijne matrix
score 4.35083245061594
seq VAHALSLPABSYG/ND

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agtactccac ctctcgccct gtgcggggag ggtaaggcgg gccacgcaac ttctcagct 120
ggaggggagag cgcacgggtg agcccgccagt tgagaaggac tctgatccgg ctacgcttc 180
caatcagctg cggaaggagc cagcgtttcg gggggttgcaa g atg gcg gcc acc agt 236
Met Ala Ala Thr Ser
-30
gga act gat gag ccg gtt tcc ggg gag ttg gtg tct gtg gca cat gcg 284
Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val Ser Val Ala His Ala

000001-100700

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-25          -20          -15          -10
ctt tct ctc cca gca gag tcg tat ggc aac gat cct gac att gag atg      332
Leu Ser Leu Pro Ala Glu Ser Tyr Gly Asn Asp Pro Asp Ile Glu Met

          -5          1          5
gct tgg gcc atg aga gca atg cag cat gct gaa gtc tat tac aag ctg      380
Ala Trp Ala Met Arg Ala Met Gln His Ala Glu Val Tyr Tyr Lys Leu

          10          15          20
att tca tca gtt gac cca cag ttc ctc aaa ctc acc aaa gta gat gac      428
Ile Ser Ser Val Asp Pro Gln Phe Leu Lys Leu Thr Lys Val Asp Asp

          25          30          35
caa att tac tct gag ttc cgg aaa aat ttt gag acc ctt agg ata gat      476
Gln Ile Tyr Ser Glu Phe Arg Lys Asn Phe Glu Thr Leu Arg Ile Asp

          40          45          50          55
gtg ttg gac cca gaa gaa ctc aag tca gaa tca gcc aaa gag aag tgg      524
Val Leu Asp Pro Glu Glu Leu Lys Ser Glu Ser Ala Lys Glu Lys Trp

          60          65          70          75
agg cca ttc tgc ttg aag ttt aat ggg att gtt gaa gac ttc aac tat      572
Arg Pro Phe Cys Leu Lys Phe Asn Gly Ile Val Glu Asp Phe Asn Tyr

          80          85
ggt act ttg ctg cga cta gat tgt tct cag ggc tac act gag gaa aac      620
Gly Thr Leu Leu Arg Leu Asp Cys Ser Gln Gly Tyr Thr Glu Glu Asn

          90          95          100
acc atc ttt gcc ccc agg ata caa ttc ttt gcc att gaa att gct cgg      668
Thr Ile Phe Ala Pro Arg Ile Gln Phe Phe Ala Ile Glu Ile Ala Arg

          105          110          115
aac cgg gaa ggc tat aac aaa gct gtt tat atc agt gtt cag gac aaa      716
Asn Arg Glu Gly Tyr Asn Lys Ala Val Tyr Ile Ser Val Gln Asp Lys

          120          125          130          135
gaa gga gag aaa gga gtc aac aat gga gga gaa aaa aga gct gac agt      764
Glu Gly Glu Lys Gly Val Asn Asn Gly Gly Glu Lys Arg Ala Asp Ser

          140          145          150
gga gaa gaa gag aac acc aag aat gga gga gag aaa gga gct gat agt      812
Gly Glu Glu Glu Asn Thr Lys Asn Gly Gly Glu Lys Gly Ala Asp Ser

          155          160          165
gga gaa gaa aaa gag gaa gga atc aac aga gaa gac aaa act gac aaa      860
Gly Glu Glu Lys Glu Glu Gly Ile Asn Arg Glu Asp Lys Thr Asp Lys

          170          175          180
gga gga gaa aaa ggg aaa gaa gct gac aaa gaa atc aac aaa agt ggt      908
Gly Gly Glu Lys Gly Lys Glu Ala Asp Lys Glu Ile Asn Lys Ser Gly

          185          190          195
gaa aaa gct atg taaggatatac aggggaacagc actctagaag ctatgactca      960
Glu Lys Ala Met

200
attgagacta caagtaccac ggtgctactt gcacagaccc ctttggttaa atgtaaaattc 1020
ttgtacaatt gaaggatacg cagaaggaca tctttctagt ctaacagtca ggagctgctc 1080
tggtcatccc cttgtatgaa ctggctctaaa gactgttagt ggggtgtagg ttgatttttc 1140
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<210> 66

<211> 881

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 101..355


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<220>
<221> sig_peptide
<222> 101..160
<223> Von Heijne matrix
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      seq LFLCYLLLF TCSG/VE

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cctccaaggt ctagtgcagg agcccgcgcg cggcgccacc atg cgg cag aag gcg 115
                                         Met Arg Gln Lys Ala
                                         -20
gta tcg ctt ttc ttg tgc tac ctg ctg ctc ttc act tgc agt ggg gtg 163
Val Ser Leu Phe Leu Cys Tyr Leu Leu Leu Phe Thr Cys Ser Gly Val
-15 -10 -5 1
gag gca ggt aag aaa aag tgc tcg gag agc tcg gac agc ggc tcc ggg 211
Glu Ala Gly Lys Lys Cys Ser Glu Ser Ser Asp Ser Gly Ser Gly
      5 10 15
ttc tgg aag gcc ctg acc ttc atg gcc gtc gga gga gga ctc gca gtc 259
Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly Gly Ile Ala Ala Val
      20 25 30
gcc ggg ctg ccc gcg ctg ggc ttc acc ggc gcc ggc atc gcg gcc aac 307
Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala Gly Ile Ala Ala Asn
      35 40 45
tcg gtg gct gcc tcg ctg atg agc tgg tct gcg atc ctg aat ggg ggc 355
Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala Ile Leu Asn Gly Gly
      50 55 60 65
tagtggccac gctgcagagc ctccggggctg gtggcagcag cgtcgtcata ggtaaatattg 415
gtgcctgatg gggctacgcc acccacaagt atctcgatag tgaggaggat gaggagtagc 475
cagcagctcc cagaaacctct tcttctctct tggcctaact ctccagttta ggatctagaa 535
ctttgccttt tttttttttt tttttttttt ttgagatggg ttctcactat attgtccagg 595
ctagagtcca gkggctattc acagatgcga acatagtaca ctgcagcctc caactcctag 655
cctcaagtga tcctcctgtc tcaacctccc aagtaggatt acaagcatgc gccgacgatg 715
cccaraatcc araactttgt ctatcactct ccccaacaac ctagatgtga aaacagaata 775
aacttcaccc agaaaaaaaa aaammacaar aaaaaaaaaa aaaaaaaaaa aaaaaaaaaam 835
aaaaaaaaaa rrraaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 881

<210> 67
<211> 524
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 173..487

<220>
<221> sig_peptide
<222> 173..301
<223> Von Heijne matrix
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      seq AGSLVATLQSVGA/AG

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catttctcgg gccaaagtgg gacccggacg gcctcaccat gatgaaacgg gcagctgctg 120
ctgcagtgagg aggagccctg gcagtggggg ctgtgccgtg gtgctcagtg cc atg ggc 178
                                         Met Gly

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ttc act ggg gca gga atc gcc gcg tcc tcc ata gca gcc aag atg atg      226
Phe Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met
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tcc gca gca gcc att gcc aac ggg ggt ggt gtt tct gcg ggg agc ctg      274
Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ser Ala Gly Ser Leu
-25 -20 -15 -10
gtg gct act ctg cag tcc gtg ggg gca gct gga ctc tcc aca tca tcc      322
Val Ala Thr Leu Gln Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser
-5 1 5
aac atc ctc ctg gcc tct gtt ggg tca gtg ttg ggg gcc tgc ttg ggg      370
Asn Ile Leu Leu Ala Ser Val Gly Ser Val Leu Gly Ala Cys Leu Gly
10 15 20
aat tca cct tct tct tct ctc cca gct gaa ccc gag gct aaa gaa gat      418
Asn Ser Pro Ser Ser Ser Leu Pro Ala Glu Pro Glu Ala Lys Glu Asp
25 30 35
gag gca aga gaa aat gta ccc cca ggt gaa cct cca aaa ccc cca ctc      466
Glu Ala Arg Glu Asn Val Pro Gln Gly Glu Pro Pro Lys Pro Pro Leu
40 45 50 55
aag tca gag aaa cat gag gaa taaaggtcac atgcagatgc aaaaaaaaaa      517
Lys Ser Glu Lys His Glu Glu
60
aaaaaaa      524

<210> 68
<211> 1472
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 210..1082

<220>
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<222> 210..311
<223> Von Heijne matrix
score 10.0571391689271
seq FLCLLSALLLTGEG/KK

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gactcctatg tgacctgttc tttagagcaag acaatcacca tctgaattcc agaagccctg      180
ttcatggttg gggatatttt ctgcactgac atg gaa tca gaa aga agc aaa agg      233
Met Glu Ser Glu Arg Ser Lys Arg
-30
atg gga aat gcc tgc att ccc ctg aaa aga att gct tat ttc cta tgt      281
Met Gly Asn Ala Cys Ile Pro Leu Lys Arg Ile Ala Tyr Phe Leu Cys
-25 -20 -15
ctc tta tct gcg ctt ttg ctg act gag ggg aag aaa cca gcg aag cca      329
Leu Leu Ser Ala Leu Leu Leu Thr Glu Gly Lys Lys Pro Ala Lys Pro
-10 -5 1 5
aaa tgc cct gcc gtg tgt act tgt acc aaa gat aat gct tta tgt gag      377
Lys Cys Pro Ala Val Cys Thr Cys Thr Lys Asp Asn Ala Leu Cys Glu
10 15 20
aat gcc aga tcc att cca cgc acc gtt cct cct gat gtt atc tca tta      425
Asn Ala Arg Ser Ile Pro Arg Thr Val Pro Pro Asp Val Ile Ser Leu
25 30 35

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tcc ttt gtg aga tct gtt ttt act gaa atc tca gaa ggg agt ttt tta	473
Ser Phe Val Arg Ser Val Phe Thr Glu Ile Ser Glu Gly Ser Phe Leu	
40 45 50	
ttc acg cca tcg ctg cag ctc ttg tta ttc aca tcg aac tcc ttt gat	521
Phe Thr Pro Ser Leu Gln Leu Leu Leu Phe Thr Ser Asn Ser Phe Asp	
55 60 65 70	
gtg atc agt gat gat gct ttt att ggt ctt cca cat cta gag tat tta	569
Val Ile Ser Asp Asp Ala Phe Ile Gly Leu Pro His Leu Glu Tyr Leu	
75 80 85	
ttc ata gaa aac aac aac atc aag tca att tca aga cat act ttc cgg	617
Phe Ile Glu Asn Asn Asn Ile Lys Ser Ile Ser Arg His Thr Phe Arg	
90 95 100	
gga cta aag tca tta att cac ttg agc ctt gca aac aac aat ctc cag	665
Gly Leu Lys Ser Leu Ile His Leu Ser Leu Ala Asn Asn Asn Leu Gln	
105 110 115	
aca ctc cca aaa gat att ttc aaa ggc ctg gat tct tta aca aat gtg	713
Thr Leu Pro Lys Asp Ile Phe Lys Gly Leu Asp Ser Leu Thr Asn Val	
120 125 130	
gac ctg agg ggt aat tca ttt aat tgt gac tgt aaa ctg aaa tgg cta	761
Asp Leu Arg Gly Asn Ser Phe Asn Cys Asp Cys Lys Leu Lys Trp Leu	
135 140 145 150	
gtg gaa tgg ctt ggc cac acc aat gca act gtt gaa gac atc tac tgc	809
Val Glu Trp Leu Gly His Thr Asn Ala Thr Val Glu Asp Ile Tyr Cys	
155 160 165	
gaa ggc ccc cca gaa tac aag aag cgc aaa atc aat agt ctc tcc tcg	857
Glu Gly Pro Pro Glu Tyr Lys Lys Arg Lys Ile Asn Ser Leu Ser Ser	
170 175 180	
aag gat ttc gat tgc atc att aca gaa ttt gca aag tct caa gac ctg	905
Lys Asp Phe Asp Cys Ile Ile Thr Glu Phe Ala Lys Ser Gln Asp Leu	
185 190 195	
cct tat caa tca ttg tcc ata gac act ttt tct tat ttg aat gat gag	953
Pro Tyr Gln Ser Leu Ser Ile Asp Thr Phe Ser Tyr Leu Asn Asp Glu	
200 205 210	
tat gta gtc atc gct cag cct ttt act gga aaa tgc att ttc ctt gaa	1001
Tyr Val Val Ile Ala Gln Pro Phe Thr Gly Lys Cys Ile Phe Leu Glu	
215 220 225 230	
tgg gac cat gtg gaa aag acc ttc cgg aat tat gac aac att aca gtt	1049
Trp Asp His Val Glu Lys Thr Phe Arg Asn Tyr Asp Asn Ile Thr Val	
235 240 245	
tta agg gaa ata cac aga ttt aca aac atg tca tagttgacct aagcgcatga	1102
Leu Arg Glu Ile His Arg Phe Thr Asn Met Ser	
250 255	
gacaccaaat tctgtggctg ccatacagaaa ttttctacag tacatgaccc ggatgaactc	1162
aatgcacgat gactcttctt atcacacttg caaatgaatg cctttcaaac attgagactg	1222
ctagaaccaa gcactaccag tatctccatc cttaactgtc cagtcacagt atgtgggaag	1282
ttacctttta taagacaaa tttaattgtg taactgttct ttgcagtga gatgtgtaaa	1342
taagcgttta atggatctgt ttaactcaaa aagaaatatt aatatgtact ttctcattta	1402
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aaaaaaaa	1472

<210> 69
 <211> 1737
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 172..1449

<220>
 <221> sig_peptide
 <222> 172..255
 <223> Von Heijne matrix
 score 5.94825670923113
 seq XVLLEPFVHQVGG/HS

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 gccgctggac tccgctgcct ccccatctc cccgccatct gcgcccggag g atg agc 177
 Met Ser
 cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc gtc ctt 225
 Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu
 -25 -20 -15
 ctg gag ccc ttt gtc cac cag gtc ggg ggg cac tca tgc gtg ctc cgc 273
 Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val Leu Arg
 -10 -5 1 5
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 Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro Gln Tyr
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 Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg Asn Leu
 40 45 50
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 Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val Asp Ile
 55 60 65 70
 gta gat aat tca gac tgt gaa cca aaa agt aag ctg cta agg tgg aca 513
 Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg Trp Thr
 75 80 85
 aca aac aaa aaa cat cat gtc tta gaa aca gaa aag acc cct aag gac 561
 Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro Lys Asp
 90 95 100
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 Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His Lys Leu
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 gaa gaa gaa ttt gag tgg cta aag aaa tct gaa gtc ttg tac tac act 657
 Glu Glu Glu Phe Glu Thr Leu Lys Lys Ser Glu Val Leu Tyr Tyr Thr
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 gta gag aag aag ggg aat ata agt tcc cag ctt aaa cac tat aac cct 705
 Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr Asn Pro
 135 140 145 150
 tgg agc atg aaa tgt cac cag caa cag tta cag aga atg aag gag aat 753
 Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys Glu Asn
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 gca aag cat cgg aac cag tac aaa ttt atc tta ctg gaa aac ctg act 801
 Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn Leu Thr
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 tcc cgc tat gag gtg cct tgt gtc ctt gac ctg aag atg ggc aca cga 849
 Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu Lys Met Gly Thr Arg
 185 190 195
 caa cat ggt gat gat gct tca gag gag aag gca gcc aac cag atc cga 897
 Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala Ala Asn Gln Ile Arg
 200 205 210

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aaa tgt cag cag agc aca tct gca gtc att ggt gtg cgt gtg tgt ggc      945
lys cys gln gln ser thr ser ala val ile gly val arg val cys gly
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atg cag gtg tac caa gca ggc agt ggg cag ctc atg ttc atg aac aag      993
met gln val tyr gln ala gly ser gly gln leu met phe met asn lys
235                               240      245
tac cat gga cgg aag cta tcg atg cag ggc ttc aag gag gca ctt ttc      1041
tyr his gly arg lys leu ser met gln gly phe lys glu ala leu phe
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cag ttc ttc cac aat ggg cgg tac ctg cgc cgt gaa ctc ctg ggc cct      1089
gln phe phe his asn gly arg tyr leu arg arg glu leu leu gly pro
265                               270      275
gtg ctc aag aag ctg act gag ctc aag gca gtg ttg gag cga cag gag      1137
val leu lys lys leu thr glu leu lys ala val leu glu arg gln glu
280                               285      290
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ser tyr arg phe tyr ser ser ser leu leu val ile tyr asp gly lys
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glu arg pro glu val val leu asp ser asp ala glu asp leu glu asp
315                               320      325
ctg tca gag gaa tca gct gat gag tct gct ggt gcc tat gcc tac aaa      1281
leu ser glu glu ser ala asp glu ser ala gly ala tyr ala tyr lys
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ccc atc ggc gcc agc tct gta gat gtg cgc atg atc gac ttt gca cac      1329
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thr thr cys arg leu tyr gly glu asp thr val val his glu gly gln
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gat gct ggc tat atc ttc ggg ctc cag agc ctg ata gac att gtc aca      1425
asp ala gly tyr ile phe gly leu gln ser leu ile asp ile val thr
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gag ata agt gag gag agt ggg gag tga gctt gct agct gctcca gtacttgaga      1479
glu ile ser glu glu ser gly glu
395
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ggtggtcctt gcagcctgga gctgatgtgc agtggcctct gtgagcccca gcctgagcca      1599
gtcccagctg tgctggagt ctttatttat tttaactatt tcttcaacat tccacatttg      1659
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score 3.71064775937629

seq YAAAGVLAGVES/RQ

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Gly Val Leu Ala Gly Val Glu Ser Arg Gln Gly Ser Ile Lys Gly Leu
-5 1 5
gtg tac tcc agc aac ttc cag aac gtg aag cag ctg tac gcg ctg gtg 149
Val Tyr Ser Ser Asn Phe Gln Asn Val Lys Gln Leu Tyr Ala Leu Val
10 15 20
tgc gaa acg cag cgc tac tcc gcc gtg ctg gat gct gtg atc gcc agc 197
Cys Glu Thr Gln Arg Tyr Ser Ala Val Leu Asp Ala Val Ile Ala Ser
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Ala Gly Leu Leu Arg Ala Glu Lys Lys Leu Arg Pro His Leu Ala Lys
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Val Leu Val Tyr Glu Leu Leu Leu Gly Lys Gly Gly Gly Gly
60 65 70
ggc cga tgg aag gct ctg ttg ggc cgc cac cag gcg agg ctc aag gct 341
Gly Arg Trp Lys Ala Leu Leu Gly Arg His Gln Ala Arg Leu Lys Ala
75 80 85
gag ttg gct cgg ctc aag gtt cat cgg ggt gtg agc cgg aat gag gac 389
Glu Leu Ala Arg Leu Lys Val His Arg Gly Val Ser Arg Asn Glu Asp
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Leu Leu Glu Val Gly Ser Arg Pro Gly Pro Ala Ser Gln Leu Pro Arg
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Phe Val Arg Val Asn Thr Leu Lys Thr Cys Ser Asp Asp Val Val Asp
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Tyr Phe Lys Arg Gln Gly Phe Ser Tyr Gln Gly Arg Ala Ser Ser Leu
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Asp Asp Leu Arg Ala Leu Lys Gly Lys His Phe Leu Leu Asp Pro Leu
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Pro Leu Tyr Arg Ala Gly His Leu Ile Leu Gln Asp Arg Ala Ser Cys
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Leu Pro Ala Met Leu Leu Asp Pro Pro Pro Gly Ser His Val Ile Asp
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Lys Asn Gln Gly Lys Ile Phe Ala Phe Asp Leu Asp Ala Lys Arg Leu
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Leu Ala Glu Glu Asp Phe Leu Ala Val Ser Pro Ser Asp Pro Arg Tyr
265 270 275 280

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Val Arg Leu His Ala Leu Ala Gly Phe Gln Gln Arg Ala Leu Cys His
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Asn Pro Gly Ala Phe Arg Leu Ala Pro Ala Leu Pro Ala Trp Pro His
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Arg Gly Leu Ser Thr Phe Pro Gly Ala Glu His Cys Leu Arg Ala Ser
380 385 390
cct gag acc aca ctc agc agt ggc ttc ttc gtt gct gta att gaa cgg 1301
Pro Glu Thr Thr Leu Ser Ser Gly Phe Phe Val Ala Val Ile Glu Arg
395 400 405
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Val Glu Val Pro Ser Ser Ala Ser Gln Ala Lys Ala Ser Ala Pro Glu
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aaaaaaaaaa 1637

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 Gly Val Leu Ala Gly Val Glu Ser Arg Gln Gly Ser Ile Lys Gly Leu
 -5 1 5
 gtg tac tcc agc aac ttc cag aac gtg aag cag ctg tac gcg ctg gtg 149
 Val Tyr Ser Ser Asn Phe Gln Asn Val Lys Gln Leu Tyr Ala Leu Val
 10 15 20
 tgc gaa acg cag cgc tac tcc gcc gtg ctg gat gct gtg atc gcc agc 197
 Cys Glu Thr Gln Arg Tyr Ser Ala Val Leu Asp Ala Val Ile Ala Ser
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 gcc ggc ctc ctc cgt gcg gag aag aag ctg cgg ccg cac ctg gcc aag 245
 Ala Gly Leu Leu Arg Ala Glu Lys Lys Leu Arg Pro His Leu Ala Lys
 45 50 55
 gtg cta gtg tat gag ttg ttg ttg gga aag ggc ttt cga ggg ggt ggg 293
 Val Leu Val Tyr Glu Leu Leu Leu Gly Lys Gly Phe Arg Gly Gly Gly
 60 65 70
 ggc cga tgg aag gct ctg ttg ggc cgg cac cag gcg agg ctc aag gct 341
 Gly Arg Trp Lys Ala Leu Leu Gly Arg His Gln Ala Arg Leu Lys Ala
 75 80 85
 gag ttg gct cgg ctc aag gtt cat cgg ggt gtg agc cgg aat gag gac 389
 Glu Leu Ala Arg Leu Lys Val His Arg Gly Val Ser Arg Asn Glu Asp
 90 95 100
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 Phe Val Arg Val Asn Thr Leu Lys Thr Cys Ser Asp Asp Val Val Asp
 125 130 135
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 Tyr Phe Lys Arg Gln Gly Phe Ser Tyr Gln Gly Arg Ala Ser Ser Leu
 140 145 150
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 Asp Asp Leu Arg Ala Leu Lys Gly Lys His Phe Leu Leu Asp Pro Leu
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 Pro Leu Tyr Arg Ala Gly His Leu Ile Leu Gln Asp Arg Ala Ser Cys
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 Leu Pro Ala Met Leu Leu Asp Pro Pro Gly Ser His Val Ile Asp
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 Lys Asn Gln Gly Lys Ile Phe Ala Phe Asp Leu Asp Ala Lys Arg Leu
 235 240 245
 gca tcc atg gcc acg ctg ctg gcc cgg gct ggc gtc tct tgc tgt gaa 869
 Ala Ser Met Ala Thr Leu Leu Ala Arg Ala Gly Val Ser Cys Cys Glu
 250 255 260
 ctg gct gag gag gac ttc ctg gcg gtc tcc ccc tcg gat cca cgc tac 917
 Leu Ala Glu Glu Asp Phe Leu Ala Val Ser Pro Ser Asp Pro Arg Tyr
 265 270 275 280
 cat gag gtc cac tac atc ctg ctg gat cct tcc tgc agt ggc tcg ggt 965
 His Glu Val His Tyr Ile Leu Leu Asp Pro Ser Cys Ser Gly Ser Gly
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 atg ccg agc aga cag ctg gag gag ccc ggg gca ggc aca cct agc ccg 1013


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Val Arg Leu His Ala Leu Ala Ala Ser Ser Ser Glu Pro Cys Ala Thr
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Arg Ser Leu Ser Leu Pro Cys Ser Gly Ser Ser Thr Pro Arg Ala Pro
      330      335      340
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Phe Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Arg Leu Asn Asp
      -20 -15 -10
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Ala Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Val Arg Pro
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Val Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro
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Gly Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu
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Ile Trp Ala Ala Met Asp	Ser Ile Pro Ala Pro Ser Ser	Gln Gln Gly	
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cac aac ctg act gaa gat gcc aga cat	cct gag agt tgg cag aac aca		494
His Asn Leu Thr Glu Asp Ala Arg	His Pro Glu Ser Trp Gln Asn Thr		
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Gly Gly Tyr Ser Glu Gly Asp Ala Val	Ser Gln Pro Gln Met Ala Leu		
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Leu Pro Gly Ser Arg Glu His Met Ala	Gln Trp Glu Val Arg Val Arg		
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Gln Thr His Val Pro Asn Arg Glu Pro	Val Gln Ala Leu Pro Ser Ser		
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Ala Ser Arg Lys Arg Leu Asp Lys Lys	Arg Ser Val Pro Val Ala Thr		
175	180	185	
gta gaa ctg gaa gaa aag agg ttc aga	act ctg cct tta gtg ccc ccc		782
Val Glu Leu Glu Glu Lys Arg Phe Arg	Thr Leu Pro Leu Val Pro Pro		
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Pro Thr Arg Pro Asp Gln Ser Gly Phe	Thr Arg Gly Arg Arg Leu Gly		
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 Val His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu
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 Tyr Ile Asn Glu Thr His Pro Gly Thr Val Thr Val Leu Asp Leu
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 Phe Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly
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 Phe Arg Glu Ala Val Val Pro Ile Met Ala Lys Ala Pro Gln Gly Val
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 80 85 90
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 Ser Val Met Asp Asp His Asn Val Asp Ser Phe Ile Ser Leu Ser Ser
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 Pro Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro Leu
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 Ile Asn Gly Glu Arg Asp His Pro Asn Ala Thr Val Trp Arg Lys Asn
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 Val Ile Thr Pro Trp Gln Ser Ser Phe Phe Gly Phe Tyr Asp Ala Asn
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 Glu Thr Val Leu Glu Met Glu Glu Gln Leu Val Tyr Leu Arg Asp Ser
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Glu Thr Cys Ile Glu Pro Trp Leu Ser	
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Phe Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly	
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Ser Val Met Asp Asp His Asn Val Asp Ser Phe Ile Ser Leu Ser Ser
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ccc acc tcc atg cgg tct aac ctc tat cgg atc tgc tat agc ccc      585
Pro Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro
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 Met Ala Phe Thr Phe Ala Ala
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 Ser Cys Val Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val
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 cca agg gaa cat cag ttc tac gag acc ctc cct tct gag atg cgc aaa 373
 Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ser Glu Met Arg Lys
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 Phe Thr Pro Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp
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 aag acc cct aag gac tgg gtg cgt cag cac cgt aaa gag gag aaa atg 613
 Lys Thr Pro Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met
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 Lys Ser His Lys Leu Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu
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 130 135 140 145
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gaa ctc ctg ggc cct gtg ctc aag aag ctg act gag ctc aag gca gtg      1141
Glu Leu Leu Gly Pro Val Leu Lys Lys Leu Thr Glu Leu Lys Ala Val
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Ile Tyr Asp Gly Lys Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala
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Glu Asp Leu Glu Asp Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly
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gcc tat gcc tac aaa ccc atc ggc gcc agc tct gta gat gtg cgc atg      1333
Ala Tyr Ala Tyr Lys Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met
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Val His Glu Gly Gln Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu
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ata gac att gtc aca gag ata agt gag gag agt ggg gag tgagcttgct      1478
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Cys																	
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cag	c	g	t	g	g	c										1222	
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ag	g	g	g	t	g	a										1462	
tat	g	t	g	t	c	a										1522	
g	g	g	t	g	g	a										1582	
acc	a	c	c	a	t	c										1642	
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Lys	His	Ala	Phe	Ala	Asp	Gly	Ala	Trp	Asp	Leu	Ser	Phe	Leu	Cys	Ala		
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Leu	Cys	Ser	Phe	Cys	Pro	Ile	Ser	Ala	Ala	Ser	Gly	Arg	Pro	Tyr	Arg		
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Phe	Asp	Ile	Glu	Arg	Lys	Gly	Lys	Ser	Ser	Val	Cys	Pro	Phe	Cys	Tyr		
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Ser Leu Met Val Thr Phe Pro Asp Val Pro Leu Gly Ile Phe Leu Phe																	
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Cys Val Cys Val Ile Ala Ile Gly Val Val Gln Ala Leu Ile Val Gly																	
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aaaccgaaac cagcgctcca aacaattggg acccgggata ttagtccagt gaggtgtgct      60
tgccggtgag cgggcctccc atccctctta aaagagttag gcatttagcc atg cct      116
                                     Met Pro
                                     -40
ccc acc cgg gac cct ttc cag cag cct aca tta gat aac gat gat tcc      164
Pro Thr Arg Asp Pro Phe Gln Gln Pro Thr Leu Asp Asn Asp Asp Ser
      -35                      -30                      -25
tac tta gga gaa ctg cgg gct tcc aag gta ctg tgg ttt ctt gcg cag      212
Tyr Leu Gly Glu Leu Arg Ala Ser Lys Val Leu Trp Phe Leu Ala Gln
      -20                      -15                      -10
att ccc agt agg gtc gcc ggt agt ctt ctt gtc tgt gtg atg agc      260
Ile Pro Ser Arg Val Ala Gly Ser Leu Leu Ser Val Cys Val Met Ser
      -5                      1                      5
aga gat ggt aac ata aag gac tct ggt gaa gac act cag tcg ggt acc      308
Arg Asp Gly Asn Ile Lys Asp Ser Gly Glu Asp Thr Gln Ser Gly Thr

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10          15          20          25
agg gaa gtc tgt ttt ctg cct gcc tcc cta tct cca tat tca agt cgg      356
Arg Glu Val Cys Phe Leu Pro Ala Ser Leu Ser Pro Tyr Ser Ser Arg

          30          35          40
cta acg ttt cag agg cgt ttt tgagcagagg aaagtagagt tctagtctag      407
Leu Thr Phe Gln Arg Arg Phe

          45
aggaacaagg ggctctggca gctcaaatca attaaccaag atccaattcc ctggagaatt      467
tttaaccctt cccactccac ccatcacttg cctggctaac atcagacact ggatcaaccc      527
taaaaaggag tccatccaca gcataccaagg atccatagtg tccctccaca ctgcagccac      587
caatggaggc tactcccgaa agaaagatgg tggcttcttc tccacctagt gttgacagat      647
ccctgaacta attatagtga aacatactgc ggcccccttc cattaataag atttgtgcaa      707
aaaaaaaaaaa aaa

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<210> 82
<211> 1029
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 223..432

<220>
<221> sig_peptide
<222> 223..336
<223> Von Heijne matrix
score 4.17665217008018
seq LVNVLFFFFTPLMT/LV

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<400> 82
gtttttgtat tggaagcagt tgtttggcct tgctgagcaa acgtctatgc cttctccatt      60
acatccaaag gagaatagcc ccatgtgaag aatggaatca gtagatgttt ggtcgctgta      120
ccatatccac tcctaggata caacaagagc aagcccaatt ctcttggtgg tgtgggcagt      180
cggtttgcac cagctaccta tctcagctct ttttgggaagc tt atg tcc tcc cca      234
                               Met Ser Ser Pro
                               -35
caa ctt cca gct ttc tta tgg gac aag ggt aca ctc acc act gcc ata      282
Gln Leu Pro Ala Phe Leu Trp Asp Lys Gly Thr Leu Thr Thr Ala Ile
          -30          -25          -20
tct aat cct gct tgc ctg gta aat gtt ctc ttc ttc ttt aca ccc ctg      330
Ser Asn Pro Ala Cys Leu Val Asn Val Leu Phe Phe Phe Thr Pro Leu
          -15          -10          -5
atg act ctg gtc act cta ctc atc ctg gtc tgg aaa gta acc aaa gac      378
Met Thr Leu Val Thr Leu Leu Ile Leu Val Trp Lys Val Thr Lys Asp
          1          5          10
aaa agc aac aag aac aga gag aca cac cca aga aag gag gca aca tgg      426
Lys Ser Asn Lys Asn Arg Glu Thr His Pro Arg Lys Glu Ala Thr Trp
          15          20          30
ctg cca taagatctg gatctcttgg tggggactcc actgaggtga agacctgatt      482
Leu Pro
gtacaaagaga ggcacggcca ctggagctgt ctcagagccc agagccaggg gagccagagc      542
tgctttatgcc accctgttcc tccattgcca gatgtccccc caggccctcat ttcttctc      602
tgccaccatc cctcttataa tgcactcctc ctgctgttct tttggttctg ccagcttctg      662
agtttgaatg tctttttttt tttttttttt tttttgkgsa tcttcaagac tgaatataga      722
aatggctcttt gatttctgca ctaacagagg aaagaaacaa gtacatggaa aagtaaaaaa      782
tgattacaaa gcctaaattt tcctctataa attgggcatg tgctgactgt ggggatattga      842
aattattggg agctcacagc atctcaagtt atataatgaa gctattctgg aagctcattt      902

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ccagaagatc cttaaaatga aatggctcac tctctgctga attaatctgg agcaagttaa 962
ctcctttttc aaatgaaatc caaattaaag aggcagtttt ttttgaaaaa ccaaaaaaaa 1022
aaaaaaa 1029

<210> 83
<211> 1788
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 769..1272

<220>
<221> sig_peptide
<222> 769..843
<223> Von Heijne matrix
score 5.65786415517206
seq AAHLLVVILPANA/AL

<400> 83
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ttatttgaac tgcagtaaag aaagctggga tgggctcctc tagggatact tccagatccc 120
tgggcgggtg tagccctggc tctcttttaa atggatttgg tttcaaagac gatcatctcc 180
gtcttctcgg atgtcatagt gccactgac atctccagct cctggccacc ctgggctttc 240
tccactttgg cctctatggt ttgcttctcc accgtcttag ccacgatact tacctctctg 300
tcatgtgatg tgacccttgt ttttgaacca ggagtggccc tgaggctcct taaaaaagag 360
ctgatcttac tgggtttcct ttgtaaagct cctgtgctag atgcagattg gtctctcccc 420
agttcctgag ttgttctcga ctctcttttg gtggagctgt ggggtggagct ctgcgcagag 480
gagccatgtc gaggccctct tacgttgctg tacccttttt cttttttgtc atctctcggtg 540
tttttatggc cagatcgcca ccggtgggaa gacgctttct gattctgtgc ccccgctctc 600
ctgcgggtgac tttcacctgc cttgcggtga tgagaacttt tctactggg atgtctgtcc 660
ttcttttctc ttctttcctt gttttcattc cagacttcag cactgggctg ggaaactttc 720
tgggtcccat ctcgttcact catgtagcct tcgctttgca aggtggag atg agg ggt 777

Met Arg Gly
-25

ccc act gct ggt cct tca gtt ctt tct gct gca cac ttg ctg gtc gta 825
Pro Thr Ala Gly Pro Ser Val Leu Ser Ala Ala His Leu Leu Val Val
-20 -15 -10
ata ctg cct gca aac gcc gca ctg aag ctg ctg tct tgg gag aga ctg 873
Ile Leu Pro Ala Asn Ala Ala Leu Lys Leu Leu Ser Trp Glu Arg Leu
-5 1 5 10
gcg gcc ccc gcc atc gag gtg gaa gta cct tcc aag gag gtg ctt gca 921
Ala Ala Pro Ala Ile Glu Val Glu Val Pro Ser Lys Glu Val Leu Ala
15 20 25
gca ccc acc aag gcc aag cta ata ccc tct gag gat atg ttg gca gca 969
Ala Pro Thr Lys Ala Lys Leu Ile Pro Ser Glu Asp Met Leu Ala Ala
30 35 40
cct gcc atg gac ttg ctg gat tca ttt tct cct gga ttt ttg ata gct 1017
Pro Ala Met Asp Leu Leu Asp Ser Phe Ser Pro Gly Phe Leu Ile Ala
45 50 55
gct ccc gcc agc gct gtg atc act tgg cct ggg cct gca gat ttg gtt 1065
Ala Pro Ala Ser Ala Val Ile Thr Trp Pro Gly Pro Ala Asp Leu Val
60 65 70
gtt gct atg ctg ata gca cct gtt gca gga ctg att gct gcc cct gct 1113
Val Ala Met Leu Ile Ala Pro Val Ala Gly Leu Ile Ala Ala Pro Ala
75 80 85 90
att gcc aca tct gtt cta ggt cct gtt gct gtt cct gcc act gcc atg 1161

Ile Ala Thr Ser Val Leu Gly Pro Val Ala Val Pro Ala Thr Ala Met
95 100 105
cca cct gct gtc ctt gct gct cct cct tca gca gcc cct gga gtg ctc 1209
Pro Pro Ala Val Leu Ala Ala Pro Pro Ser Ala Ala Pro Gly Val Leu
110 115 120
gtg gat gga gaa gcc gca cta gcc gtt cgg tgg gag gca tgt tgg att 1257
Val Asp Gly Glu Ala Ala Leu Ala Val Pro Trp Glu Ala Cys Trp Ile
125 130 135
ccc tct ccc cca gca taagcagaag aggtggctgc agatacatca caaggttgt 1312
Pro Ser Pro Pro Ala
140
agagcccagt ctactctga tccctctctc tgtggagctc tgcagcctat accaagggga 1372
agagaaacag atgagattga gatgactgaa agggagatca gaactttcta ctctctctt 1432
atcctggagt taattcaagg gcttataatt agaagaacct gggtcgggtg tggtggtctc 1492
cgctgtaat cccaacactt tgggaggcca agggaggcag atcgcttgag gccaggagtt 1552
caagaccagc cttgccaaaca tagcaaaacc cgcactctac taaaaataca aaaaattagc 1612
tggacaggat ggcgcatgcc tgtaatccca gctactcagt aggtctgaggt agggagtatcg 1672
cttgaactcg gatggcggag gctgcagtga gccaaagactg cgccactcca ctgcactcca 1732
gctcgggcaa cagagtgaga cactgtttaa aaaaaagaaa gaaaaaaaaa aaaaaa 1788

<210> 84
<211> 805
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 30..527

<220>
<221> sig_peptide
<222> 30..74
<223> Von Heijne matrix
score 6.88924532952647
seq PLLIICLLPAIEG/KN

<400> 84
actggggcac agtaggagga acccagaag atg ctg cct ctc ctg atc atc tgt 53
Met Leu Pro Leu Leu Ile Ile Cys
-15 -10
ctc ctg cct gcc att gaa ggg aag aac tgc ctc cgc tgc tgg cca gaa 101
Leu Leu Pro Ala Ile Glu Gly Lys Asn Cys Leu Arg Cys Trp Pro Glu
-5 1 5
ctg tct gcc ttg ata gac tat gac ctg cag atc ctc tgg gtg acc cca 149
Leu Ser Ala Leu Ile Asp Tyr Asp Leu Gln Ile Leu Trp Val Thr Pro
10 15 20 25
ggg cca ccc aca gaa ctt tct caa aat cgt gac cat ttg gaa gaa gaa 197
Gly Pro Pro Thr Glu Leu Ser Gln Asn Arg Asp His Leu Glu Glu Glu
30 35 40
aca gcc aaa ttc ttc act caa gta cac caa gcc att aaa acg tta cga 245
Thr Ala Lys Phe Phe Thr Gln Val His Gln Ala Ile Lys Thr Leu Arg
45 50 55
gat gat aaa aca gta ctt ctg gaa gag atc tac acg cac aag aat ctc 293
Asp Asp Lys Thr Val Leu Leu Glu Glu Ile Tyr Thr His Lys Asn Leu
60 65 70
ttt act gag agg ctg aat aag ata tct gat ggg ctg aag gag aag gac 341
Phe Thr Glu Arg Leu Asn Lys Ile Ser Asp Gly Leu Lys Glu Lys Asp
75 80 85


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ata cag tcc aca ctg aag gtc acc agc tgt gct gac tgc agg act cac      389
Ile Gln Ser Thr Leu Lys Val Thr Ser Cys Ala Asp Cys Arg Thr His
90          95          100          105
ttc ctc tcc tgc aat gac ccc act ttc tgc cca gcc agg aac cgg cgg      437
Phe Leu Ser Cys Asn Asp Pro Thr Phe Cys Pro Ala Arg Asn Arg Arg
          110          115          120
acc tcc ctg tgg gct gtg agt ctc agc agt gct cta ctc ctg gcc ata      485
Thr Ser Leu Trp Ala Val Ser Leu Ser Ser Ala Leu Leu Leu Ala Ile
          125          130          135
gct gga gat gtt tct ttt act ggc aaa gga aga agg agg cag      527
Ala Gly Asp Val Ser Phe Thr Gly Lys Gly Arg Arg Arg Gln
          140          145          150
taaagcagga acagggcagc ccgcatgtct tccagaagtg aacagaggcc gcagctacca      587
ccgtcacaaa gtteactcat ctctgggtccc cggtgacccc atccccccat accctccatc      647
ctgggtcctg gggccccc aaa gctctgaggg ctaggagact gcgctgtctc gtggtttgcc      707
tactcctaca cctttgtaaa gagtctcttc attaaaaacc ctcttcataa aaaaaaaaaa      767
aaaaaaaaaa aaaaaaaaaa aataaaaaaa aaaaaaaa      805

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<210> 85
<211> 814
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 39..506

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<220>
<221> sig_peptide
<222> 39..83
<223> Von Heijne matrix
      score 5.91494342964539
      seq ILMLTFIICGLT/RV

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<400> 85
attcctcagg acacagagct tcctctctccc caggagcc atg aat atc ctg atg ctg      56
Met Asn Ile Leu Met Leu
          -15          -10
acc ttc att atc tgt ggg ttg cta act cgg gtg acc aaa ggt agc ttt      104
Thr Phe Ile Ile Cys Gly Leu Leu Thr Arg Val Thr Lys Gly Ser Phe
          -5          1          5
gaa ccc caa aaa tgt tgg aag aat aat gta gga cat tgc aga aga cga      152
Glu Pro Gln Lys Cys Trp Lys Asn Asn Val Gly His Cys Arg Arg Arg
          10          15          20
tgt tta gat act gaa agg tac ata ctt ctt tgt agg aac aag cta tca      200
Cys Leu Asp Thr Glu Arg Tyr Ile Leu Leu Cys Arg Asn Lys Leu Ser
          25          30          35
tgc tgc att tct ata ata tca cat gaa tat act cga cga cca gca ttt      248
Cys Cys Ile Ser Ile Ile Ser His Glu Tyr Thr Arg Arg Pro Ala Phe
          40          45          50          55
cct gtg att cac cta gag gat ata aca ttg gat tat agt gat gtg gac      296
Pro Val Ile His Leu Glu Asp Ile Thr Leu Asp Tyr Ser Asp Val Asp
          60          65          70
tct ttt act ggt tcc cca gta tct atg ttg aat gat ctg ata aca ttt      344
Ser Phe Thr Gly Ser Pro Val Ser Met Leu Asn Asp Leu Ile Thr Phe
          75          80          85
gac aca act aaa ttt gga gaa acc atg aca cct gag acc aat act cct      392
Asp Thr Thr Lys Phe Gly Glu Thr Met Thr Pro Glu Thr Asn Thr Pro

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90 95 100
 gag act act atg cca cca tcc gag gcc act act ccc gag act act atg 440
 Glu Thr Thr Met Pro Pro Ser Glu Ala Thr Thr Pro Glu Thr Thr Met
 105 110 115
 cca cca tct gag act gct act tcc gag act atg cca cca cct tct cag 488
 Pro Pro Ser Glu Thr Ala Thr Ser Glu Thr Met Pro Pro Ser Gln
 120 125 130 135
 aca gct ctt act cat aat taattaacat ttacttctgg tatggaacaa 536
 Thr Ala Leu Thr His Asn

140
 ctagaaatcac tgctggaaat aatatccaaa gagctgatto taccaatcca atttcaccag 596
 gaaaattcca tcagggattg gatgaccatg gggatggaca taattgctac taccaacaca 656
 acagccaaga gagttgcctt acaattagaa atgtgtagac agaaatgtat agaagataca 716
 aggattctct taattggact taaattcttt atctgtcttc ctccgatgta ctcaaatata 776
 tgagctaatt tttgtcttaa gtgaaaaaaa aaaaaaaa 814

<210> 86
 <211> 598
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 115..429

<220>
 <221> sig_peptide
 <222> 115..210
 <223> Von Heijne matrix
 score 8.2583062681354
 seq LVAAMVLLSVVFC/LY

<400> 86
 attctaccag ctctggctga gcttgagctt ccaaaagtga gctgagctgt tcaaccttgg 60
 atcttaatta ctctagcag ggataattag gtccctcttt ctcaagattac aggc atg 117
 Met
 gca aag atg ttt gat ctc agg acg aag atc atg atc ggc atc gaa agc 165
 Ala Lys Met Phe Asp Leu Arg Thr Lys Ile Met Ile Gly Ile Glu Ser
 -30 -25 -20
 agc tta ctg gtt gcc gcg atg gtg ctc cta agt gtt gtg ttc tgt ctt 213
 Ser Leu Leu Val Ala Ala Met Val Leu Leu Ser Val Val Phe Cys Leu
 -15 -10 -5 1
 tac ttc aaa gta gct aag gca cta aaa gct gca aag gac cct gat gct 261
 Tyr Phe Lys Val Ala Lys Ala Leu Lys Ala Ala Lys Asp Pro Asp Ala
 5 10 15
 gtg gct gta aaa aat cac aac cca aag gtg tgt tgg gcc acg aac 309
 Val Ala Val Lys Asn His Asn Pro Asp Lys Val Cys Trp Ala Thr Asn
 20 25 30
 agc cag gcc aaa gcc acc acc atg gag tct tgt cca tct ctc cag tgc 357
 Ser Gln Ala Lys Ala Thr Thr Met Glu Ser Cys Pro Ser Leu Gln Cys
 35 40 45
 tgt gaa ggt tgt aga atg cat gcc agt tct gat tcc ctg cca cct tgc 405
 Cys Glu Gly Cys Arg Met His Ala Ser Ser Asp Ser Leu Pro Pro Cys
 50 55 60 65
 tgt tgt gac ata aat gag ggc ctc tgacttggga aagctgggca caaaaatctt 459
 Cys Cys Asp Ile Asn Glu Gly Leu
 70
 catgagcaat atttcttct taatagaatg ttttattatt caagtcaagt tctagagtgt 519

ttacatacta ttatataatg tacagtggtta ttttctgtac ttctgaataa atgtgcaata 579
 ttgcaaaaaa aaaaaaaaaa 598

<210> 87
 <211> 699
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 332..574

<220>
 <221> sig_peptide
 <222> 332..412
 <223> Von Heijne matrix
 score 7.96491294552426
 seq ILGLFCCLPLAIP/AV

<400> 87
 aatccccgtg ggttggtgat caaggaagag catagtgcca gacctaggtg cccctcctggg 60
 aatgttccag gagggcagga gtaggaggag gagtggttaga gtagagggga aatgatgaga 120
 gcagaaaagga gagtctcgct ctgtcaccca ggctggagtg cagtggcagg atcttggttc 180
 acttcaacct ccacctcccg agttctgcct cagcctccca agtagctggg attacaggtc 240
 cagtcaactcc acgcttgtag agtccaatta acaagagcaa gttctggtag aaagaaggtc 300
 actttattcc agagctcagg tgtttgaact g atg tct gat gag gat gaa tcc 352
 Met Ser Asp Glu Asp Glu Ser
 -25
 agc gac tac ctc tgc ctg tcc atc ctg ggc ctc ttc tgt tgc ctt ccc 400
 Ser Asp Tyr Leu Cys Leu Ser Ile Leu Gly Leu Phe Cys Leu Pro
 -20 -15 -10 -5
 cta gcc atc cca gcc gtg atc ttt tct tgc ctg aca aag aac tac aat 448
 Leu Ala Ile Pro Ala Val Ile Phe Ser Cys Leu Thr Lys Asn Tyr Asn
 1 5 10
 aaa tcc agt gac tat gag ctg gca gcc aag acc tcc aaa caa gcc tac 496
 Lys Ser Ser Asp Tyr Glu Leu Ala Ala Lys Thr Ser Lys Gln Ala Tyr
 15 20 25
 tac tgg gcc atc gcg agc atc act gtg gga atc tta ggt acc atc ttg 544
 Tyr Trp Ala Ile Ala Ser Ile Thr Val Gly Ile Leu Gly Thr Ile Leu
 30 35 40
 tac acc tac ctg ata tac tta ctt aga ttg taaactgctt cccagctctt 594
 Tyr Thr Tyr Leu Ile Tyr Leu Leu Arg Leu
 45 50
 gaacaaacca ccaaataatc accacagtgc aatttaaaaa aaaaaaaaaa aaaaaaaaaa 654
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gaaaaaaaaa aaaaa 699

<210> 88
 <211> 905
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 133..417

<220>
 <221> sig_peptide
 <222> 133..213

<223> Von Heijne matrix
score 11.106948594338
seq LTSLILVTLISA/FV

<400> 88
atttccaggg agctgaggag ctgagggcag agctagcttt tgggtattttt ggatgttatt 60
gccagtttcc tcccagggcc attgttacca cctgatcatt tgagtttttag tttctctagc 120
agatgctgac ta atg act gac cag gat cga atc atc aat tta gtt gtt ggc 171
Met Thr Asp Gln Asp Arg Ile Ile Asn Leu Val Val Gly
-25 -20 -15
agc tta aca tcc tta ttg att cta gta acg ctg ata agt gct ttt gtt 219
Ser Leu Thr Ser Leu Leu Ile Leu Val Thr Leu Ile Ser Ala Phe Val
-10 -5 1
ttc cct caa cta cct cca aaa ccg ttg aat ata ttc ttt gct gtc tgc 267
Phe Pro Gln Leu Pro Pro Lys Pro Leu Asn Ile Phe Phe Ala Val Cys
5 10 15
atc tct ttg agt agt att act gcc tgc ata atc tac tgg tat cga caa 315
Ile Ser Leu Ser Ser Ile Thr Ala Cys Ile Ile Tyr Trp Tyr Arg Gln
20 25 30
gga gac tta gaa ccg aaa ttt aga aag cta att tac tat atc ata ttt 363
Gly Asp Leu Glu Pro Lys Phe Arg Lys Leu Ile Tyr Tyr Ile Ile Phe
35 40 45 50
tct atc atc atg ttg tgt ata tgt gca aac ctg tac ttc cat gat gtg 411
Ser Ile Ile Met Leu Cys Ile Cys Ala Asn Leu Tyr Phe His Asp Val
55 60 65
gga agg tgaggctgcc aaggagaagt acttaccagg actcttcaaa atgatacatt 467
Gly Arg
aggacagtga gtaattttttg gataaggat gctgaagaat ctctctgcaga agtctgatac 527
atgattttca tgtaatttgt aaatgttaat tccctcttgc aaggagagaca tatcctagat 587
cactttgtctt tttctttaag gagctgatgt tgcacctaaa cattccaacc cttaaagcta 647
aaacagcaca aaaaaatttc acttttgaaa tgaaattttt ataattgtat ggcaaaaggc 707
tatgtaaaaa caaatcttgc atctttaagac aaatattctt ttatttctgt taaactgaat 767
atacaattgt tccttaggca accaactttt gcttataact acaattttaat ttcacgttga 827
caaaacacag tgaaaagaca actttgtgaa gatctaatta caataataaa taaaaataat 887
tacaaaaaaa aaaaaaaa 905

<210> 89
<211> 514
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 113..364

<220>
<221> sig_peptide
<222> 113..172
<223> Von Heijne matrix
score 4.37180298395146
seq SLLLSLPPHQGLT/FS

<400> 89
ttttttacat ggtgttccca cagctgggag gacacccaca tgggtcggcgt gcaggatatt 60
tcgctggacc ctagaaaagc caccacgacc tgtgggcat gatgctaccc ca atg gct 118
Met Ala
-20
gct gct gct gtt cct tct ctt ctt ctt tct ctt cct cct cac cag ggg 166

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Ala Ala Ala Val Pro Ser Leu Leu Leu Ser Leu Pro Pro His Gln Gly
      -15          -10          -5
ctc act ttc tcc aac aaa ata caa cct ttt gga gct caa gga gtc ttg      214
Leu Thr Phe Ser Asn Lys Ile Gln Pro Phe Gly Ala Gln Gly Val Leu
      1          5          10
cat ccg gaa cca gga ctg cga gac tgg ctg ctg cca acg tgc tcc aga      262
His Pro Glu Pro Gly Leu Arg Asp Trp Leu Leu Pro Thr Cys Ser Arg
      15          20          25          30
caa ttg cga gtc gca ctg ccg gag aag ggg tcc gag ggc agt ctg tgt      310
Gln Leu Arg Val Ala Leu Pro Glu Lys Gly Ser Glu Gly Ser Leu Cys
      35          40          45
caa acg cag ctg cca gct act cca tgc ttc ctg cct tcg aat acg gtg      358
Gln Thr Gln Leu Pro Ala Thr Pro Cys Phe Leu Pro Ser Asn Thr Val
      50          55          60
aga acg tgaagtcatg agctgctgct aaggcatgtg gcaaccttga agagaaggtc      414
Arg Thr
aagagctacc agccaccaaa agaatgccag cacttctctgt gtctttgctt tggattcatg      474
agaaatatac gttcctattt gcttcaaaaa aaaaaaaaaa      514

<210> 90
<211> 518
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 9..380

<220>
<221> sig_peptide
<222> 9..104
<223> Von Heijne matrix
      score 4.73369226787171
      seq AVFAVLFFVFLFA/ML

<400> 90
acatccta atg gtg gtg gtt gaa cca gga gcc agt tta ttc cca aat ggt      50
      Met Val Val Val Glu Pro Gly Ala Ser Leu Phe Pro Asn Gly
      -30          -25          -20
gtt cct tgg ctg tat gct gtg ttt gct gtg ctt ttt gta ttt ttt ctt      98
Val Pro Trp Leu Tyr Ala Val Phe Ala Val Leu Phe Val Phe Phe Leu
      -15          -10          -5
ttt gcc atg tta tct ccc ttt tta ctt gag ata gac cag cac ata aag      146
Phe Ala Met Leu Ser Pro Phe Leu Met Asp Gln His Ile Lys
      1          5          10
aaa ttc ttg atc aga tgc agg tat tct ctg cat aac act gtg cat aag      194
Lys Phe Leu Ile Arg Cys Arg Tyr Ser Leu His Asn Thr Val His Lys
      15          20          25          30
gac aaa aaa aac agt gag ata aag atg gac cat cta gaa agg cca ggc      242
Asp Lys Lys Asn Ser Glu Ile Lys Met Asp His Leu Glu Arg Pro Gly
      35          40          45
tgt cca ctg gag tca cca agg aga gga gtt ctg gga ggg aag aaa aat      290
Cys Pro Leu Glu Ser Pro Arg Arg Gly Val Leu Gly Gly Lys Lys Asn
      50          55          60
ggg atg gga aac gac cca tta cta ttt gtg aaa gtg aca aaa gaa ccc      338
Gly Met Gly Asn Asp Pro Leu Leu Phe Val Lys Val Thr Lys Glu Pro
      65          70          75
agg gat tct gag gct gaa atc tat acc cct ggg cct tca gtt      380

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 <222> 185..253
 <223> Von Heijne matrix
 score 9.49395175807817
 seq SLLFICFFGESFC/IC

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 tagctcctgg tattttctgc ttcccttctg aggggaattta gttattttat tttattattt 120
 agctaattta gctatttttaa aatagctaaa ttttagctac ttttttttca attgacaaag 180
 aagg atg tct aat caa aga cta ccg ctg att ttt tct ctg ttg ttt atc 229
 Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile
 -20 -15 -10
 tgc ttc ttc ggg gag agt ttc tgc att tgt gat gga act gtc tgg aca 277
 Cys Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr
 -5 1 5
 aag gtt gga tgg gag att ctt cca gaa gaa gta cat tat tgg aaa ggt 325
 Lys Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Gly
 10 15 20
 tgt tta tat ctc att tat aat tta tta caa gct gtc ttc ttc gtc tta 373
 Cys Leu Tyr Leu Ile Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu
 25 30 35 40
 ttt gtt ttg tct gtg cat tac ctg tgg aag aaa tgg aag aaa cac caa 421
 Phe Val Leu Ser Val His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln
 45 50 55
 aaa aag ctg aaa aag caa gcc tcc tta gaa aaa cct ggt aat gat cta 469
 Lys Lys Leu Lys Lys Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu
 60 65 70
 gaa agc cca ttg atc aac aac att gac caa aca ctc cac aga gtg gca 517
 Glu Ser Pro Leu Ile Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala
 75 80 85
 acc aca gca tca gtg ata tac aag atc tgg gag cac agg tct cac cat 565
 Thr Thr Ala Ser Val Ile Tyr Lys Ile Trp Glu His Arg Ser His His
 90 95 100
 cct tcc tct aag aaa att aag cac tgc aaa tta aag aag aag agt aaa 613
 Pro Ser Ser Lys Lys Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys
 105 110 115 120
 gaa gaa gga gcc aga aga tac taaataaatg catatgcaaa tgtagcttag 664
 Glu Glu Gly Ala Arg Arg Tyr
 125
 tcaattatag atatcacaaa agaaatctat catctaagga ttaaaaaattg ttctttggaa 724
 aaaaaaaaaaaa aaa 737

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 <213> Homo sapiens

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 <222> 53..646

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 <222> 53..91
 <223> Von Heijne matrix
 score 4.95353272042967

seq MLLGRLTSQLLRA/VP

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Leu Gly Arg Leu Thr Ser Gln Leu Leu Arg Ala Val Pro Trp Ala Gly
-10
ggc cgc ccg cct tgg ccc gtc tct gga gtg ctg ggc agc cgg gtc tgc      154
Gly Arg Pro Pro Trp Pro Val Ser Gly Val Leu Gly Ser Arg Val Cys
10
ggg ccc ctt tac agc aca tcg ccg gcc ggc cca ggt agg gcg gcc tct      202
Gly Pro Leu Tyr Ser Thr Ser Pro Ala Gly Pro Gly Arg Ala Ala Ser
25
ctc cct cgc aag ggg gcc cag ctg gag ctg gag gag atg gtc ccc agg      250
Leu Pro Arg Lys Gly Ala Gln Leu Glu Leu Glu Met Val Pro Arg
40
aag atg tcc gtc agc ccc ctg gag agc tgg ctc acg gcc cgc tgc ttc      298
Lys Met Ser Val Ser Pro Leu Glu Ser Trp Leu Thr Ala Arg Cys Phe
55
ctg ccc aga ctg gat acc ggg acc gca ggg act gtg gct cca ccg caa      346
Leu Pro Arg Leu Asp Thr Gly Thr Ala Gly Thr Val Ala Pro Pro Gln
70
tcc tac cag tgt ccg ccc agc cag ata ggg gaa ggg gcc gag cag ggg      394
Ser Tyr Gln Cys Pro Pro Ser Gln Ile Gly Glu Gly Ala Glu Gln Gly
90
gat gaa ggc gtc gcg gat gcg cct caa att cag tgc aaa aac gtg ctg      442
Asp Glu Gly Val Ala Asp Ala Pro Gln Ile Gln Cys Lys Asn Val Leu
105
aag atc cgc cgg cgg aag atg aac cac cac aag tac cgg aag ctg gtg      490
Lys Ile Arg Arg Arg Lys Met Asn His His Lys Tyr Arg Lys Leu Val
120
aag aag acg cgg ttc ctg cgg agg aag gtc cag gag gga cgc ctg aga      538
Lys Lys Thr Arg Phe Leu Arg Arg Lys Val Gln Glu Gly Arg Leu Arg
135
cgc aag cag atc aag ttc gag aaa gac ctg agg cgc atc tgg ctg aag      586
Arg Lys Gln Ile Lys Phe Glu Lys Asp Leu Arg Arg Ile Trp Leu Lys
150
gcg ggg cta aag gaa gcc ccc ccc gaa ggc tgg cag acc ccc aag atc tac      634
Ala Gly Leu Lys Glu Ala Pro Glu Gly Trp Gln Thr Pro Lys Ile Tyr
170
ctg cgg ggc aaa tgagtctggc gcgcaccttc ccgccgttg ctgctgtgat      686
Leu Arg Gly Lys
185
ccgtagtaat aaattctcag aggacccaaa aaaaaaaaaa aa      728

<210> 94
<211> 582
<212> DNA
<213> Homo sapiens

<220>
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<222> 247..510

<220>
<221> sig_peptide
<222> 247..318

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<223> Von Heijne matrix
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seq FCALEVVLPSDC/RS

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gggaacattc ttttaagcgtg tgcgtcttggc acgagacata aggcagttca acatcaagcc 120
cttgccctga acagtttcaa atggccaagaa ctggcgaatt actactttgg tttcaatggg 180
tggtccaaaa ggatcatcaa gcttcaggag ctttctgacc ttgaagaaag ggaaatgaa 240
gatagc atg gtg cca ctt ccg aag caa agc ctg aag ttc ttc tgt gct 288
Met Val Pro Leu Pro Lys Gln Ser Leu Lys Phe Phe Cys Ala
-20 -15
tta gaa gtg gtg ttg cca tcc tgt gat tgc agg agt cct ggc att ggc 336
Leu Glu Val Val Leu Pro Ser Cys Asp Cys Arg Ser Pro Gly Ile Gly
-10 -5 1 5
ttg gtg gag gag cct atg gat aag gtg gag gaa gga cca tta tca ttc 384
Leu Val Glu Glu Pro Met Asp Lys Val Glu Glu Gly Pro Leu Ser Phe
10 15 20
ctt atg aaa agg aag aca gcc cag aag ctt gct att cag aag gct ttg 432
Leu Met Lys Arg Lys Thr Ala Gln Lys Leu Ala Ile Gln Lys Ala Leu
25 30 35
tca gat gca ttc cag aaa ctg ttg att gtt gtt cta ggt aag act gtc 480
Ser Asp Ala Phe Gln Lys Leu Leu Ile Val Val Leu Gly Lys Thr Val
40 45 50
ttg atc atc ctt gaa gta ctt cag ttt cag taagcaata aactcatttt 530
Leu Ile Ile Leu Glu Val Leu Gln Phe Gln
55 60
gaaaagttaa ttgaataaaa atattgatat ctaaagcaaa aaaaaaaaaa aa 582

<210> 95
<211> 1913
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 143..592

<220>
<221> sig_peptide
<222> 143..277
<223> Von Heijne matrix
score 5.94057630118762
seq VLVDLAILGQAYA/FA

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ggacatgagg ccagaccttg tgaccttggt ggcaaggggc agtggtctga tgtgaggtcc 120
cagagacggc aggttcatca ag atg gtg ctc atg tgg acc agt ggt gac gcc 172
Met Val Leu Met Trp Thr Ser Gly Asp Ala
-45 -40
ttc aag acg gcc tac ttc ctg ctg aag ggt gcc cct ctg cag ttc tcc 220
Phe Lys Thr Ala Tyr Phe Leu Leu Lys Gly Ala Pro Leu Gln Phe Ser
-35 -30 -25 -20
gtg tgc ggc ctg ctg cag gtg ctg gtg gac ctg gcc atc ctg ggg cag 268
Val Cys Gly Leu Leu Gln Val Leu Val Asp Leu Ala Ile Leu Gly Gln
-15 -10 -5
gcc tac gcc ttc gcc cca ccc cca gaa gcc ggc gcc cca cgc cgt gca 316

Ala Tyr Ala Phe Ala Pro Pro Pro Glu Ala Gly Ala Pro Arg Arg Ala	
1 5 10	
ccc cac tgg cac caa ggc cct ctg aca gtg ggg agg acg agg atg tgg	364
Pro His Trp His Gln Gly Pro Leu Thr Val Gly Arg Thr Arg Met Trp	
15 20 25	
gac cgc cag ccg cgg gca ctg gtg ggc cct gac ctc ccc gcg ggg agg	412
Asp Arg Gln Pro Arg Ala Leu Val Gly Pro Asp Leu Pro Ala Gly Arg	
30 35 40 45	
gtg ggt gcc gtg gcc cct gca ggt gtg gca gag atg ggg cac ggg cat	460
Val Gly Ala Val Ala Pro Ala Gly Val Ala Glu Met Gly His Gly His	
50 55 60	
tgg ggt ctc cat cag cct ctg tgg ggt gtc tca ggg tgg gca gtg ggg	508
Trp Gly Leu His Gln Pro Leu Trp Gly Val Ser Gly Trp Ala Val Gly	
65 70 75	
gtg ggg ctg gga cgc tgt ttg tgc tca gcg ggg aca gcc agg gtt gat	556
Val Gly Leu Gly Arg Cys Leu Cys Ser Ala Gly Thr Ala Arg Val Asp	
80 85 90	
ctg gcc ccg agg gtt ttg gat gtt ttt agg atg aca taaaaagcaa	602
Leu Ala Pro Arg Val Leu Asp Val Phe Arg Met Thr	
95 100 105	
gtgtttttccc catttctctct tatgaaacac cgtctgagcc caagggtacac attggggcggc	662
ctgcaggaac ctgctccagg tggacacacg gccagcagc cgcgaaacctt gaagctgggg	722
tgaccgcagg agacctgtga aggcctgtga gcggagccct cgaccocgtg acacctgggc	782
cagacaccct gcttggaactg ggggtggcctc tgctaccagg ggggtctggca cgggggaggg	842
ctgggggcttt ctctgcctgg tacacacgga aaggcggctg tgcggacgca gggtcaccgt	902
gctccggggtt ttctgacagt cgtgtgttcc tgggcctttg gagtggctgc gaagcctgaa	962
cgcccttgttg atcccgctgtg tccagcccgg ctgagcatcg ccagggtcag ctcatgctgc	1022
tcttgtcagc ctctggttct cctcgagtcc ttggggacgt ggcagatgcc agcgaccatc	1082
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ccctgggctt ttggcctgaa gcaaatctct gagtgggggg tactggggcc tgcgcgatcc	1382
tgtcctgtcc actgcccacc cccgtgtgct ggctccctca cttctggctg cagtgggagc	1442
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gagttttctt cggaaaacct cttgaatgtc tgagtgaagg tctctcttag ccttttggcc	1742
tgtgagatgc tttgaaaatt tttatttttt taagatgaag caagatgtct gtacgcggtaa	1802
ttgcctcaca ttaaaactgtc gccgactgca ggccgagtga ctgctgaaatg taccctgtgt	1862
ggcgacttgg aatcaataaa ccatttgttg atctcaaaaa aaaaaaaaaa a	1913

<210> 96
 <211> 670
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 33..458

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 <222> 33..89
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Met Ala Thr Ala Ser Pro Ser
-15
gtc ttt Cta ctc atg gtc aac ggg cag gtg gag agc gcc cag ttt cca 101
Val Phe Leu Leu Met Val Asn Gly Gln Val Glu Ser Ala Gln Phe Pro
-10 -5 1
gag tat gat gac ttc tac tgc aag tac tgc ttt gtg tac ggc cag gac 149
Glu Tyr Asp Asp Phe Tyr Cys Lys Tyr Cys Phe Val Tyr Gly Gln Asp
5 10 15 20
tgg gcc ccc aca gcg ggt ctg gag gag ggg atc tca cag atc aca tcc 197
Trp Ala Pro Thr Ala Gly Leu Glu Glu Gly Ile Ser Gln Ile Thr Ser
25 30 35
aag agc caa gat gtg cgg caa gca ctg gtg tgg aac ttc ccc att gat 245
Lys Ser Gln Asp Val Arg Gln Ala Leu Val Trp Asn Phe Pro Ile Asp
40 45 50
gtc acc ttt aaa agc acc aac ccc tac ggc tgg cca cag atc gtg ctc 293
Val Thr Phe Lys Ser Thr Asn Pro Tyr Gly Trp Pro Gln Ile Val Leu
55 60 65
agc gtg tat gga cca gat gtg ttc ggg aac gat gtg gtt cga ggc tat 341
Ser Val Tyr Gly Pro Asp Val Phe Gly Asn Asp Val Val Arg Gly Tyr
70 75 80
ggg gcc gtg cac gtg ccc ttc tca cct ggc cgg cac aaa agg acc atc 389
Gly Ala Val His Val Pro Phe Ser Pro Gly Arg His Lys Arg Thr Ile
85 90 95 100
ccc atg ttt gtc cca gaa tct acg tct aaa ctg cag aag ttt aca aga 437
Pro Met Phe Val Pro Glu Ser Thr Ser Lys Leu Gln Lys Phe Thr Arg
105 110 115
tct gca agc tgc tcc acc cac tggagacaaa tagaacagg tccctggga 488
Ser Ala Ser Cys Ser Thr His
120
gtgctgagtc acggggtcc cttcagccct gttccagcag cagaaggccg ggcgatttta 548
ccctgtgcc tgtgaaaaat ctttgtgtct gagggggcag aggaaaaact cttgtcagat 608
gggaaaaaatg ctcatgacat aatgtgacat taaaagggtgg gaaacaaaaa aaaaaaaaaa 668
aa 670

<210> 97
<211> 939
<212> DNA
<213> Homo sapiens

<220>
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<222> 1..336

<220>
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<222> 1..81
<223> Von Heijne matrix
score 3.68137078794859
seq AHLCSDSLPEQQ/QD

<400> 97
act tcc gaa gag aga acc gcc atg aag aga gaa ggg ggt gcc gcc cac 48
Thr Ser Glu Glu Arg Thr Ala Met Lys Arg Glu Gly Gly Ala Ala His
-25 -20 -15
ctc tgc tcc gac agc ctc ccg gag tcc cag cag caa gac ggc aac cac 96

Leu	Cys	Ser	Asp	Ser	Leu	Pro	Glu	Ser	Gln	Gln	Gln	Asp	Gly	Asn	His		
-10						-5					1			5			
gca	ccc	aac	ttc	tcc	agc	cac	ggc	tca	tgc	cgc	cgt	cgc	cag	cgg	scc	144	
Ala	Pro	Asn	Phe	Ser	Ser	His	Gly	Ser	Cys	Arg	Arg	Arg	Gln	Arg	Xaa		
			10					15					20				
gac	atg	aca	agg	cgc	tgc	atg	ccc	gct	agg	cca	ggg	ttc	ccc	tca	tcc	192	
Asp	Met	Thr	Arg	Arg	Cys	Met	Pro	Ala	Arg	Pro	Gly	Phe	Pro	Ser	Ser		
			25				30					35					
cca	gcc	ccg	ggg	tcg	tcg	ccc	ccg	cgc	tgc	cat	ctg	aga	ccc	ggg	agt	240	
Pro	Ala	Pro	Gly	Ser	Ser	Pro	Pro	Arg	Cys	His	Leu	Arg	Pro	Gly	Ser		
		40					45				50						
acc	gcc	cat	gct	gca	gcg	gga	aag	aga	aca	gag	agt	cct	ggg	gac	agg	288	
Thr	Ala	His	Ala	Ala	Ala	Gly	Lys	Arg	Thr	Glu	Ser	Pro	Gly	Asp	Arg		
		55				60					65						
tac	cgt	gca	gag	ggc	ttg	aga	agg	ggc	cgg	gtc	gcg	ggg	gca	agg	gta	336	
Tyr	Arg	Ala	Glu	Gly	Leu	Arg	Arg	Gly	Arg	Val	Ala	Gly	Ala	Arg	Val		
		70			75					80			85				
tgaggggagg	gctgcagacc	gccgctcttc	cagttccgc	catcctccgc	gagctcaggc											396	
gttggcattt	cggggcttgg	caaatacccg	ccccgcctcc	gcgcaggggc	tactggggagt											456	
tggaagtttg	ttctctgtag	ttgggcagct	gctcttggtc	tagtgaccac	cagcctggac											516	
agctacggag	aaccgcctt	aggtagaaag	aaagtgtatt	ttttcctttg	caagagtttg											576	
acccgggacc	ctaactgctt	aatgcataatt	tagatcgttt	tctgtacgtt	gtcagttcta											636	
ctgatcctag	tggttttagta	atataaacct	tttctatggt	gtgggtgaaa	ttatgtaacc											696	
tgtgatgagg	gaatcccttc	cacgaattac	ttttagtgcc	agcgtgcacg	ctagtgtcata											756	
cttaaaagaa	cttgcagatt	tggaatgtga	cgtgttttct	ctttcagtaa	cttcacgcct											816	
ctccaagagg	ctaatttttt	tgtaaaagatt	ttgtgggagc	tatgtaatga	gatggggagt											876	
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 174..443

<220>
 <221> sig_peptide
 <222> 174..269
 <223> Von Heijne matrix
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 seq SSIAFCQVGFLTA/QP

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ctagatgacc	gactttaccc	acttcaaagt	ctaccttgac	cctagcactc	tctccacctc											120	
gcattctcac	ctcagccat	cagttgggta	ggccaaacag	tcaccatcaa	ttc atg											176	
					Met												
ccc tgc cta gac caa cag ctc act gtt cat gcc cta ccc tgc cct gcc																224	
Pro Cys Leu Asp Gln Gln Leu Thr Val His Ala Leu Pro Cys Pro Ala																	
-30			-25				-20										
cag ccc tcc tct ctg gcc ttc tgc caa gtg ggg ttc tta aca gca cag																272	
Gln Pro Ser Ser Leu Ala Phe Cys Gln Val Gly Phe Leu Thr Ala Gln																	
-15			-10				-5							1			
cct tca cct ccg aga agg cgc aat ggg aaa gac aga tac acg ttg gtt																320	
Pro Ser Pro Pro Arg Arg Arg Asn Gly Lys Asp Arg Tyr Thr Leu Val																	

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      5          10          15
ctg caa cac cag gaa tgc cag gat gat tta gcc acc tcc tca ctt gtc      368
Leu Gln His Gln Glu Cys Gln Asp Asp Leu Ala Thr Ser Ser Leu Val
      20          25          30
tac ctt tcc ctc ccc tgc ttc aaa gac ttg ggt cga tcg aag cac caa      416
Tyr Leu Ser Leu Pro Cys Phe Lys Asp Leu Gly Arg Ser Lys His Gln
      35          40          45
agc atc act gtt gct gac act aac aag tagtgccaag ggattgcctt      463
Ser Ile Thr Val Ala Asp Thr Asn Lys
      50          55
taaggaagat caggagcgga acatctgggt gcaaagaaaa tctttctaat agccccattc      523
tagtgaccac cttcaacctc ctcatagcag gagagtttgg gagtagggga cttaggatgt      583
ttgtttcttt taatcaattc agaaaatatg tatgtttgaa ataaaaataa aaatacttga      643
gccccaaaaa aaaaaaaa      661

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<210> 99
<211> 647
<212> DNA
<213> Homo sapiens

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<220>
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<222> 282..521

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<220>
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<223> Von Heijne matrix
score 3.64439944832387
seq LEPLGLSSSAACNG/KE

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tgtgaaagaa tctcctgatg tcataatttc cgggtgtcac cggaacattt gatcatcatt      180
cctttggcaa ttccagcctt ctgtggaag gccagtagaa agcattgatt tattcacctc      240
tacaggaatc agactcagcc tcttttgggt ttcagtgaag t atg cct ttt caa ttt      296
Met Pro Phe Gln Phe
      -35
gga acc cag cca agg agg ttt cca gtg gaa gga gga gat tct tca att      344
Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly Gly Asp Ser Ser Ile
      -30          -25          -20          -15
gag ctg gaa cct ggg ctg agc tcc agt gct gcc tgt aat ggg aag gag      392
Gly Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala Cys Asn Gly Lys Glu
      -10          -5          1
atg tca cca acc agg caa ctc cgg agg tgc cct gga agt cat tgc ctg      440
Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro Gly Ser His Cys Leu
      5          10          15
aca ata act gat gtt ccc gtc act gtt tat gca aca acg aga aag cca      488
Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala Thr Thr Arg Lys Pro
      20          25          30
cct gca caa agc agc aag gaa atg cat cct aaa tagcaccatt aagtcctttg      541
Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys
      35          40          45
tcaaggtctg actagggtcaa gggtaatgga ccagtatcat ctgggtgatct ggtaaacaaa      601
taaaagtggg ggcaccttta gatgatgaca aaaaaaaaaa aaaaaa      647

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<210> 100

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<211> 1006
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 251..643

<220>
 <221> sig_peptide
 <222> 251..295
 <223> Von Heijne matrix
 score 3.74215118492367
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 ttcttgactt taattagtat ctaggaaagt ctaaaactttg gacctacctc tttttttgat 180
 actcattttt gtacttttgc tctctgggat tggtttctta aagaatctgg atccttttta 240
 atatgtcaaa atg agt ctg ctg atg ttt aca caa cta ctg ctg tct ggt gga 289
 Met Ser Leu Leu Met Phe Thr Gln Leu Leu Cys Gly
 -15 -10 -5
 ttt tta tat gtt cgg gtt gat gga tgc cgt ctt cgc cag gag gac ttt 337
 Phe Leu Tyr Val Arg Val Asp Gly Ser Arg Leu Arg Gln Glu Asp Phe
 1 5 10
 ccc cgc cgg att gtt gag cat cct tcc gat gtc atc gtc tct aag ggc 385
 Pro Pro Arg Ile Val Glu His Pro Ser Asp Val Ile Val Ser Lys Gly
 15 20 25 30
 gag ccc acg act ctg aac tgc aag gcg gag ggc cgg cca acg ccc acc 433
 Glu Pro Thr Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr Pro Thr
 35 40 45
 att gag tgg tac aaa gat ggg gag cga gtg gag act gac aag gac gat 481
 Ile Glu Trp Tyr Lys Asp Gly Glu Arg Val Glu Thr Asp Lys Asp Asp
 50 55 60
 ccc cgg tcc cac agg atg ctt ctg ccc agc gga tcc tta ttc ttc ttg 529
 Pro Arg Ser His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe Phe Leu
 65 70 75
 cgc atc gtg cac ggg cgc agg agt aaa cct gat gaa gga agc tac gtt 577
 Arg Ile Val His Gly Arg Arg Ser Lys Pro Asp Glu Gly Ser Tyr Val
 80 85 90
 tgt gtt gcg agg aac tat ctt ggt gaa gca gtg agt cga aat gcg tct 625
 Cys Val Ala Arg Asn Tyr Leu Gly Glu Ala Val Ser Arg Asn Ala Ser
 95 100 105 110
 ctg gaa gtg gca tgt aag tgaacataat gaacctcatg tgcacattta 673
 Leu Glu Val Ala Cys Lys
 115
 cttttattta tttcaagtaa gttttgatgt gttcccatag acgctgaaac cttaaagaatc 733
 aatcaacaca ctgcataatt ttacttggtc ttotccaagag aagtctggtc aagatagtat 793
 caagccagggt tgttttagta agtttgttta tatgaaatca agatgaccaa tatgttatta 853
 taagaaagca ggccggggcg ggtggctcac gcctgtaatc ccagcacttt gggaggcgga 913
 ggcggggcga tcacgaggtc agggagatcga gaccatcctg ggtagcacgg tggggccccc 973
 tctctacaaa aaatacaaaa aaaaaaaaaa aaa 1006

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 <222> 179..475

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 <222> 179..295
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 score 4.14109371250204
 seq PSLIAGLFVGCCLA/GY

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 gcgctgggtgc ggagactgct tccggactcc aggtaccgcg cttggcgcca gctggcccca 120
 gactttctgtc ttttcagctg cagtgaaaggc tcggggctgc agaattgcaa ccttgcca 178
 atg gac ctg atc ggt ttt ggt tat gca gcc ctg gtg aca ttt gga agc 226
 Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser
 -35 -30 -25
 att ttt gga tat aag cgg aga ggt ggt gtt ccg tct ttg att gct ggt 274
 Ile Phe Gly Tyr Lys Arg Arg Gly Gly Val Pro Ser Leu Ile Ala Gly
 -20 -15 -10
 ctt ttt gtt gga tgt ttg gcc ggc tat gga gct tac cgt gtc tcc aat 322
 Leu Phe Val Gly Cys Leu Ala Gly Tyr Gly Ala Tyr Arg Val Ser Asn
 -5 1 5
 gac aaa cga gat gta aaa gtg tca ctg ttt aca gct ttc ttc ctg gct 370
 Asp Lys Arg Asp Val Lys Val Ser Leu Phe Thr Ala Phe Phe Leu Ala
 10 15 20 25
 acc ata atg ggt gtg aga ttt aag agg tcc aag aaa ata atg cct gct 418
 Thr Ile Met Gly Val Arg Phe Lys Arg Ser Lys Lys Ile Met Pro Ala
 30 35 40
 ggt ttg gtt gca ggt tta agc ctg atg atc ctg aga ctt gtc ttg 466
 Gly Leu Val Ala Gly Leu Ser Leu Met Met Ile Leu Arg Leu Val Leu
 45 50 55
 ttg ctg ctg tgagcatctg gaggaacaga aaactaagtt catgtcatcc 515
 Leu Leu Leu
 60
 tgctgtaatg ggcagagcat attttttttg tatttaaaag ataaacttca atatggaatg 575
 ctagaaacac aaatagcact gtcacctcta atatgaacat tagtttgagg tagttttttt 635
 ctaaagcaaa aattttaact gttttctaata tgtaagcac tattttcatt aaaagtgtct 695
 aatgaatcat gatatactct tccattttgt gtgtctattt tttatatatt tggatttttt 755
 tgaaaattcc aaatactcat gtctcaagta agcttaaaact acaactgtgc acataaagga 815
 agtctttaagt ggagttcaca gaatgataat gtatctattt gtcattttgt ttatatattga 875
 aattattaga aattatgctt ttccattttt aattgtattg ctgccagtcg tatttttttc 935
 tttaaaaaat tttattctta gcacactgtt atgtcctaac tgaatgtatt cagtattcaa 995
 ataaaagaca ttttgggtcca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1055
 aaaa 1059

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 <211> 514
 <212> DNA
 <213> Homo sapiens

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 <221> CDS
 <222> 34..327

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<221> sig_peptide
<222> 34..162
<223> Von Heijne matrix
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      seq LGDALLFLRPAGS/CA

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agagacccat ggggttcgcc tgaagccccc gga atg tgt gag aca ctt ctt act      54
                               Met Cys Glu Thr Leu Leu Thr
                               -40
agt aaa tgg gct tca gta tcc ccc atc cct gca ctc ctg cag gaa ggt      102
Ser Lys Trp Ala Ser Val Ser Pro Ile Pro Ala Leu Leu Gln Glu Gly
-35                               -30                               -25
gag aat cgg gac agt cgc agg ctg gga gac gct ctg ctt ttc ctg cgt      150
Glu Asn Arg Asp Ser Arg Arg Leu Gly Asp Ala Leu Leu Phe Leu Arg
-20                               -15                               -10                               -5
cct gct ggg agc tgc gcg ctc cag gta tcc tgg cct gcc gcc cta gcc      198
Pro Ala Gly Ser Cys Ala Leu Gln Val Ser Trp Pro Ala Ala Leu Ala
1                               5                               10
ggc cca agg agc cac aca gga cag ttg acc caa cac ttc tgc cac ctg      246
Gly Pro Arg Ser His Thr Gly Gln Leu Thr Gln His Phe Cys His Leu
15                               20                               25
aag aac gac acc tgc att cct cca tct ctg gga cca cca agg aac tca      294
Lys Asn Asp Thr Cys Ile Pro Pro Ser Leu Gly Pro Pro Arg Asn Ser
30                               35                               40
ggg agc ttg gaa tct ctc aga tca aaa aga tac tgactcatcg gatagccatg      347
Gly Ser Leu Glu Ser Leu Arg Ser Lys Arg Tyr
45                               50                               55
gcacacctgaa aacggcccttc ctgtgtgtga cattatttgc aacaagcaac aagtttataa      407
gcaccttgggt aaaattgcac gtgagggtta aaatattaaa gtcagtgcggt caacttgaaa      467
taaatgatga gttattgatt actgctaaag aaaaaaaaaa aaaaaaa      514

<210> 103
<211> 1158
<212> DNA
<213> Homo sapiens

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<222> 303..953

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<222> 303..359
<223> Von Heijne matrix
      score 5.47911600153114
      seq LCCSGCVPSLCCS/SY

<400> 103
aaaaacttcc gccgccgcgt ccgccgcctc cggaactaaa cgggggtgagg tcacattcgg      60
ttatctctaa cgttggaataa cgaaggagct aacacccatt atggagatta accacttttc      120
atcaggtttt taacttaagt cgtgagggaat acaacgggtga acacaagatt cattttattt      180
tcacaccatc gggacgtatc ctgttgttga gttctctggg tcagacctct gaagacttct      240
cagatggatc ctagtctctg ggcttgcctt gaaattactc gctgctcagg gagagagttg      300
aa atg gtt ggc atc ctc cca ctc tgt tgc tcc ggc tgt gtc ccc tgc      347
Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys Val Pro Ser
-15                               -10                               -5
ctc tgt tgt tcc agc tat gtc ccc tet gtt gct cca act gca gct cat      395

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Leu Cys Cys Ser Ser Tyr Val Pro Ser Val Ala Pro Thr Ala Ala His
      1      5      10
tct gtt aga gtt cct cat tca gct ggt cac tgt ggc cag agg gtg ttg      443
Ser Val Arg Val Pro His Ser Ala Gly His Cys Gly Gln Arg Val Leu
      15      20      25
gcc tgc tcc ctt cct caa gta ttc tta aag cca tgg att ttt gtg gag      491
Ala Cys Ser Leu Pro Gln Val Phe Leu Lys Pro Trp Ile Phe Val Glu
      30      35      40
cat ttt tct tcc tgg ctc tcc ctt gag tta ttt tcc ttt ctt cgc tat      539
His Phe Ser Ser Trp Leu Ser Leu Glu Leu Phe Ser Phe Leu Arg Tyr
      45      50      55      60
ctt ggg act ctt ctt tgt gct tgc gga cat cgg ttg aga gaa gga cga      587
Leu Gly Thr Leu Leu Cys Ala Cys Gly His Arg Leu Arg Glu Gly Arg
      65      70      75
ctt ctt cct tgt ctc ctt ggt gtt ggc tgc tgg ttg ctc ttc aac aac      635
Leu Leu Pro Cys Leu Leu Gly Val Gly Ser Trp Leu Leu Phe Asn Asn
      80      85      90
tgg act gga ggc tct tgg ttt tct ctt cat ctt caa caa gtc agt ctc      683
Trp Thr Gly Gly Ser Trp Phe Ser Leu His Leu Gln Gln Val Ser Leu
      95      100      105
tct caa ggg tct cac gtt gca gca ttc tta cca gag gcc att ggg cct      731
Ser Gln Gly Ser His Val Ala Ala Phe Leu Pro Glu Ala Ile Gly Pro
      110      115      120
gga gtt cca gtt cca gtg tct gga gag tcc acc tca gct cag caa tct      779
Gly Val Pro Val Pro Val Ser Gly Glu Ser Thr Ser Ala Gln Gln Ser
      125      130      135      140
cat gcc ggt tgg caa ttg tca gca gaa gcc gat gcc tgc cca tca gtt      827
His Ala Gly Trp Gln Leu Ser Ala Glu Ala Asp Ala Cys Pro Ser Val
      145      150      155
ctt tac tct gag gtg tta gag tgg aat aaa aat ata aat act tat act      875
Leu Tyr Ser Glu Val Leu Glu Trp Asn Lys Asn Ile Asn Thr Tyr Thr
      160      165      170
agt ttt cat gac ttc tgc tta ata ttg ggt att ttt ktt gtt ttg ttt      923
Ser Phe His Asp Phe Cys Leu Ile Leu Gly Ile Phe Xaa Val Leu Phe
      175      180      185
tgt ttt ggc ggt gat agg ctt acc tta cat taaaccaggc cttagccttt      973
Cys Phe Gly Gly Asp Arg Leu Thr Leu His
      190      195
ctgtggccttt gttatggcaa agcctcatat tactctctag tctggttcag caggacagtc      1033
aggtccacac ctggggctgt ttgttttcta cgtttacctc aacataaggt accttatcat      1093
tgtcagcctt catctcttga tccaaaataa aataaaatgc cacaggtcaa aaaaaaaaaa      1153
aaaaa

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<210> 104
 <211> 1563
 <212> DNA
 <213> Homo sapiens

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 <222> 97..645

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 <222> 97..156
 <223> Von Heijne matrix
 score 8.42885652997473
 seq AVVGCLLVPPAEA/NK

<220>
 <221> misc_feature
 <222> 972
 <223> n=a, g, c or t

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gtgtccggct ttgtctggccc agcaagcctg ataagc atg aag ctc tta tct ttg      114
                                         Met Lys Leu Leu Ser Leu
                                         -20
gtg gct gtg gtc ggg tgt ttg ctg gtg ccc cca gct gaa gcc aac aag      162
Val Ala Val Val Gly Cys Leu Leu Val Pro Pro Ala Glu Ala Asn Lys
                                         -10
agc tct gaa gat atc cgg tgc aaa tgc atc tgt cca cct tat aga aac      210
Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile Cys Pro Pro Tyr Arg Asn
                                         5
atc agt ggg cac att tac aac cag aat gta tcc cag aag gac tgc aac      258
Ile Ser Gly His Ile Tyr Asn Gln Asn Val Ser Gln Lys Asp Cys Asn
                                         20
tgc ctg cac gtg gtg gag ccc atg cca gtg cct ggc cat gac gtg gag      306
Cys Leu His Val Val Glu Pro Met Pro Val Pro Gly His Asp Val Glu
                                         35
gcc tac tgc ctg ctg tgc gag tgc agg tac gag gag cgc agc acc acc      354
Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr
                                         55
acc atc aag gtc atc att gtc atc tac ctg tcc gtg gtg ggt gcc ctg      402
Thr Ile Lys Val Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu
                                         70
ttg ctc tac atg gcc ttc ctg atg ctg gtg gac cct ctg atc cga aag      450
Leu Leu Tyr Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys
                                         85
ccg gat gca tac act gag caa ctg cac aat gag gag gag aat gag gat      498
Pro Asp Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp
                                         100
gct cgc tct atg gca gca gct gct gca tcc ctc ggg gga ccc cga gca      546
Ala Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
                                         115
aac aca gtc ctg gag cgt gtg gaa ggt gcc cag cag cgg tgg aag ctg      594
Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys Leu
                                         135
cag gtg cag gag cag cgg aag aca gtc ttc gat cgg cac aag atg ctc      642
Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys Met Leu
                                         150
agc tagatgggct ggtgtgggtg ggtcaaggcc ccaacaccat ggctgccagc      695
Ser
ttccaggctg gacaagcagc ggggctactt ctcccttccc tcggttccag tcttcccttt      755
aaaaagcctgt ggcatttttc ctcccttccc ctacttttag aaatgttgta ctggctatt      815
ttgattaggg aagaggggat tggctctcta tctctgttgt ctctcttggt cttctgggtt      875
gaagggaggg ggaaggcagc cccasaaggg aatggagaca ttcagggcgg cctcaggagt      935
ggatgcgata ttgtctctcc tkggcctccc actcttngcc gccttcacgc tctgagtctt      995
gggaatgttg ttacccttgg aagataaagy ctgggtcttc aggaactcag tgtctgggag      1055
gaaagcatgg ccagacattc agcatgtgtt ctttctgca gtggttctta tcaccacctc      1115
cctccagccc ccagcgctcc agccccagcc ccagctccag ccttgaggac agctctgatg      1175
ggagagcttg gcccccctag cccactgggt cttcagggtg cactggaagc tgggtgtcgc      1235
tgtccctctg gcactctctg cactggggca tggagtgcoc actcactact tgcctgcggg      1295
ccctcactc gaacttgagg ggtctgggca gtccctctcc tccccagtgt ccacagtcac      1355
tgagccagac ggtcggttgg aacatgagac tcgaggctga cgttggtatc gaacaccaca      1415

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gcccctgtac ttgggttgcc tcttgtccct gaacttogg ttaccagtgc atggagagaa 1475
aattttgtcc tcttgtctta gagttgtgtg taaatcaagg aagccatcat taaattgttt 1535
tattttcttc taaaaaaaaa aaaaaaaaaa 1563

<210> 105
<211> 1621
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..820

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<221> sig_peptide
<222> 80..118
<223> Von Heijne matrix
score 5.76690322882439
seq MLVLRSA LTRALA/SR

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acctttccac tcgggaaacc ttcagaggag tctcagaaag gacacggctg gctgcttttc 60
tcacgcgcga agccgcgcc atg ctc gtc ctc aga agc gcc ctg act cgg gcg 112
Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala
-10 -5
ctg gcc tca cgg acg ctg gcg cct cag atg tgc tca tct ttt gct acg 160
Leu Ala Ser Arg Thr Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr
1 5 10
gga ccc aga caa tac gat gga ata ttc tat gaa ttt cgt tct tat tac 208
Gly Pro Arg Gln Tyr Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr
15 20 25 30
ctt aag ccc tca aag atg aat gag ttc ctg gaa aat ttt gag aaa aac 256
Leu Lys Pro Ser Lys Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn
35 40 45
gct cat ctt cgg aca gct cac tct gaa ttg gtt gga tac tgg agt gta 304
Ala His Leu Arg Thr Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val
50 55 60
gaa ttt gga ggc aga atg aat aca gtg ttt cat att tgg aag tat gat 352
Glu Phe Gly Gly Arg Met Asn Thr Val Phe His Ile Trp Lys Tyr Asp
65 70 75
aat ttt gct cat cga act gaa gtt cag aaa gcc ttg gcc aaa gat aag 400
Asn Phe Ala His Arg Thr Glu Val Gln Lys Ala Leu Ala Lys Asp Lys
80 85 90
gaa tgg caa gaa caa ttc ctc att cca aat ttg gct ctc att gat aaa 448
Glu Trp Gln Glu Gln Phe Leu Ile Pro Asn Leu Ala Leu Ile Asp Lys
95 100 105 110
caa gag agt gag att act tat ctg gta cca tgg tgc aaa tta gaa aaa 496
Gln Glu Ser Glu Ile Thr Tyr Leu Val Pro Trp Cys Lys Leu Glu Lys
115 120 125
cct cca aaa gaa gga gtc tat gaa ctg gcc act ttt cag atg aaa cct 544
Pro Pro Lys Glu Gly Val Tyr Glu Leu Ala Thr Phe Gln Met Lys Pro
130 135 140
ggg ggg cca gct ctg tgg ggt gat gca ttt aaa agg gca gtt cat gct 592
Gly Gly Pro Ala Leu Trp Gly Asp Ala Phe Lys Arg Ala Val His Ala
145 150 155
cat gtc aat cta ggc tac aca aaa cta gtt gga gtg ttc cac aca gag 640
His Val Asn Leu Gly Tyr Thr Lys Leu Val Gly Val Phe His Thr Glu
160 165 170

tac gga gca ctc aac aga gtt cat gtt ctt tgg tgg aat gag agt gca	688
Tyr Gly Ala Leu Asn Arg Val His Val Leu Trp Asn Glu Ser Ala	
175 180 185 190	
gat agt cgt gca gct ggg aga cat aag tcc cat gag gat ccc aga gtt	736
Asp Ser Arg Ala Ala Gly Arg His Lys Ser His Glu Asp Pro Arg Val	
195 200 205	
gtg gca gct gtt cgg gaa agt gtc aac tac cta gta tct cag cag aat	784
Val Ala Ala Val Arg Glu Ser Val Asn Tyr Leu Val Ser Gln Gln Asn	
210 215 220	
atg ctt ctg att cct aca tcg ttt tca cca ctg aaa tagttttcta	830
Met Leu Leu Ile Pro Thr Ser Phe Ser Pro Leu Lys	
225 230	
ctgaaataca aaacatttca ttaactgcta taggatctct ctgctaattg tgcttaaaatt	890
ctcccaagag gttctcactt ttatttgaag gaggtggtaa gtttaatttgc tatgtttctt	950
gcattatgaa ggctacatct gtgctttgta agtaccactt caaaaaatag ttctgtttac	1010
ttctgcagtg gtatttcagtg gtctgtcata cattaaaaat acctgtcact gttttaagat	1070
cttgactctt catttggtttc agaatagctc ttctactgta ttctgacaac tctttgcttt	1130
atagcatttt gttgtattca aatgataatg gtagcatttc catgcttgtg acagcatttt	1190
taagttatta atatatttta tcaacctttc catcatgtct gttttccctgg ttttttttgg	1250
ttgttttttg accagtaaaa tttattttgt aataccaaat aggattttaag aaaattaacg	1310
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tttcacatta gttatttgtc acttacttgg aaaatgatgc tgttaggtcc tggattataa	1430
aatctagaaa agactgtgtg gtttatgtgc tgaaatgtct ttattttataa ttaattttaa	1490
ctactatttta ctttatttcg gatcctgttt aacaaagata cttgagacat ccatttgttt	1550
taatgaaatc tgtatggata tggaaatgct tgccttaata aaagcctaca tatacaaaaa	1610
aaaaaaaaa a	1621

<210> 106
 <211> 557
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 77..388

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 <221> sig_peptide
 <222> 77..217
 <223> Von Heijne matrix
 score 4.57105404339594
 seq FLYLTLNQSCIFA/NY

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aacaccctcc ctggaccctc tgcctggagg acggggaatc acagcagctg gtttggggtg	60
cctcccaaac caaaag atg ttc tct ccg cgc caa gct ttg acg ccc gac ccc	112
Met Phe Ser Pro Arg Gln Ala Leu Thr Pro Asp Pro	
-45 -40	
ctg cac tct ccc gcc tac tca ccg gtc cta ggg ggt tgg tcc cgc ttt	160
Leu His Ser Pro Ala Tyr Ser Pro Val Leu Gly Trp Ser Arg Phe	
-35 -30 -25 -20	
cgt agt gtg gat ttt cgt ttc ctc tac ttg act cta aat caa tcc tgt	208
Arg Ser Val Asp Phe Arg Phe Leu Tyr Leu Thr Leu Asn Gln Ser Cys	
-15 -10 -5	
ata ttc gca aac tac aaa gag gcg cat gca aat aga tac tgt act gag	256
Ile Phe Ala Asn Tyr Lys Glu Ala His Ala Asn Arg Tyr Cys Thr Glu	
1 5 10	
ggc aga tac acg cgc gag atc cag agg ctt aca tcc cca gcc gct tgg	304

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Gly Arg Tyr Thr Arg Glu Ile Gln Arg Leu Thr Ser Pro Ala Ala Trp
  15                20                25
ccc acc aga gac aag aac agg atg ata agc aat gga atg gca ttg aac      352
Pro Thr Arg Asp Lys Asn Arg Met Ile Ser Asn Gly Met Ala Leu Asn
  30                35                40                45
tct cct gct gaa gga ctt gca ttt caa tgt aga ttc tgaggctggg      398
Ser Pro Ala Glu Gly Leu Ala Phe Gln Cys Arg Phe
  50                55
tgaaaaattc tctgtcacct ttactacagc attctcaccc atttatattt ctttccctt      458
ctacatctct attactgttg cactatgtta tgcattacac catggcaaaa ttaatcaatt      518
aatacaataa aagcttaatt ttaaaaaaaaa aaaaaaaaaa      557

<210> 107
<211> 600
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 139..513

<220>
<221> sig_peptide
<222> 139..201
<223> Von Heijne matrix
      score 5.86857787719223
      seq IVMGVQVVGRAFA/RA

<400> 107
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tgaccgcccg accacgcttg atccccggcc gcggggccag gaagtcggag tttgagcccc      120
ggaggcagag cggttgcc atg gcc aag tac ctg gcc cag atc att gtg atg      171
               Met Ala Lys Tyr Leu Ala Gln Ile Ile Val Met
               -20                -15
ggc gtg cag gtg gtg ggc agg gcc ttt gca cgg gcc ttg cgg cag gag      219
Gly Val Gln Val Val Gly Arg Ala Phe Ala Arg Ala Leu Arg Gln Glu
-10                -5                1                5
ttt gca gcc agc cgg gcc gca gct gat gcc cga gga cgc gct gga cac      267
Phe Ala Ala Ser Arg Ala Ala Ala Asp Ala Arg Gly Arg Ala Gly His
      10                15                20
cgg tct gca gcc gct tcc aac ctc tcc gcc ctc agc ctc cag gag gca      315
Arg Ser Ala Ala Ala Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala
      25                30                35
cag cag att ctc aac gtg tcc aag ctg agc cct gag gag gtc cag aag      363
Gln Gln Ile Leu Asn Val Ser Lys Leu Ser Pro Glu Glu Val Gln Lys
      40                45                50
aac tat gaa cac tta ttt aag gtg aat gat aaa tcc gtg ggt ggc tcc      411
Asn Tyr Glu His Leu Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser
      55                60                65                70
ttc tac ctg cag tca aag gtg gtc cgc gca aag gag cgc ctg gat gag      459
Phe Tyr Leu Gln Ser Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu
      75                80                85
gaa ctc aaa atc cag gcc cag gag gac aga gaa aaa ggg cag atg ccc      507
Glu Leu Lys Ile Gln Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro
      90                95                100
cat acg tgactgctcg gctcccccg cccaccccg cgctctaat ttatagcttg      563
His Thr
gtaataaatt tcttttctac aaaaaaaaa aaaaaaaa      600

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<210> 108
 <211> 1129
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 81..986

<220>
 <221> sig_peptide
 <222> 81..134
 <223> Von Heijne matrix
 score 5.03543461931947
 seq ITLLGLAVNVVTT/LV

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 tccagtggtat cccgctctgg atg gcc ccc aac tcc atc acc ctg ctg ggg ctg 113
 Met Ala Pro Asn Ser Ile Thr Leu Leu Gly Leu
 -15 -10
 gcc gtc aac gtg gtc acc acg ctc gtg ctc atc tcc tac tgt ccc acg 161
 Ala Val Asn Val Val Thr Thr Leu Val Leu Ile Ser Tyr Cys Pro Thr
 -5 1 5
 gcc acc gaa gag gca cca tac tgg aca tac ctt tta tgt gca ctg gga 209
 Ala Thr Glu Glu Ala Pro Tyr Trp Thr Tyr Leu Leu Cys Ala Leu Gly
 10 15 20 25
 ctt ttt att tac cag tca ctg gat gct att gat ggg aaa caa gcc aga 257
 Leu Phe Ile Tyr Gln Ser Leu Asp Ala Ile Asp Gly Lys Gln Ala Arg
 30 35 40
 aga aca aac tct tgt tcc cct tta ggg gag ctc ttt gac cat ggc tgt 305
 Arg Thr Asn Ser Cys Ser Pro Leu Gly Glu Leu Phe Asp His Gly Cys
 45 50 55
 gac tct ctt tcc aca gta ttt atg gca gtg gga gct tca att gcc gct 353
 Asp Ser Leu Ser Thr Val Phe Met Ala Val Gly Ala Ser Ile Ala Ala
 60 65 70
 cgc tta gga act tat cct gac tgg ttt ttt ttc tgc tct ttt att ggg 401
 Arg Leu Gly Thr Tyr Pro Asp Trp Phe Phe Phe Cys Ser Phe Ile Gly
 75 80 85
 atg ttt gtg ttt tat tgc gct cat tgg cag act tat gtt tca ggc atg 449
 Met Phe Val Phe Tyr Cys Ala His Trp Gln Thr Tyr Val Ser Gly Met
 90 95 100 105
 ttg aga ttt gga aaa gtg gat gta act gaa att cag ata gct tta gtg 497
 Leu Arg Phe Gly Lys Val Asp Val Thr Glu Ile Gln Ile Ala Leu Val
 110 115 120
 att gtc ttt gtg ttg tct gca ttt gga gga gca aca atg tgg gac tat 545
 Ile Val Phe Val Leu Ser Ala Phe Gly Gly Ala Thr Met Trp Asp Tyr
 125 130 135
 acg ggc acc agt gtc ttg tca cct gga ctc cac ata gga cta att att 593
 Thr Gly Thr Ser Val Leu Ser Pro Gly Leu His Ile Gly Leu Ile Ile
 140 145 150
 ata ctg gca ata atg atc tat aaa aag tca gca act gat gtg ttt gaa 641
 Ile Leu Ala Ile Met Ile Tyr Lys Lys Ser Ala Thr Asp Val Phe Glu
 155 160 165
 aag cat cct tgt ctt tat atc cta atg ttt gga tgt gtc ttt gct aaa 689
 Lys His Pro Cys Leu Tyr Ile Leu Met Phe Gly Cys Val Phe Ala Lys
 170 175 180 185


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agt gag tct gga agg agt gct ctg tat aca att gca aag aac aaa atg      532
Ser Glu Ser Gly Arg Ser Ala Leu Tyr Thr Ile Ala Lys Asn Lys Met
60              65              70              75
gtc atc ttt aag gta cct gat tgc atg cac tta aat gca gat tat ttt      580
Val Ile Phe Lys Val Pro Asp Cys Met His Leu Asn Ala Asp Tyr Phe
      80              85              90
gga gtt tgaaggga ctattaaatga aatctttctt ttccctctct tctctttttc      636
Gly Val
cctccccgc cactgattca gtgagctgga gattggatca cagccgaagg agtaaagggtg      696
ctgcaatgat gttagctgtg gccactgtgg atttttcgca agaacattaa taaactaaaa      756
acttcaaaaa aaaaaaaaaa aa      778

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<222> 59..745

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<222> 59..160
<223> Von Heijne matrix
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      seq LGAAALALLLANT/DV

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Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
      -30              -25              -20
att ggt gca gga gcc ctg ggg gct gct gcc ttg gca ttg ctg ctt gcc      154
Ile Gly Ala Gly Ala Leu Gly Ala Ala Leu Ala Leu Leu Leu Ala
      -15              -10              -5
aac aca gac gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg gag tac      202
Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
      1              5              10
ctg gag gat ata gac ctg aaa aca ctg gag aag gaa cca agg act ttc      250
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
      15              20              25              30
aaa gca aag gag cta tgg gaa aaa aat gga gct gtg att atg gcc gtg      298
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
      35              40              45
cgg agg cca ggc tgt ttc ctc tgt cga gag gaa gct gcg gat ctg tcc      346
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
      50              55              60
tcc ctg aaa agc atg ttg gac cag ctg gcc gtc ccc ctc tat gca gtg      394
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
      65              70              75
gta aag gag cac atc agg act gaa gtg aag gat ttc cag cct tat ttc      442
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
      80              85              90
aaa gga gaa atc ttc ctg gat gaa aag aaa aag ttc tat ggt cca caa      490
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
      95              100              105              110

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agg cgg aag atg atg ttt atg gga ttt atc cgt ctg gga gtg tgg tac 538
Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
115 120 125

aac ttc ttc cga gcc tgg aac gga ggc ttc tct gga aac ctg gaa gga 586
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
130 135 140

gaa ggc ttc atc ctt ggg gga gtt ttc gtg gtg gga tca gga aag cag 634
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln
145 150 155

ggc att ctt ctt gag cac cga gaa aaa gaa ttt gga gac aaa gta aac 682
Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe Gly Asp Lys Val Asn
160 165 170

cta ctt tct gtt ctg gaa gct gct aag atg atc aaa cca cag act ttg 730
Leu Leu Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln Thr Leu
175 180 185 190

gcc tca gag aaa aaa tgattgtgtg aaactgcccc gctcagggat aaccagggac 785
Ala Ser Glu Lys Lys
195

attcacctgt gttcatggga tgtattgttt cactcgtgt cctaaggag tgagaaaccc 845
atttatactc tactctcagt atggattatt aatgtatttt aatattctgt ttaggcccac 905
taaggcaaaa tagcccaaaa acaagactga caaaaatctg aaaaactaag gaggattatt 965
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cgggtgtggt ggcaggcacc tgtagtccca gctacccggg aggctgaggc aggagaatca 1205
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<213> Homo sapiens

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<222> 59..160
<223> Von Heijne matrix
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seq LGAAALALLLANT/DV

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atg tct ttc ctg cag gac cca agt ttc ttc acc atg ggg atg tgg tcc 106
Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
-30 -25 -20

att ggt gca gga gcc ctg ggg gct gct gcc ttg gca ttg ctg ctt gcc 154
Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu Leu Ala
-15 -10 -5

aac aca gac gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg gag tac 202
Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
1 5 10

ctg gag gat ata gac ctg aaa aca ctg gag aag gaa cca agg act ttc 250
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
15 20 25 30

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aaa gca aag gag cta tgg gaa aaa aat gga gct gtg att atg gcc gtg      298
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
                               35                               40                               45
cgg agg cca gcc tgt ttc ctc tgt cga gag gaa gct gcg gat ctg tcc      346
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
                               50                               55                               60
tcc ctg aaa agc atg ttg gac cag ctg gcc gtc ccc ctc tat gca gtg      394
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
                               65                               70                               75
gta aag gag cac atc agg act gaa gtg aag gat ttc cag cct tat ttc      442
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
                               80                               85                               90
aaa gga gaa atc ttc ctg gat gaa aag aaa aag ttc tat ggt cca caa      490
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
                               95                               100                               105
agg cgg aag atg atg ttt atg gga ttt atc cgt ctg gga gtg tgg tac      538
Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
                               115                               120                               125
aac ttc ttc cga gcc tgg aac gga gcc ttc tct gga aac ctg gaa gga      586
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
                               130                               135                               140
gaa gcc ttc atc ctt ggg gga gtt ttc gtg gtg gga tca gga agc agg      634
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Ser Arg
                               145                               150                               155
gca ttc ttc ttg agc acc gag gaa aaa aag aat ttg gag aca aag      676
Ala Phe Phe Leu Ser Thr Glu Lys Lys Asn Leu Glu Thr Lys
                               160                               165                               170
taaacctact ttctgttctg gaagctgcta agatgatcaa accacagact ttggcctcag      736
agaaaaaatg attgtgtgaa actgccccagc tcagggataa ccaggggacat tcacctgtgt      796
tcattgggatg tattgtttcc actcgtgtcc ctaaggagtg agaaaccccat ttatactcta      856
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gggaaatagg aggtttaaaa ttgactgccca ggctgggtgc agtggctcac acctgtaatc      1036
ccagcacttt gggaggccaa ggtgagcaag tcacttgagg tcgggagttc gagaccagcc      1096
tgagcaacat gccgaaaccc cgtctctact aaaaatacaa aaatcacccc ggtgtggttg      1156
caggcacctg tagtcccagc taccggggag gctgaggcag gagaatcact tgaacctggg      1216
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<213> Homo sapiens

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<222> 15..278

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score 12.2610572403264
seq PLFLLLLLGSVTA/DI

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Met Ala Ala Glu Gly Trp Ile Trp Arg Trp Gly Trp

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00224023-1007400

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                                     -40          -35
ggc cgg cgg tgc ctg gga agg cct ggg ctt ctc ggc ccc ggc cct ggc      98
Gly Arg Arg Cys Leu Gly Arg Pro Gly Leu Leu Gly Pro Gly Pro Gly
      -30          -25          -20
ccc act aca cct ctc ttt ctt ctt ttg ttg ttg ggg tct gtg act gcg      146
Pro Thr Thr Pro Leu Phe Leu Leu Leu Leu Leu Gly Ser Val Thr Ala
      -15          -10          -5
gat ata act gac ggc aac att gaa cat ctc aag cgg gag cat tcg ctc      194
Asp Ile Thr Asp Gly Asn Ile Glu His Leu Lys Arg Glu His Ser Leu
1          5          10          15
att aag ccc tac caa ggg gtc ggt tcc agc tcc ccc tct ggg act tcc      242
Ile Lys Pro Tyr Gln Gly Val Gly Ser Ser Ser Pro Ser Gly Thr Ser
      20          25          30
agg gca gca cta tgc tca cga gcc agt acg tac gtc tgacccctga      288
Arg Ala Ala Leu Cys Ser Arg Ala Ser Thr Tyr Val
      35          40
cgagcgcagc aaagaggggt ctatctggaa ccaccagccg tgcttctctca aagactggga      348
aatgcacgtc cactctaaaag tccacggcac agggaagaag aacctccatg gagacggcat      408
cgcccttggtg tacacccggg accgcctcgt gccagggcct gtgttttgaa gcaaaagataa      468
cttcaccggc ttatgccatct tccctggacac ctaccccaat gatgagacca ctgagcgcgt      528
gttccccgtac atctcgggtga tgggtgaacaa tgggtccctg tcctacgacc acagcaagga      588
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ccttcctgtt caccctgagc tgcttctctga gacagatgct caagtgaggc tgcaggcgcg      1548
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aaaaaaaaa

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<210> 113
<211> 1634
<212> DNA
<213> Homo sapiens

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<222> 167..619

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<221> sig_peptide
<222> 167..262
<223> Von Heijne matrix
score 6.8501239662158
seq LLSSCLPPSTAS/AV

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gtacttcoga gagagattaa agattcaatg gaactctgcg tctctcatct ggaacccagg 60

acacagaaca agggaggggaa gaaaagctca gccttaaaaca tagcaagggtg aaacctttgt 120
 cctggggaat agtctggccc gtccttgga accacactca gactca atg gac tct 175
 Met Asp Ser
 -30
 gcc tca aat ccc acc aac ctt gtc agc acc tcc caa agg cac cgg ccc 223
 Ala Ser Asn Pro Thr Asn Leu Val Ser Thr Ser Gln Arg His Gln Pro
 -25 -20 -15
 ttg ctt tca tcc tgt ggc ctc cca cca agc act gcc tca gct gtg cgc 271
 Leu Leu Ser Ser Cys Gly Leu Pro Pro Ser Thr Ala Ser Ala Val Arg
 -10 -5 1
 agg cta tgc tcc agg gga gtg tta aaa gga tca aat gaa aga agg gat 319
 Arg Leu Cys Ser Arg Gly Val Leu Lys Gly Ser Asn Glu Arg Arg Asp
 5 10 15
 atg gaa tca ttt tgg aaa cta aat cgt tcc cca ggg tgc gac cga tac 367
 Met Glu Ser Phe Trp Lys Leu Asn Arg Ser Pro Gly Ser Asp Arg Tyr
 20 25 30 35
 ctg gag agc cgc gat gcc tct cga ctg agt ggc cgg gac ccc tcc tca 415
 Leu Glu Ser Arg Asp Ala Ser Arg Leu Ser Gly Arg Asp Pro Ser Ser
 40 45 50
 tgg aca gtc gag gat gtg atg cag ttt gtc cgg gaa gct gat cct cag 463
 Trp Thr Val Glu Asp Val Met Gln Phe Val Arg Glu Ala Asp Pro Gln
 55 60 65
 ctt gga ccc cac gct gac ctg ttt cgc aaa cac gag atc gat ggc aag 511
 Leu Gly Pro His Ala Asp Leu Phe Arg Lys His Glu Ile Asp Gly Lys
 70 75 80
 gcc ctg ctg ctg ctg cgc agt gac atg atg atg aag tac atg ggc ctg 559
 Ala Leu Leu Leu Leu Arg Ser Asp Met Met Met Lys Tyr Met Gly Leu
 85 90 95
 aag ctg ggg cct gca ctc aag ctc tcc tac cac att gac cgg ctg aag 607
 Lys Leu Gly Pro Ala Leu Lys Leu Ser Tyr His Ile Asp Arg Leu Lys
 100 105 110 115
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 Gln Gly Lys Phe
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 tccaccact cgcctgtcca caggcttctc tgtaagcaag tcagcagcac agctactcac 1559
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 aaaaaaaaaa aaaaa 1634

<210> 114
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 <212> DNA
 <213> Homo sapiens

<220>
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<222> 223..417

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<221> sig_peptide

<222> 223..270

<223> Von Heijne matrix
score 4.19788230215007
seq LACVRETSVAVA/CK

<400> 114

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cctatccccg gccccgctcg ggcctttccc cttgcgcctt ggctcggctg gctcgacgag 180
cagtaagtgc gtacccgccc tccgaagccg ggcgtgcacg gg atg gca gag ttg 234
Met Ala Glu Leu
-15
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gcg tgc gtg cgt gag tcc acc agt gtg gca tgg gca tgt aag gtg cgc 282
Ala Cys Val Arg Glu Ser Thr Ser Val Ala Trp Ala Cys Lys Val Arg
-10 -5 1
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gga ggg act gca cct tct cca tca ggt gca gaa ggc cac gtc atg ctg 330
Gly Gly Thr Ala Pro Ser Pro Ser Gly Ala Glu Gly His Val Met Leu
5 10 15 20
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aac aag agc cga gaa gta gaa tgc cca gtg tca agc cgt cca cgt tgt 378
Asn Lys Ser Arg Glu Val Glu Ser Pro Val Ser Ser Arg Pro Arg Cys
25 30 35
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ggg atg ccc act gtt ccc cca gga tca ctc aag acc ctg tgacttgtgg 427
Gly Met Pro Thr Val Pro Pro Gly Ser Leu Lys Thr Leu
40 45
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tcaactgatga gtggaccaag tgaagtccac aagatggctg ctgtggctcc aggcatacac 487
tccacatgca aatccatcca gaggcaggaa ctgggaatat gcttggaggt gcccaggaca 547
gcaagtgggc tgtctgtata aacctcccct ccacttggga aggaaaaatca ccccccaagt 607
cgattttctg tccatcttat tgatcagaga gcgttataaa ttcaccattt aaataatctg 667
gacaagggga aaaaaaaaaa aaaaaa 693
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<210> 115

<211> 784

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 166..732

<220>

<221> sig_peptide

<222> 166..237

<223> Von Heijne matrix
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seq KMVHLLVLSGANG/MQ

<400> 115

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ggcgctggga gtgaggtacc agattcagcc catttggccc cgacgcctct gttctcgaaa 120
tccgggtgct gcggatttag gtccccgttc ctaacggact gcaag atg gag gaa ggc 177
Met Glu Glu Gly
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ggg aac cta gga ggc ctg att aag atg gtc cat cta ctg gtc ttg tca 225
Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu Leu Val Leu Ser
-20 -15 -10 -5
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-35	-30	-25	-20	
tta agt gat cca gaa tta aga ctt ctt ctg ccc tgt ttg gta cgg atg				206
Leu Ser Asp Pro Glu Leu Arg Leu Leu Leu Pro Cys Leu Val Arg Met				
	-15	-10	-5	
gca ctt tgt gca cct gct gac cag agc caa agc tgg gct cag gat aag				254
Ala Leu Cys Ala Pro Ala Asp Gln Ser Gln Ser Trp Ala Gln Asp Lys				
	1	5	10	
aaa ctc atc ctt cgc ctt ctt tct gga gtg gaa gct gtc aac tcc att				302
Lys Leu Ile Leu Arg Leu Leu Ser Gly Val Glu Ala Val Asn Ser Ile				
	15	20	25	
gtt gca ttg ttg tcc gtg gac ttt cat gct tta gaa caa gat gcc agc				350
Val Ala Leu Leu Ser Val Asp Phe His Ala Leu Glu Gln Asp Ala Ser				
	30	35	40	
aaa gaa cag cag ctt aga ccg agt ctt gcc ctg ttg ccc agg ctg gag				398
Lys Glu Gln Gln Leu Arg Pro Ser Leu Ala Leu Leu Pro Arg Leu Glu				
	50	55	60	
tgc ggt ggc gtg atc tgc gct cac tgc aac ctc cac ctc ctg ggt tca				446
Cys Gly Gly Val Ile Ser Ala His Cys Asn Leu His Leu Leu Gly Ser				
	65	70	75	
agt gat tct tct gcc tca gtc tcc cga gta gat ggg act aca ggc acg				494
Ser Asp Ser Ser Ala Ser Val Ser Arg Val Asp Gly Thr Thr Gly Thr				
	80	85	90	
cgc cac cat gcc cgg ctt ttt tgt att att agt aga gac gag gtt tca				542
Arg His His Ala Arg Leu Phe Cys Ile Ile Ser Arg Asp Glu Val Ser				
	95	100	105	
cca tat tgg cca ggc tgg tct cga act ccc aac ctt gtg atc cac ctg				590
Pro Tyr Trp Pro Gly Trp Ser Arg Thr Pro Asn Leu Val Ile His Leu				
	110	115	120	
cct cag cct ccc aaa gta ctg gga tta ccg gcg tgagccactg tgcctggcct				643
Pro Gln Pro Pro Lys Val Leu Gly Leu Pro Ala				
	130	135		
atgtgggtgga gtatttatta tacgtaggat gtgaatccct gaaatacaca ggcaactaa				703
atagcatttc agaagtaaca gaacatttta gaacacttta tacatccttt tatagcttat				763
ttcaataaaa gataattttt atacaaaaaa aaaaaaaaaa a				804

<210> 117

<211> 484

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 30..335

<220>

<221> sig_peptide

<222> 30..71

<223> Von Heijne matrix

score 4.49063834776683

seq FLTALLWRGRIPG/RQ

<400> 117

gcagagtctt	gagcagcgcg	gcaggcacc	atg ttc	ctg act	gcg ctc	ctc tgg	
			Met Phe	Leu Thr	Ala Leu	Leu Trp	53

cgc ggc	cgc att	ccc ggc	cgt cag	tgg atc	ggg aag	cac cgg	cgg ccg	
Arg Gly	Arg Ile	Pro Gly	Arg Gln	Trp Ile	Gly Lys	His Arg	Arg Pro	101
-5		1		5			10	

cgg ttc gtg tgc ttg cgc gcc aag cag aac atg atc cgc cgc ctg gag 149
 Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg Leu Glu
 15 20 25
 atc gag cgc gag aac cat tac tgg ctg agc atg ccc tac atg acc cgg 197
 Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met Thr Arg
 30 35 40
 gag cag gag cgc gcc cac gcc cgc gtg cgc agg agg gag gcc ttc gag 245
 Glu Gln Glu Arg Gly His Ala Val Arg Arg Arg Glu Ala Phe Glu
 45 50 55
 gcc ata aag cgc gcc gcc act tcc aag ttc ccc cgc cat aga ttc att 293
 Ala Ile Lys Ala Ala Ala Thr Ser Lys Phe Pro His Arg Phe Ile
 60 65 70
 cgc gag cag ctg gac cat ctg aat gtc acc aag aaa tgg tcc 335
 Ala Asp Gln Leu Asp His Leu Asn Val Thr Lys Lys Trp Ser
 75 80 85
 taatcctgag tcgtcacccct tggattttat ggatcacgga gctgaccatc tttacctggt 395
 cctggaactg aaaaactgta gcttgtgtga aaatgagcct ttggaccagt cttattataa 455
 acaaacaaac acaaaaaaaaa aaaaaaaaaa 484

<210> 118
 <211> 985
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..752

<220>
 <221> sig_peptide
 <222> 21..107
 <223> Von Heijne matrix
 score 3.61056351168286
 seq FPLYLLNFLGLWS/WI

<400> 118
 gtttttttcc cttctgagca atg gag ctt acc atc ttt atc ctg aga ctg gcc 53
 Met Glu Leu Thr Ile Phe Ile Leu Arg Leu Ala
 -25 -20
 att tac atc ctg aca ttt ccc ttg tac ctg ctg aac ttt ctg gcc ttg 101
 Ile Tyr Ile Leu Thr Phe Pro Leu Tyr Leu Leu Asn Phe Leu Gly Leu
 -15 -10 -5
 tgg agc tgg ata tgc aaa aaa tgg ttc ccc tac ttc ttg gtg agg ttc 149
 Trp Ser Trp Ile Cys Lys Lys Trp Phe Pro Tyr Phe Leu Val Arg Phe
 1 5 10
 act gta ata tac aac gaa cag atg gca agc aag aag cgg gag ctg ttc 197
 Thr Val Ile Tyr Asn Glu Gln Met Ala Ser Lys Lys Arg Glu Leu Phe
 15 20 25 30
 agt aac ctg cag gag ttt cgc gcc ccc tcc ggg aaa ctg tcc ctg ctg 245
 Ser Asn Leu Gln Glu Phe Ala Gly Pro Ser Gly Lys Leu Ser Leu Leu
 35 40 45
 gaa gtg gcc tgt gcc acg ggg gcc aac ttc aag ttc tac cca cct ggg 293
 Glu Val Gly Cys Gly Thr Gly Ala Asn Phe Lys Phe Tyr Pro Pro Gly
 50 55 60
 tgc agg gtg acc tgt att gac ccc aac ccc aac ttt gag aag ttt ttg 341
 Cys Arg Val Thr Cys Ile Asp Pro Asn Pro Asn Phe Glu Lys Phe Leu
 65 70 75
 atc aag agc att gca gag aac cga cac ctg cag ttt gag cgc ttt gtg 389


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Ile Lys Ser Ile Ala Glu Asn Arg His Leu Gln Phe Glu Arg Phe Val
  80                      85                      90
gta gct gcc ggg gag aac atg cac cag gtg gct gat ggc tct gtg gat 437
Val Ala Ala Gly Glu Asn Met His Gln Val Ala Asp Gly Ser Val Asp
  95                      100                      105                      110
gtg gtg gtc tgc acc ctg gtg ctg tgc tct gtg aag aac cag gag cgg 485
Val Val Val Cys Thr Leu Val Leu Cys Ser Val Lys Asn Gln Glu Arg
  115                      120                      125
att ctc cgc gag gtg tgc aga gtg ctg aga ccg gga ggg gct ttc tat 533
Ile Leu Arg Glu Val Cys Arg Val Leu Arg Pro Gly Gly Ala Phe Tyr
  130                      135                      140
ttc atg gag cat gtg gca gct gag tgt tgc act tgg aat tac ttc tgg 581
Phe Met Glu His Val Ala Ala Glu Cys Ser Thr Trp Asn Tyr Phe Trp
  145                      150                      155
caa caa gtc ctg gat cct gcc tgg cac ctt ctg ttt gat ggg tgc aac 629
Gln Gln Val Leu Asp Pro Ala Trp His Leu Leu Phe Asp Gly Cys Asn
  160                      165                      170
ctg acc aga gag agc tgg aag gcc ctg gag cgg gcc agc ttc tct aag 677
Leu Thr Arg Glu Ser Trp Lys Ala Leu Glu Arg Ala Ser Phe Ser Lys
  175                      180                      185                      190
ctg aag ctg cag cac atc cag gcc cca ctg tcc tgg gag ttg gtg cgc 725
Leu Lys Leu Gln His Ile Gln Ala Pro Leu Ser Trp Glu Leu Val Arg
  195                      200                      205
cct cat atc tat gga tat gct gtg aaa tagtgtgagc tggcagttaa 772
Pro His Ile Tyr Gly Tyr Ala Val Lys
  210                      215
gagctgaatg gctcaaagaa tttaaagcctt cagttttaca tttaaaatgc taggtgggtg 832
cctgtaatcc caggtactctt gaaggctgag gcaggagaat ctcttgaacc cagaaggcga 892
aggttgagct gaaccgagat catgccattg tactctagcc tgggtgacaa gagcaagact 952
cgctctcaaa aaaaaataaa aaaaaaaaaa aaa 985

<210> 119
<211> 839
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 185..715

<220>
<221> sig_peptide
<222> 185..253
<223> Von Heijne matrix
      score 9.49395175807817
      seq SLLFICFFGESFC/IC

<400> 119
atattttgct gactggcaag gttatatgaa gtgcttttat tgaagcacca tttaactaa 60
cagctcctgg tattttctgc ttcccttcgt agggaaattta gttattttat ttattatttt 120
agctaattta gctatttttaa aatagctaaa ttttagctac ttttttttca attgacaaag 180
aagg atg tct aat caa aga cta ccg ctg att ttt tct ctg ttg ttt atc 229
      Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile
      -20                      -15                      -10
tgc ttc ttc ggg gag agt ttc tgc att tgt gat gga act gtc tgg aca 277
Cys Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr
      -5                      1                      5
aag gtt gga tgg gag att ctt cca gaa gaa gta cat tat tgg aaa gtt 325

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Lys Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Val
 10 15 20
 aag ggt tct cca tct cac tgc cct tat ctt ctg gat aaa cta tgc 373
 Lys Gly Ser Pro Ser His Cys Leu Pro Tyr Leu Leu Asp Lys Leu Cys
 25 30 35 40
 tgc gac ttt gct aac atg gat ata ttt cag ggt tgt tta tat ctc att 421
 Cys Asp Phe Ala Asn Met Asp Ile Phe Gln Gly Cys Leu Tyr Leu Ile
 45 50 55
 tat aat tta tta caa gct gtc ttc ttc gtc tta ttt gtt ttg tct gtg 469
 Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe Val Leu Ser Val
 60 65 70
 cat tac ctg tgg aag aaa tgg aag aaa cac caa aaa aag ctg aaa aag 517
 His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys Lys Leu Lys Lys
 75 80 85
 caa gcc tcc tta gaa aaa cct ggt aat gat cta gaa agc cca ttg atc 565
 Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu Glu Ser Pro Leu Ile
 90 95 100
 aac aac att gac caa aca ctc cac aga gtg gca acc aca gca tca gtg 613
 Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala Thr Thr Ala Ser Val
 105 110 115 120
 ata tac aag atc tgg gag cac agg tct cac cat cct tcc tct aag aaa 661
 Ile Tyr Lys Ile Trp Glu His Arg Ser His His Pro Ser Ser Lys Lys
 125 130 135
 att aag cac tgc aaa tta aag aag aag agt aaa gaa gaa gga gcc aga 709
 Ile Lys His Cys Lys Leu Lys Lys Ser Lys Glu Glu Gly Ala Arg
 140 145 150
 aga tac taaataaatg catatgcaaa tgtagcttac tcaattatag atatcacaaa 765
 Arg Tyr
 agaaatctat catctaagga ttaaaaaattg ttctttggaa acctttataa aaaaaaaaga 825
 aaaaaaaaaa aaaa 839

 <210> 120
 <211> 583
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 54..527

 <220>
 <221> sig_peptide
 <222> 54..116
 <223> Von Heijne matrix
 score 6.80928714315144
 seq ALXSLNLAPPTVA/AP

 <400> 120
 aacgtcatct aggagcaccg agcagcttgg ctaaaagtaa gggtgtctgtg ctg atg 56
 Met
 gcc ctg tgc gca ctg acc cgc gct ctg ccs tct ctg aac ctg gcg ccc 104
 Ala Leu Cys Ala Leu Thr Arg Ala Leu Pro Ser Leu Asn Leu Ala Pro
 -20 -15 -10 -5
 ccg acc gtc gcc gcc cct gcc ccg agt ctg ttc ccc gcc gcc cag atg 152
 Pro Thr Val Ala Ala Pro Ala Pro Ser Leu Phe Pro Ala Ala Gln Met
 1 5 10
 atg aac aat gcc ctc ctc caa cag ccc tct gcc ttg atg ttg ctc ccc 200
 Met Asn Asn Gly Leu Leu Gln Gln Pro Ser Ala Leu Met Leu Leu Pro

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      15              20              25
tgc cgc cca gtt ctt act tct gtg gcc ctt aat gcc aac ttt gtg tcc      248
Cys Arg Pro Val Leu Thr Ser Val Ala Leu Asn Ala Asn Phe Val Ser
      30              35              40
tgg aag agt cgt acc aag tac acc att aca cca gtg aag atg agg aag      296
Trp Lys Ser Arg Thr Lys Tyr Thr Ile Thr Pro Val Lys Met Arg Lys
      45              50              55              60
tct ggg ggc cga gac cac aca ggt gct gga aac gtg cgt aga aca gta      344
Ser Gly Gly Arg Asp His Thr Gly Ala Gly Asn Val Arg Arg Thr Val
      65              70              75
ggc cga gta tcc aac gtt gat cat aac aaa cgg gtc att ggc aag gca      392
Gly Arg Val Ser Asn Val Asp His Asn Lys Arg Val Ile Gly Lys Ala
      80              85              90
ggg cgc aac cgc tgg ctg ggc aag agg cct aac agt ggg cgg tgg cac      440
Gly Arg Asn Arg Trp Leu Gly Lys Arg Pro Asn Ser Gly Arg Trp His
      95              100              105
cgc aag ggg ggc tgg gct ggc cga aag att cgg cca cta ccc ccc atg      488
Arg Lys Gly Gly Trp Ala Gly Arg Lys Ile Arg Pro Leu Pro Pro Met
      110              115              120
aag agt tac gtg aag ctg cct tct gct tct gcc caa agc tgatatccct      537
Lys Ser Tyr Val Lys Leu Pro Ser Ala Ser Ala Gln Ser
      125              130              135
gtactctaataaaaatgccccccccccctcaaaaaaaaaaaaaa      583

<210> 121
<211> 1024
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 129..686

<220>
<221> sig_peptide
<222> 129..185
<223> Von Heijne matrix
      score 6.45239823575329
      seq  SVFLLMVNGQVES/AQ

<400> 121
cttcgcgaag gtgtcgctgc caagaaacgt gtctcgcgcg ctacgcgcgc tgtttctagg      60
gcaacgcggc cgtctcttag caaccgcgcg cggcctagggt gggcccccc ggcaccccc      120
gacctgcc atg gcg acc gcg agt cct agc gtc ttt cta ctc atg gtc aac      170
      Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn
      -15              -10
ggg cag gtg gag agc gcc cag ttt cca gag tat gat gac ctc tac tgc      218
Gly Gln Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Leu Tyr Cys
      -5              1              5              10
aag tac tgc ttt gtg tac ggc cag gac tgg gcc ccc aca gcg ggt ctg      266
Lys Tyr Cys Phe Val Tyr Gly Gln Asp Trp Ala Pro Thr Ala Gly Leu
      15              20              25
gag gag ggg atc tca cag atc aca tcc aag agc caa gat gtg cgg caa      314
Glu Glu Gly Ile Ser Gln Ile Thr Ser Lys Ser Gln Asp Val Arg Gln
      30              35              40
gca ctg gtg tgg aac ttc ccc att gat gtc acc ttt aaa agc acc aac      362
Ala Leu Val Trp Asn Phe Pro Ile Asp Val Thr Phe Lys Ser Thr Asn
      45              50              55

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ccc tac ggc tgg cca cag atc gtg ctc agc gtg tat gga cca gat gtg      410
Pro Tyr Gly Trp Pro Gln Ile Val Leu Ser Val Tyr Gly Pro Asp Val
60          65          70          75
ttc ggg aac gat gtg gtt cga ggc tat ggg gcc gtg cac gtg ccc ttc      458
Phe Gly Asn Asp Val Val Arg Gly Tyr Gly Ala Val His Val Pro Phe
80          85          90
tca cct ggc cgg cac aaa agg acc atc ccc atg ttt gtc cca gaa tct      506
Ser Pro Gly Arg His Lys Arg Thr Ile Pro Met Phe Val Pro Glu Ser
95          100          105
acg tct aaa ctg cag aag ttt aca agc tgg ttc atg ggg cgg cgg ccc      554
Thr Ser Lys Leu Gln Lys Phe Thr Ser Trp Phe Met Gly Arg Arg Pro
110          115          120
gag tac aca gac ccc aag gtg gtg gct cag ggt gaa ggc cgg gaa gct      602
Glu Tyr Thr Asp Pro Lys Val Val Ala Gln Gly Glu Gly Arg Glu Ala
125          130          135
atc aca gct ccc cgg aaa gct gtc ttc tct gtc cat ggc ctc acc tca      650
Ile Thr Ala Pro Arg Lys Ala Val Phe Ser Val His Gly Leu Thr Ser
140          145          150          155
ccc agg gca ctg gcc ttg gtc cac atc aag ggg acc tgaagcttcc      696
Pro Arg Ala Leu Ala Leu Val His Ile Lys Gly Thr
160          165
ctgaagcctc tagcctgtgg tgtgcacgta caagcctcag gccccatttg tccagcctgt      756
cagcagctgg gaaatactaa gtcacctct tctgggtatg tttaatcttc caatttttct      816
caacattact gaaatgtcta aatgtggaaa agttgacatc attttacagt gaacaccaca      876
taccaccac ctagatttta ccattaccaa ttctctgttc cgtacttgta tattcacata      936
tatccaacta ttcacccctg ctccaatcca tctattttt attgcatctc aaaataaact      996
gtgaaatcag gaaaaaaaa aaaaaaaa      1024

<210> 122
<211> 760
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 165..614

<220>
<221> sig_peptide
<222> 165..305
<223> Von Heijne matrix
      score 5.10820788278539
      seq ALGLALCSTKALS/VG

<400> 122
aatttcgat gccaggcacc ctcaaggcac agaggctggg gctcatgttg ggggcacttg      60
gcctctcag gcctcgaagg cttctcctgg gctgatgcga gctggggaac gggagggacg      120
gacgtgggag cgagaacgtc acactggagg cagctggttg cacg atg ggg gac aga      176
                               Met Gly Asp Arg
                               -45
gtg aaa ggt agc aag tca aga gcc ttc gtg tca cca tgg cca cac acc      224
Val Lys Gly Ser Lys Ser Arg Ala Phe Val Ser Pro Trp Pro His Thr
-40          -35          -30
ccg atg gct tcc ggc ttg agg gac ccc tgg ctg cag ccc aca gcc ctg      272
Pro Met Ala Ser Gly Leu Arg Asp Pro Trp Leu Gln Pro Thr Ala Leu
-25          -20          -15
ggc ctt gca ctg tgc tct acg aag gcc ctg tcc gtg ggc tct gcc cct      320
Gly Leu Ala Leu Cys Ser Thr Lys Ala Leu Ser Val Gly Ser Ala Pro

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-10          -5          1          5
ttg ccc ccg cga aat tcc aac acc atg gcg gcg gct gcc ctg gct gcc      368
Leu Pro Pro Arg Asn Ser Asn Thr Met Ala Ala Ala Leu Ala Ala
          10          15          20
ccc agc ctg ggc ttc gat ggg gtg att ggg gtg ctc gtg gct gat acc      416
Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu Val Ala Asp Thr
          25          30          35
agc ctc acg gac atg cac gtg gtg gat gta gag ctg agc gga ccc cgg      464
Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu Ser Gly Pro Arg
          40          45          50
ggc ccc acg ggc cga agc ttt gct gtg cac acc cgc aga gag aac cct      512
Gly Pro Thr Gly Arg Ser Phe Ala Val His Thr Arg Glu Asn Pro
          55          60          65
gcc gag cca ggc gcg gtc acc ggc tcc gcc acc gtc acg gcc ttc tgg      560
Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val Thr Ala Phe Trp
          70          75          80          85
cgg agc ctc ctg gcc tgc tgc cag ctc ccc tcc agg ccg ggg atc cat      608
Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg Pro Gly Ile His
          90          95          100
ctc tgc tgagaagcct cctccctccc gagacaagat catctgcctg gctctcacc      664
Leu Cys
accaccatcc caccctctgcc ctgccccact tccccagggt ctccctctctg actcagtaaa      724
gatcaccgct gcctccctca aaaaaaaaaa aaaaaa      760

<210> 123
<211> 594
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 192..476

<220>
<221> sig_peptide
<222> 192..326
<223> Von Heijne matrix
      score 6.60884760057354
      seq FILLLLSGPAEM/SA

<400> 123
acctttatgtg aaaaagacta cagcaaatca tactgaggtg aatgaagaca gtgaaatgaa      60
ggagaagcca ggtcctcttt atgttttcgc agctgggtca aggggtttgg ggttttctat      120
ctaggttaaa gattgcgtaa tacacagctg gagccataga cattaatgca tgtttatcac      180
acgcaacaac g atg ctg cat cat gtg att aca gct ggg cct gtg ctg ctt      230
      Met Leu His His Val Ile Thr Ala Gly Pro Val Leu Leu
      -45          -40          -35
cta cac ctc cct cgc cct gac act tcc acc agg ttg ctc ctc acc tcc      278
Leu His Leu Pro Arg Pro Asp Thr Ser Thr Arg Leu Leu Leu Thr Ser
      -30          -25          -20
gtc tct gct ttt atc ctc tta ctg ctc ctt tca gga cca gca gaa atg      326
Val Ser Ala Phe Ile Leu Leu Leu Leu Leu Ser Gly Pro Ala Glu Met
      -15          -10          -5
tca gct tcc cag gaa tcc ttc cct gga tct ctg cag caa gaa ata gct      374
Ser Ala Ser Gln Glu Ser Phe Pro Gly Ser Leu Gln Gln Glu Ile Ala
      1          5          10          15
tct ctg atc act gta gca ctt ggt tct tta ata tct tta tct tgc tct      422
Ser Leu Ile Thr Val Ala Leu Gly Ser Leu Ile Ser Leu Ser Cys Ser

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      20              25              30
acc ttg tta tat ttt tct tgt gaa ctt aaa att ccc tgt gag gac gta      470
Thr Leu Leu Tyr Phe Ser Cys Glu Leu Lys Ile Pro Cys Glu Asp Val
      35              40              45
aac ctt tgaaggatg tctcatatct ctgaacctct ttaaaatgcc tagcatccct      526
Asn Leu
      50
gtgtgggtgc caattgcttg tgtattgaat taaattgtga ttgttaacct gaaaaaaaaa      586
aaaaaaaaa      594

<210> 124
<211> 559
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 16..297

<220>
<221> sig_peptide
<222> 16..93
<223> Von Heijne matrix
      score 6.65836819891491
      seq FCGSACLLAVIRA/FF

<400> 124
ttacacaggg gataa atg gca gca atc gag att gaa gtc aag cct aac cag      51
      Met Ala Ala Ile Glu Ile Glu Val Lys Pro Asn Gln
      -25              -20              -15
ggc ttt tgc ggg agc gca tgc ctt ttg gct gta att cgt gca ttt ttt      99
Gly Phe Cys Gly Ser Ala Cys Leu Leu Ala Val Ile Arg Ala Phe Phe
      -10              -5              1
ttt aag aaa aac gcc tgc ctt ctg cgt gag att ctc cag agc aaa ctg      147
Phe Lys Lys Asn Ala Cys Leu Leu Arg Glu Ile Leu Gln Ser Lys Leu
      5              10              15
ggc ggc atg ggc cct gtg gtc ttt tcg tac aga ggg ctt cct ctt tgg      195
Gly Gly Met Gly Pro Val Val Phe Ser Tyr Arg Gly Leu Pro Leu Trp
      20              25              30
ctc ttt gcc tgg ttg ttt cca aga tgt act gtg cct ctt act ttc ggt      243
Leu Phe Ala Trp Leu Phe Pro Arg Cys Thr Val Pro Leu Thr Phe Gly
      35              40              45              50
ttt gaa aac atg agg ggg ttg ggc gtg gta gct tac gcc tgt aat ccc      291
Phe Glu Asn Met Arg Gly Leu Gly Val Val Ala Tyr Ala Cys Asn Pro
      55              60              65
agc act tagggagcc gaggcgggag gatggcttga ggtccgtagt tgagaccagc      347
Ser Thr
ctggccaaca tggatgaagcc tggctctcac aaaaaataa taacaaaaat tagccgggtg      407
tgggtggctcg tgcctgtggt cccagctgct ccggtggctg aggcgggagg atctcttgag      467
cttaggcttt tgagctatca tggcgccagt gcactccagc gtggccaaca gagcgagacc      527
ctgtctctca aaaaacaaaa aaaaaaaaaa aa      559

<210> 125
<211> 744
<212> DNA
<213> Homo sapiens

<220>

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<221> CDS
 <222> 216..635

<220>
 <221> sig_peptide
 <222> 216..335
 <223> Von Heijne matrix
 score 4.38054120608596
 seq ITLVSAAPGKVIC/EM

<400> 125
 gcttcgtcac aagggtgcga tgaaagtcag tgagcaaato gcggaccacc ggggctgcca 60
 gctcgccctga ctcccggcct cttgcgctcc taggggcgga gaagggtgcg ggctcttcgc 120
 cctttgtgtc ctccttcttt cactaacctc tggactttcc agctcttccg aagttcgttc 180
 ttgcgcaaaag cccaaaggct ggaanaaccgt ccacg atg acc agc atg act cag 233
 Met Thr Ser Met Thr Gln
 -40 -35
 tct ctg cgg gag gtg ata aag gcc atg acc aag gct cgc aat ttt gag 281
 Ser Leu Arg Glu Val Ile Lys Ala Met Thr Lys Ala Arg Asn Phe Glu
 -30 -25 -20
 aga gtt ttg gga aag att act ctt gtc tct gct gct cct ggg aaa gtg 329
 Arg Val Leu Gly Lys Ile Thr Leu Val Ser Ala Ala Pro Gly Lys Val
 -15 -10 -5
 att tgt gaa atg aaa gta gaa gaa gag cat acc aat gca ata ggc act 377
 Ile Cys Glu Met Lys Val Glu Glu Glu His Thr Asn Ala Ile Gly Thr
 1 5 10
 ctc cac ggc ggt ttg aca gcc acg tta gta gat aac ata tca aca atg 425
 Leu His Gly Gly Leu Thr Ala Thr Leu Val Asp Asn Ile Ser Thr Met
 15 20 25 30
 gct ctg cta tgc acg gaa agg gga gca ccc gga gtc agt gtc gat atg 473
 Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro Gly Val Ser Val Asp Met
 35 40 45
 aac ata acg tac atg tca cct gca aaa tta gga gaa gat ata gtg att 521
 Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp Ile Val Ile
 50 55 60
 aca gca cat gtt ctg aag caa gga aaa aca ctt gca ttt acc tct gtg 569
 Thr Ala His Val Leu Lys Gln Gly Lys Thr Leu Ala Phe Thr Ser Val
 65 70 75
 gat ctg acc aac aag gcc aca gga aaa tta ata gca caa gga aga cac 617
 Asp Leu Thr Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln Gly Arg His
 80 85 90
 aca aaa cac ctg gga aac tgagagaaca gcagaatgac ctaagaanaac 665
 Thr Lys His Leu Gly Asn
 95 100
 ccaacaatga atatcaagta tagatttgac tcaaacatt gtaatttttg aaataaacta 725
 gcaaaaaaaaa aaaaaaaaaa 744

<210> 126
 <211> 824
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 164..280

<220>
 <221> sig_peptide

<222> 164..268
 <223> Von Heijne matrix
 score 5.73290676305402
 seq TLPLCPVTSPVWG/WS

<400> 126
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 gcggggccag aggggtgcgc ataggctgct gggtcgcaaa acc atg gac ccg gga 175
 Met Asp Pro Gly
 -35
 tgg ccc cac ttc aag ctg acc cac agc cgc tgc atg gct gtg ctt ttc 223
 Trp Pro His Phe Lys Leu Thr His Ser Arg Cys Met Ala Val Leu Phe
 -30 -25 -20
 ctt ggc act ctg ccc ttg tgt cct gtg acc agc cct gtg tgg ggc tgg 271
 Leu Gly Thr Leu Pro Leu Cys Pro Val Thr Ser Pro Val Trp Gly Trp
 -15 -10 -5 1
 agt cca ggg tgaccatcag gccctgggtg ggcgatgggg tgccctgggac 320
 Ser Pro Gly
 ctggctcagc ccgactgccc tcctcccaca gcctggcagc aggtgcaaca gcagctggat 380
 ggtggcccgag ccggtgaggg cgggccaagg cctgtgcagt acgtggagag gacccccaat 440
 ccccggtcgc agaactttgt gcccatctac ctgacgagc ggtggcgca gcagttcctg 500
 gcgagaatca ccagctgttc ctagtggctg ctgggagggg gcgctgctac acggccgacc 560
 tgtcgccagg agagaagcat gggccctcgc ccccccactg cgcctggctg ggtgcccggc 620
 acacctgaag tgcagcatt tggacttttg cactttttt tcccttggcc ccgctgtccc 680
 aaccaagctg ccatggccta gggccgaacc cgtctgacct cagccctgct cactgtgccc 740
 agggaccagc gaccagcccc tggggctggc agggaggagc tccaggctaa taaagtggag 800
 aaactgtcaa aaaaaaaaaa aaaa 824

<210> 127
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..301

<220>
 <221> sig_peptide
 <222> 68..190
 <223> Von Heijne matrix
 score 4.68908216483476
 seq AYLLYILLTGALQ/FG

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 tgcagtt atg tcg gcg tcg gta gtg tct gtc att tcg cgg ttc tta gaa 109
 Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Gly
 -40 -35 -30
 gag tac ttg agc tcc act ccg cag cgt ctg aag ttg ctg gac gcg tac 157
 Glu Tyr Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr
 -25 -20 -15
 ctg ctg tat ata ctg ctg acc ggg gcg ctg cag ttc ggt tac tgt ctc 205
 Leu Leu Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu
 -10 -5 1 5
 ctc gtg ggg acc ttc ccc ttc aac tct ttt ctc tcg ggc ttc atc tct 253
 Leu Val Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser

<220>
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 <222> 22..66
 <223> Von Heijne matrix
 score 4.68058603039206
 seq VLAGSLLGPTSRs/AA

<400> 129
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 Met Ala Val Leu Ala Gly Ser Leu Leu Gly
 -15 -10
 ccc acg agt agg tgc gca gcg ttg ctg ggt ggc agg tgg ctc cag ccc 99
 Pro Thr Ser Arg Ser Ala Ala Leu Leu Gly Gly Arg Trp Leu Gln Pro
 -5 1 5 10
 cgg gcc tgg ctg ggg ttc cca gac gcc tgg ggc ctc ccc acc ccg cag 147
 Arg Ala Trp Leu Gly Phe Pro Asp Ala Trp Gly Leu Pro Thr Pro Gln
 15 20 25
 cag gcc cgg ggc aag gct cgc ggg aat gag tat cag ccg agc aat atc 195
 Gln Ala Arg Gly Lys Ala Arg Gly Asn Glu Tyr Gln Pro Ser Asn Ile
 30 35 40
 aaa cgc aag aac aag cac gcc tgg gtc cgg cgc ctg agc acg ccg gcc 243
 Lys Arg Lys Asn Lys His Gly Trp Val Arg Arg Leu Ser Thr Pro Ala
 45 50 55
 ggc gtg cag gtc atc ctt cgc cga atg ctc aag ggc cgc aag tgc ctg 291
 Gly Val Gln Val Ile Leu Arg Arg Met Leu Lys Gly Arg Lys Ser Leu
 60 65 70 75
 agc cat tgaggatcgc gacgcagtcg gcggggaccc tcattggaagc atcgccctcg 347
 Ser His
 cctcggacct tgcctggcgc tatttttgca gggagctggg gacgcaggaac gcctcggacc 407
 tgagtgtctc ccatattgtg ggtttgaagt ctggatggga gccttgccaa gtcccttttt 467
 aggcttttta attaggaagc atttcgaacc tgcgcaacag accaaagaac agtacaaaga 527
 acatccgtgt acccagtaac ctgactaccg actacctaca acccgctccct gccccatcct 587
 gagttctttt gaagctgac tcaggcatcg gattatttct tctgtaataa tttcagaatg 647
 tatctctcca agatgagagc tcattaaaaa ataattacaa agcttatcac atccaaaaaga 707
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 aaaaaaaaaa 776

<210> 130
 <211> 998
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 9..845

<220>
 <221> sig_peptide
 <222> 9..134
 <223> Von Heijne matrix
 score 6.13963522287438
 seq RSLALAAPSSNG/SP

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 Met Ala Ala Pro Val Arg Arg Thr Leu Leu Gly Val Ala Gly
 -40 -35 -30

ggt tgg cgg cgg ttc gag agg ctc tgg gcc ggc agt cta agc tct cgc 98
 Gly Trp Arg Arg Phe Glu Arg Leu Trp Ala Gly Ser Leu Ser Ser Arg
 -25 -20 -15
 agc ctg gct ctt gca gcc gca ccc tca agc aac gga tcc cca tgg cgc 146
 Ser Leu Ala Leu Ala Ala Ala Pro Ser Ser Asn Gly Ser Pro Trp Arg
 -10 -5 1
 ttg ttg ggc gcg ttg tgc ctg cag cgg cca cct gta gtc tcc aag ccg 194
 Leu Leu Gly Ala Leu Cys Leu Gln Arg Pro Pro Val Val Ser Lys Pro
 5 10 15 20
 ttg acc cca ttg cag gaa gag atg gcg tct cta ctg cag cag att gag 242
 Leu Thr Pro Leu Gln Glu Met Ala Ser Leu Leu Gln Gln Ile Glu
 25 30 35
 ata gag aga agc ctg tat tca gac cac gag ctt cgt gct ctg gat gaa 290
 Ile Glu Arg Ser Leu Tyr Ser Asp His Glu Leu Arg Ala Leu Asp Glu
 40 45 50
 aac cag cga ctg gca aag aag aaa gct gac ctt cat gat gaa gaa gat 338
 Asn Gln Arg Leu Ala Lys Lys Lys Ala Asp Leu His Asp Glu Glu Asp
 55 60 65
 gaa cag gat ata ttg ctg gcg caa gat ttg gaa gat atg tgg gag cag 386
 Glu Gln Asp Ile Leu Leu Ala Gln Asp Leu Glu Asp Met Trp Glu Gln
 70 75 80
 aaa ttt cta cag ttc aaa ctt gga gct cgc ata aca gaa gct gat gaa 434
 Lys Phe Leu Gln Phe Lys Leu Gly Ala Arg Ile Thr Glu Ala Asp Glu
 85 90 95 100
 aag aat gac cga aca tcc ctg aac agg aac cta gac agg aac ctt gtc 482
 Lys Asn Asp Arg Thr Ser Leu Asn Arg Asn Leu Asp Arg Asn Leu Val
 105 110 115
 ctg tta gtc aga gag aag ttt gga gac cag gat gtt tgg ata ctg ccc 530
 Leu Leu Val Arg Glu Lys Phe Gly Asp Gln Asp Val Trp Ile Leu Pro
 120 125 130
 cag gca gag tgg cag cct ggg gag acc ctt cga gga aca gct gaa cga 578
 Gln Ala Glu Trp Gln Pro Gly Glu Thr Leu Arg Gly Thr Ala Glu Arg
 135 140 145
 acc ctg gcc aca ctc tca gaa aac aac atg gaa gcc aag ttc cta gga 626
 Thr Leu Ala Thr Leu Ser Glu Asn Asn Met Glu Ala Lys Phe Leu Gly
 150 155 160
 aat gca ccc tgt ggg cac tac aca ttc aag ttc ccc cag gca atg cgg 674
 Asn Ala Pro Cys Gly His Tyr Thr Phe Lys Phe Pro Gln Ala Met Arg
 165 170 175 180
 aca gag agt aac ctc gga gcc aag gtg ttc ttc ttc aaa gca ctg cta 722
 Thr Glu Ser Asn Leu Gly Ala Lys Val Phe Phe Lys Ala Leu Leu
 185 190 195
 tta act gga gac ttt tcc cag gct ggg aat aag ggc cat cat gtt tgg 770
 Leu Thr Gly Asp Phe Ser Gln Ala Gly Asn Lys Gly His His Val Trp
 200 205 210
 gtc att aag gat gag ctg ggt gac tat ttg aaa cca aaa tac ctg gcc 818
 Val Ile Lys Asp Glu Leu Gly Asp Tyr Leu Lys Pro Lys Tyr Leu Ala
 215 220 225
 caa gtt agg agg ttt gtt tca gac ctc tgatgggccc agctgcctgt 865
 Gln Val Arg Arg Phe Val Ser Asp Leu
 230 235
 ggacggtgct cagacaagtc tgggattaga gcctcaagga cattgtgtga ttgcctcaca 925
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 aaaaaaaaaa aaa 998

<210> 131
 <211> 779
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 27..578

<220>

<221> sig_peptide

<222> 27..119

<223> Von Heijne matrix
score 4.50637135496675
seq TALMVGAAASLLEG/RP

<400> 131

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      -30                               -25
cag gaa cac atg ctt ctc acc cct ctc act gct ctg atg gtg ggg gct      101
Gln Glu His Met Leu Leu Thr Pro Leu Thr Ala Leu Met Val Gly Ala
      -20                               -15                               -10
gct tct ctg ctt gag ggc cgg cca cag atc tca gct cca tac tcc cga      149
Ala Ser Leu Leu Glu Gly Arg Pro Gln Ile Ser Ala Pro Tyr Ser Arg
      -5                               1                               5                               10
gct gca tgt tgc agc cct ggg gca ctg gga tgt cct gca gct cgg gtt      197
Ala Ala Cys Cys Ser Pro Gly Ala Leu Gly Cys Pro Ala Ala Arg Val
      15                               20                               25
ggg att ctg gat ctg atg tat tcc tgg gtt gcc agg aaa gtg ctc agg      245
Gly Ile Leu Asp Leu Met Tyr Ser Trp Val Ala Arg Lys Val Leu Arg
      30                               35                               40
tgc agc aat act ggg ctg cag ggg ctg cac tgt gca cca gct tat gca      293
Cys Ser Asn Thr Gly Leu Gln Gly Leu His Cys Ala Pro Ala Tyr Ala
      45                               50                               55
gca cag ctt ggt atg gac cct ggg agg ggc caa cga gca gga ggg cct      341
Ala Gln Leu Gly Met Asp Pro Gly Arg Gly Gln Arg Ala Gly Gly Pro
      60                               65                               70
gta gag cag aca tac ttc agt ccc atg ggg aag ctg ccc act ctt tcg      389
Val Glu Gln Thr Tyr Phe Ser Pro Met Gly Lys Leu Pro Thr Leu Ser
      75                               80                               85                               90
tgg ctg gaa ggc tgt aca gca gtc atg acg ctg gca tct gct tgg ctt      437
Trp Leu Glu Gly Cys Thr Ala Val Met Thr Leu Ala Ser Ala Trp Leu
      95                               100                               105
ctg ggg agc cct cgg gaa act tac aat cat gag aag gtg aag gag aag      485
Leu Gly Ser Pro Arg Glu Thr Tyr Asn His Glu Lys Val Lys Glu Lys
      110                               115                               120
cag tgt cca ttc tcc agt atg gtt ttg ggg gag tat ggc ttc cta cct      533
Gln Cys Pro Phe Ser Ser Met Val Leu Gly Glu Tyr Gly Phe Leu Pro
      125                               130                               135
act gtg gac cac ctg tca act ctg ggc tgt aac atg aga gaa ttg      578
Thr Val Asp His Leu Ser Thr Leu Gly Cys Asn Met Arg Glu Leu
      140                               145                               150
tgaacttctg tcttgtttga gccatggttt cattctcttt ttcagccatg tagcctgtgc      638
tgtaactcag taccacattta gcaactagtg aaagtcgaatg tgggtaaatt tgtcattctt      698
cagggttagaa catttcttcc ttttattctt gtgttttttgg ctataataaac tgggaaatta      758
tagtaaaaaa aaaaaaaaaa a      779
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<210> 132

<211> 1025

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 408..710

<220>

<221> sig_peptide

<222> 408..533

<223> Von Heijne matrix

score 5.66440183652506

seq QLCFHLISWLYSWA/SQ

<400> 132

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gacaaaaaca atagctacta caaacaatat gagtttataa ttatgtgctg atgtattcga 180
agatgtgttg acagtcgtga gtgtgtatcc taggaaaggc gagctggact ctgtctccat 240
ggtggctctc accccaggga cctaggaaca gcctgtcacc acacaattac ttttataacc 300
ctggagatga aaatctcctt gtccctcaaaa tacttccaga agaacaacca gatgggaagg 360
accttggttg ggactctttc cagttcactt ggggcagagg gaattta atg gct cac 416
Met Ala His
-40
gta gct gaa aag gat ggg cta gat tgg gct tca ggc tgc atc cca gga 464
Val Ala Glu Lys Asp Gly Leu Asp Trp Ala Ser Gly Cys Ile Pro Gly
-35 -30 -25
ctc caa aca ggg atc tgt ctc ttt ggc tct cag ctc tgc ttt cat ttg 512
Leu Gln Thr Gly Ile Cys Leu Phe Gly Ser Gln Leu Cys Phe His Leu
-20 -15 -10
agt tgg ctt tat tct tgg gct tca cag tgt ggc ccc aca gca cca gtt 560
Ser Trp Leu Tyr Ser Trp Ala Ser Gln Cys Gly Pro Thr Ala Pro Val
-5 1 5
att gat aaa aag agc tcc cct ttg ctg aca gaa ctg ctg gat ttg gtt 608
Ile Asp Lys Lys Ser Ser Pro Leu Leu Thr Glu Leu Leu Asp Leu Val
10 15 20 25
ctc att ggt cca gac gag gaa ggt atc cag cct caa gtc atc att gtg 656
Leu Ile Gly Pro Asp Glu Glu Gly Ile Gln Pro Gln Val Ile Ile Val
30 35 40
gcc agg aag atg gaa tac acc aaa tgg aca ggc ctg gca tgt acc cac 704
Ala Arg Lys Met Glu Tyr Thr Lys Trp Thr Gly Leu Ala Cys Thr His
45 50 55
aga gac tgagagttgg tgctggtggt tgtggtggca gatgatatta cctgaagaag 760
Arg Asp
ggacgaatgg gtgctgggca ggacaaagca tcagctgtcc agttcaggcc tctcctcttt 820
ccctggtgtc ttcatttttc tccgtctccc tctgtgccct taccctctgc ccaatctcat 880
tactctggtt cttgggagtt gccttctgag gatactccac tgggggtacc tgagcctgga 940
ttagagggca gggggaggat attgcctagc caaagtgggt gttcaataaa gaaccatttg 1000
gagatggcaa aaaaaaaaaa aaaaa 1025
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<210> 133

<211> 607

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 247..501

<220>
 <221> sig_peptide
 <222> 247..306
 <223> Von Heijne matrix
 score 6.43040298500966
 seq LLLVTLVASTVPG/NS

<400> 133
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 ttgattttca caactctgct tcaagtggcat atgtttagct ttttgtcttc tgaattaatt 120
 gggcttctga tgggtccctag aggtatcagc tactcagtca gaaaacatac atgggggaaga 180
 aactgaagtt catgccacaa actgtagcag ctttgaaca gaagggacca gacaacctca 240
 aggaga atg ggc cca aat acc aaa aat tta ctc ttg gtg acc ctt gtt 288
 Met Gly Pro Asn Thr Lys Asn Leu Leu Leu Val Thr Leu Val
 -20 -15 -10
 gct tct act gta cca ggc aac tct ctt ggg cag gat ttt act ttt gca 336
 Ala Ser Thr Val Pro Gly Asn Ser Leu Gly Gln Asp Phe Thr Phe Ala
 -5 1 5 10
 cac tta gaa aga tcc tgc acc agg gaa aat cgg tct cct ggg gag gta 384
 His Leu Glu Arg Ser Cys Thr Arg Glu Asn Arg Ser Pro Gly Glu Val
 15 20 25
 ttc cag caa cca tgc aag tct gga ggc ggg ggg gtt gga gaa cca aat 432
 Phe Gln Gln Pro Cys Lys Ser Gly Gly Val Gly Glu Pro Asn
 30 35 40
 gcc caa ggg cag cta ctt agc cag cac cca cta cct gcc ttc att aat 480
 Ala Gln Gly Gln Leu Leu Ser Gln His Pro Leu Pro Ala Phe Ile Asn
 45 50 55
 tgt tct cac ggg cag gcc ttt tgaaccaccc tggtacagaa caccaacctt 531
 Cys Ser His Gly Gln Ala Phe
 60 65
 ggtgctttag gctgtctgtg ccattttctag gcaatgaacg agtagttact gtaccaaccc 591
 aaaaaaaaaa aaaaaa 607

<210> 134
 <211> 774
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 333..602

<220>
 <221> sig_peptide
 <222> 333..416
 <223> Von Heijne matrix
 score 4.79986448293481
 seq VPALPLLSLCA/MV

<400> 134
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 ctctgctcta tcaggattcg attcttggtg ttaaacaaga caacgctgaa ggctcggtgc 120
 agcagccctg caaaggtttt tccagcgctc ttgggaggtg ggctgtgcc tgccctggccc 180
 acctggccca cctggcccac cattacctga aggggaagcat gaacagcctt tgacctggga 240
 gtggcgactg ctgagagggg actgtctgta cacaagcaat gtacgcttat gggacctgag 300
 tggagcccca acccacgcag ggcgtgktct tc atg gct ttt cct ggc caa tct 353
 Met Ala Phe Pro Gly Gln Ser
 -25

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gat acc aag atg cag tgg cca gaa gta cct gca ctt cca ctg tca      401
Asp Thr Lys Met Gln Trp Pro Glu Val Pro Ala Leu Pro Leu Leu Ser
-20      -15      -10
agt ctg tgc atg gct atg gtg agg aag agc tct gca ctg ggc aag gaa      449
Ser Leu Cys Met Ala Met Val Arg Lys Ser Ser Ala Leu Gly Lys Glu
-5      1      5      10
gtt ggc cgt cga gtg aag gaa atg gtg atg ctg gtg gcc cct ttc cgg      497
Val Gly Arg Arg Val Lys Glu Met Val Met Leu Val Ala Pro Phe Arg
15      20      25
cag tca agt tcc cta tca agg aca ttc agt tct cgg aaa gtg gtg aag      545
Gln Ser Ser Ser Leu Ser Arg Thr Phe Ser Ser Arg Lys Val Val Lys
30      35      40
gca cat gct tcc ctg cat ggt gcc cgc ctc tct cca ctc tct aga aat      593
Ala His Ala Ser Leu His Gly Ala Arg Leu Ser Pro Leu Ser Arg Asn
45      50      55
att aga ggc taggctgctg ctgtatgtca gggctagtcc ctcttctatg      642
Ile Arg Gly
60
aatccagaat aactctgaag aagccgagta acaggcatga agtgaagaga aatcgctgta      702
acaggaagac agcaaagcag atgctaata ccaactatt taacgaactg gaaccaacaa      762
aaaaaaaaaa aa      774

<210> 135
<211> 611
<212> DNA
<213> Homo sapiens

<220>
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<222> 110..376

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<221> sig_peptide
<222> 110..208
<223> Von Heijne matrix
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      seq LVPHSPLPGALSS/AP

<220>
<221> misc_feature
<222> 347
<223> n=a, g, c or t

<400> 135
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gcctgcgcag agccagaggc ctcagaagcc acaggaacat ggcctaggc atg gct cag      118
      Met Ala Gln

cca gca gcc ccc tcc ctg acg cgg ccc ttc ctg gca gag gcc ccg aca      166
Pro Ala Ala Pro Ser Leu Thr Arg Pro Phe Leu Ala Glu Ala Pro Thr
-30      -25      -20      -15
gca ctg gtc cca cac agc ccc ctg cct ggg gcc ctg tca agc gcc cct      214
Ala Leu Val Pro His Ser Pro Leu Pro Gly Ala Leu Ser Ser Ala Pro
-10      -5      1
ggc ccg aag cag ccc ccg acg gca agc aca ggc ccg gag ctg ctg ctg      262
Gly Pro Lys Gln Pro Pro Thr Ala Ser Thr Gly Pro Glu Leu Leu Leu
5      10      15
ctg cct ctt tcc tcc ttc atg ccc tgc ggg gcg gct gca cca gcc agg      310
Leu Pro Leu Ser Ser Phe Met Pro Cys Gly Ala Ala Ala Pro Ala Arg

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      20      25      30
gtg tca tca cag cgg gct act cct agg gat aag ccc ncc ggt ccc etc 358
Val Ser Ser Gln Arg Ala Thr Pro Arg Asp Lys Pro Xaa Gly Pro Leu
35      40      45      50
atc cct ggc cag tgt ccc tgacccccat ctactccttc ctgggggacct 406
Ile Pro Gly Gln Cys Pro
      55
ctcagcgcca gccattggc gcctgcgttg cccgcaccca ggccttcgcg caggccctgt 466
gctagcgtgt tcgcaccagg aacgcaggtg ctgggctgtc ggggaggcct caggccacct 526
ccaggaacag aacacagttt taagtttgat tttttttatt tcaaaatgct ttgcaattaa 586
atgaattact gttcaaaaaa aaaaaa 611

<210> 136
<211> 925
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 22..417

<220>
<221> sig_peptide
<222> 22..66
<223> Von Heijne matrix
      score 5.47092708754574
      seq RVLCAFAAGAVRA/LR

<400> 136
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      Met Asn Arg Val Leu Cys Ala Pro Ala Ala
      -15      -10
ggg gcc gtc cgg gcg ctg agg ctc ata gcc tgg gct tcc cga agc ctt 99
Gly Ala Val Arg Ala Leu Arg Leu Ile Gly Trp Ala Ser Arg Ser Leu
-5      1      5      10
cat ccg ttg ccc ggt tcc cgg gat cgg gcc cac cct gcc gcc gag gaa 147
His Pro Leu Pro Gly Ser Arg Asp Arg Ala His Pro Ala Ala Glu Glu
      15      20      25
gag gac gac cct gac cgc ccc att gag ttt tcc tcc agc aaa gcc aac 195
Glu Asp Asp Pro Asp Arg Pro Ile Glu Phe Ser Ser Ser Lys Ala Asn
      30      35      40
cct cac cgc tgg tgc gtc ggc cat acc atg gga aag gga cat cag cgg 243
Pro His Arg Trp Ser Val Gly His Thr Met Gly Lys Gly His Gln Arg
      45      50      55
ccc tgg tgg aag gtg ctg ccc ctc agc tgc ttc ctc gtg gcg ctg atc 291
Pro Trp Trp Lys Val Leu Pro Leu Ser Cys Phe Leu Val Ala Leu Ile
      60      65      70      75
atc tgg tgc tac ctg agg gag gag agc gag gcg gac cag tgg ttg aga 339
Ile Trp Cys Tyr Leu Arg Glu Glu Ser Glu Ala Asp Gln Trp Leu Arg
      80      85      90
cag gtg tgg gga gag gtg cca gag ccc agt gat cgt tct gag gag cct 387
Gln Val Trp Gly Glu Val Pro Glu Pro Ser Asp Arg Ser Glu Glu Pro
      95      100      105
gag act cca gct gcc tac aga gcg aga act tgacgggggtg cccgctgggg 437
Glu Thr Pro Ala Ala Tyr Arg Ala Arg Thr
      110      115
ctggcaggaa gggagccgac agccgccctt cggatttgat gtcacgtttg cccgtgactg 497
tcctggctgat gcgtgcgtcc tcagcactga aggacttggc tgggtgatgg ggcacttggc 557

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tatgctgatt	cgcgtagaagg	cggagcagaa	tctcagcaga	tcggaactg	ctctcgcct	617
ggctcttgat	gtccaaggat	tccatcggca	agacttctca	gatccttggg	gaaggtttca	677
gttgcaactgt	atgctgttgg	atttgccaag	tctttgtata	acataatcat	gtttccaaag	737
cacttctggt	gacacttgto	atccagtgtt	agtttgcagg	taatttgctt	tctgagatag	797
aatatctggc	agaagtgtga	aactgtattg	catgctgcgg	cctgtgcaag	gaacacttcc	857
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aaaaaaaa						925

<210> 137
 <211> 674
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..367

<220>
 <221> sig_peptide
 <222> 62..103
 <223> Von Heijne matrix
 score 4.49063834776683
 seq FLTALLWRGRIPG/RQ

<400> 137		
acgccacggc	gtctgctggc	ggccgcggag
c atg ttc ctg act gcg ctc ctc tgg cgc gcg att ccc gcc cgt cag		60
Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln		109
-10	-5	1
tgg atc ggg aag cac cgg cgg cgg ttc gtg tgc ttg cgc gcc aag		157
Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys		
5	10	15
cag aac atg atc cgc cgc ctg gag atc gat gcg gag aac cat tac tgg		205
Gln Asn Met Ile Arg Arg Leu Glu Ile Asp Ala Glu Asn His Tyr Trp		
20	25	30
ctg agc atg ccc tac atg acc cgg gag cag gag cgc gcc cac gcc gsg		253
Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Xaa		
35	40	45
dtg cgc agg agg gag gcc ttc gag gcc ata aag gcg gcc gcc act tcc		301
Xaa Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser		
55	60	65
aag ttc ccc cgg cat aga ttc att gcg gac cag ctc gac cat ctc aat		349
Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn		
70	75	80
gtc acc aag aaa tgg tcc taatcctgag tagtcacccct tggattttat		397
Val Thr Lys Lys Trp Ser		
85		
ggatcacgga	gctgaccatc	tttaacctggt
aaatgagcct	ttggaccagt	ctttattaaa
atatactagag	ctcctaaaccc	cccaataactt
tagtctgata	ggaagatagg	gatttcoctca
aataaagcca	caatgattcg	aaaaaaaaaa
		674

<210> 138
 <211> 1725
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 107..1618

<220>
 <221> sig_peptide
 <222> 107..178
 <223> Von Heijne matrix
 score 6.19650168602189
 seq LGLYSLVLSGALA/YA

<400> 138
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 cagtgtgccca gggtcctctg cggcctctctc aagccctgtc caggct atg ggc atc 115
 Met Gly Ile
 aag aca gca ttg ccg gcg gct gag ctg ggc ctc tac tct ctg gtg ctg 163
 Lys Thr Ala Leu Pro Ala Ala Glu Leu Gly Leu Tyr Ser Leu Val Leu
 -20 -15 -10
 agt ggg gcc ctg gcc tat gct ggc cgg ggc ctc ctt gag gct tca caa 211
 Ser Gly Ala Leu Ala Tyr Ala Gly Arg Gly Leu Leu Glu Ala Ser Gln
 -5 1 5 10
 gat ggg gcc cac agg aag gcc ttc cgg gag tct gtg cga cct ggc tgg 259
 Asp Gly Ala His Arg Lys Ala Phe Arg Glu Ser Val Arg Pro Gly Trp
 15 20 25
 gag tac att ggc cgg aag atg gat gtg gct gac ttc gag tgg gtg atg 307
 Glu Tyr Ile Gly Arg Lys Met Asp Val Ala Asp Phe Glu Trp Val Met
 30 35 40
 tgg ttc acc tcc ttt cgc aac gtc atc atc ttt gcc ctc tcc gga cat 355
 Trp Phe Thr Ser Phe Arg Asn Val Ile Ile Phe Ala Leu Ser Gly His
 45 50 55
 gtg ctg ttt gct aaa ctc tgc acg atg gtt gcc cca aag ctc cgc tcc 403
 Val Leu Phe Ala Lys Leu Cys Thr Met Val Ala Pro Lys Leu Arg Ser
 60 65 70 75
 tgg atg tat gct gtg tac ggg gcc ttg gct gtg atg ggc aca atg ggc 451
 Trp Met Tyr Ala Val Tyr Gly Ala Leu Ala Val Met Gly Thr Met Gly
 80 85 90
 cct tgg tac ctg ctg ctg ctt ggt cac tgt gtg ggc ctc tat gtg 499
 Pro Trp Tyr Leu Leu Leu Leu Gly His Cys Val Gly Leu Tyr Val
 95 100 105
 gcc tgc ctt ttg ggc cag ccc tgg ctc tgt ctt ggc ctt ggc ttg gcc 547
 Ala Ser Leu Leu Gly Gln Pro Trp Leu Cys Leu Gly Leu Gly Leu Ala
 110 115 120
 agc ctg gcc tcc ttc aag atg gac ccc cta atc tct tgg cag agc ggg 595
 Ser Leu Ala Ser Phe Lys Met Asp Pro Leu Ile Ser Trp Gln Ser Gly
 125 130 135
 ttt gta aca ggc act ttt gat ctt caa gag gtg ctg ttt cat ggg ggc 643
 Phe Val Thr Gly Thr Phe Asp Leu Gln Glu Val Leu Phe His Gly Gly
 140 145 150 155
 agc agc ttc aca gtg ctg cgt tgc acc agc ttt gca ctg gag agc tgt 691
 Ser Ser Phe Thr Val Leu Arg Cys Thr Ser Phe Ala Leu Glu Ser Cys
 160 165 170
 gcc cac cct gac cgc cac tac tcc tta gct gac ctg ctc aag tac agc 739
 Ala His Pro Asp Arg His Tyr Ser Leu Ala Asp Leu Leu Lys Tyr Ser
 175 180 185
 ttc tac ctg ccc ttc ttc ttc ttc ggg ccc atc atg acc ttt gat cgc 787
 Phe Tyr Leu Pro Phe Phe Phe Gly Pro Ile Met Thr Phe Asp Arg
 190 195 200
 ttc cat gct cag gtg agc cag gtg gag cca gtg aga cgc gag ggt gag 835

Phe His Ala Gln Val Ser Gln Val Glu Pro Val Arg Arg Glu Gly Glu
 205 210 215
 ctg tgg cac atc cga gcc cag gca ggc cta agc gtg gtc gcc atc atg 883
 Leu Trp His Ile Arg Ala Gln Ala Gly Leu Ser Val Val Ala Ile Met
 220 225 230 235
 gcc gtc gac atc ttc ttt cac ttc ttc tac atc ctc act atc ccc agc 931
 Ala Val Asp Ile Phe Phe His Phe Phe Tyr Ile Leu Thr Ile Pro Ser
 240 245 250
 gac ctc aag ttc gcc aac cgc ctc cca gac att gcc ctc gct ggc cta 979
 Asp Leu Lys Phe Ala Asn Arg Leu Pro Asp Ile Ala Leu Ala Gly Leu
 255 260 265
 gcc tat tca aac ctg gtg tat gac tgg gtg aag gcg gcc gtc ctc ttt 1027
 Ala Tyr Ser Asn Leu Val Tyr Asp Trp Val Lys Ala Ala Val Leu Phe
 270 275 280
 ggt gtt gtc aac act gtg gca tgc ctc gac cac ctg gac cca ccc cag 1075
 Gly Val Val Asn Thr Val Ala Cys Leu Asp His Leu Asp Pro Pro Gln
 285 290 295
 cct ccc aag tgc atc acc gca ctc tac gtc ttt gcg gaa acg cac ttt 1123
 Pro Pro Lys Cys Ile Thr Ala Leu Tyr Val Phe Ala Glu Thr His Phe
 300 305 310 315
 gac cgt ggc atc aac gac tgg ctt tgc aaa tat gtg tat aac cac att 1171
 Asp Arg Gly Ile Asn Asp Trp Leu Cys Lys Tyr Val Tyr Asn His Ile
 320 325 330
 ggt ggg gag cat tcc gct gtg atc cca gag ctg gca gcc aca gtg gcc 1219
 Gly Gly Glu His Ser Ala Val Ile Pro Glu Leu Ala Thr Val Ala
 335 340 345
 aca ttt gcc atc acc aca ctg tgg ctt ggg cct tgt gac att gtc tac 1267
 Thr Phe Ala Ile Thr Thr Leu Trp Leu Gly Pro Cys Asp Ile Val Tyr
 350 355 360
 ctg tgg tca ttc ctt aac tgc ttt ggc ctc aac ttt gag ctc tgg atg 1315
 Leu Trp Ser Phe Leu Asn Cys Phe Gly Leu Asn Phe Glu Leu Trp Met
 365 370 375
 caa aaa ctg gca gag tgg ggg ccc cta gca cga att gag gcc tct ctg 1363
 Gln Lys Leu Ala Glu Trp Gly Pro Leu Ala Arg Ile Glu Ala Ser Leu
 380 385 390 395
 tca gtg cag atg tcc cgt agg gtc cgg gcc ctg ttt gga gcc atg aac 1411
 Ser Val Gln Met Ser Arg Arg Val Arg Ala Leu Phe Gly Ala Met Asn
 400 405 410
 ttc tgg gcc atc atc atg tac aac ctt gtg agc ctg aac agc ctc aaa 1459
 Phe Trp Ala Ile Ile Met Tyr Asn Leu Val Ser Leu Asn Ser Leu Lys
 415 420 425
 ttc aca gag ctg gtt gcc cgg cgc ctg cta ctc aca ggg ttc ccc cag 1507
 Phe Thr Glu Leu Val Ala Arg Arg Leu Leu Leu Thr Gly Phe Pro Gln
 430 435 440
 acc acg ctg tcc atc ctg ttt gtc acc tac tgt ggc gtc cag ctg gta 1555
 Thr Thr Leu Ser Ile Leu Phe Val Thr Tyr Cys Gly Val Gln Leu Val
 445 450 455
 aag gag cgt gag cga acc ttg gca ctg gag gag gag cag aag cag gac 1603
 Lys Glu Arg Glu Arg Thr Leu Ala Leu Glu Glu Gln Lys Gln Asp
 460 465 470 475
 aaa gag aag ccg gag taggaggag cgggtagagg gatgggctct gctcagctat 1658
 Lys Glu Lys Pro Glu
 480
 tcttgggcca gatggggcct gaccgataga ataaaagact tttctacaac aaaaaaaaaa 1718
 aaaaaaa 1725

<210> 139
 <211> 1474

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 16..471

<220>
<221> sig_peptide
<222> 16..93
<223> Von Heijne matrix
score 5.809301698725
seq FCVCVIAIGVVQA/LI

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<400> 139
tacacgtttt cgтта atg gtg acc ttc cct gat gtg cct ctg ggc atc ttc      51
                Met Val Thr Phe Pro Asp Val Pro Leu Gly Ile Phe
                -25                      -20                      -15

ttg ttc tgt gtg tgt gtg atc gcc atc ggg gtc gtg cag gca ctg att      99
Leu Phe Cys Val Cys Val Ile Ala Ile Gly Val Val Gln Ala Leu Ile
                -10                      -5                      1

gta ggg tac gca ttc cac ttc cgg cac ctg ctg agc cgg cag atc cag      147
Val Gly Tyr Ala Phe His Phe Pro His Leu Leu Ser Pro Gln Ile Gln
                5                      10                      15

cgc tct gcc cac agg gct ctg tac cga cga cac gtc ctg ggc atc gtc      195
Arg Ser Ala His Arg Ala Leu Tyr Arg Arg His Val Leu Gly Ile Val
                20                      25                      30

ctc caa ggc cgg gcc ctg tgc ttt gca gcg gcc atc ttc tct ctc ttc      243
Leu Gln Gly Pro Ala Leu Cys Phe Ala Ala Ala Ile Phe Ser Leu Phe
                35                      40                      45                      50

ttt gtc ccc ttg tct tac ctg ctg atg gtg act gtc atc ctc ctc ccc      291
Phe Val Pro Leu Ser Tyr Leu Leu Met Val Thr Val Ile Leu Leu Pro
                55                      60                      65

tat gtc agc aag gtc acc ggc tgg tgc aga gac agg ctc ctg ggc cac      339
Tyr Val Ser Lys Val Thr Gly Trp Cys Arg Asp Arg Leu Leu Gly His
                70                      75                      80

agg gag ccc tcg gct cac cca gtg gaa gtc ttc tcg ttt gac ctc cac      387
Arg Glu Pro Ser Ala His Pro Val Glu Val Phe Ser Phe Asp Leu His
                85                      90                      95

gag cca ctc agc aag gag cgc gtg gaa gcc ttc agc gac gga gtc tac      435
Glu Pro Leu Ser Lys Glu Arg Val Glu Ala Phe Ser Asp Gly Val Tyr
                100                      105                      110

gcc atc gtg gcc acg ctt ctc atc ctg gac atc tgg tgaggacccc      481
Ala Ile Val Ala Thr Leu Leu Ile Leu Asp Ile Trp
                115                      120                      125

gcgtcacctg cccagctat caggtggcca atgtgtcttg agtcctctggc gtctcctct      541
ggaaccacca gaaaggcaca ggggtcttgg ctccaccctc ctctggatgc ctagagtttt      601
gtgtgaggtc agggcagccc ccacttcagg gaggacaacc ttccggcggg cccctccctt      661
ccagcgggcc cctcccttcc cagaggctcc caccccaagc acagccgagg atgggggtgcc      721
agggtgaggt cagcaccagc agccaactgc ttctctcact cctctcagag gggctcagca      781
gccatgggta tccctctgcc ccaggcctca cccctgcccc aacaccagcc cctcctagtc      841
cctagtccct ccattccct cgggctccct cccagtcccc cccatcgctt cgcagccct      901
tctgctccct ttggctggct gttgttctct tccagcgtct gtcctccgc ggctcatct      961
gcctcttcgt ctgttagagc gcgcgtctcg tctcagtcgt cactgttttg gttttgttg      1021
ggtttttttt tttttttttt tttagagacag tctgtctgtg tcgcccaggc tggagtatag      1081
ttgctcaagc tcagctcact gcaacctccg cctccagggt tcaagcaatt cctctgcctc      1141
agcctcccaa gtagtggga ttacaagcac ccaccacat gccagctaa cttttgtcat      1201
ttttaataga gatgaggttt caccaagttg gccaggctgg tcttgaactc ctgacctcag      1261

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gtgatctgcc cacctcggcc tcccaaagtg ctgggattac aggtgtaagc caccgtgccc 1321
ggccatcgta atgttttgaat ttgctttttt acatcttcca tcctttttgga gtgtcttggt 1381
ccctcgtcac agttcagcac tgtgaccacc ttgggggttag acactatggt tttatatcct 1441
gtacttgata ttctccaaaa aaaaaaaaaa aaa 1474

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<210> 140
<211> 653
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 222..374

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<220>
<221> sig_peptide
<222> 222..299
<223> Von Heijne matrix
      score 4.28353322771141
      seq ILFKFSLCPYAAA/LS

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<400> 140
taataatggt gttaaattat tgccttctca tctgcgtgtc tcttatgttc tgcttaaaga 60
gattgtcagt ttgttcaagc tctttttagt tgttgctcct ccagtgcccta gctttgagct 120
ttgtacacgg tagttattga gttgagtaac atagtttggt ctgagtcatt tgttccacat 180
gcttgaagac ttggcttaac ctagtagata ataggaaaaga a atg gaa atg ctc ttt 236
                                         Met Glu Met Leu Phe
                                         -25
gat gaa aga gcc cct ctc tta ttc atc ctt ttt aaa ttt tct ttg tgc 284
Asp Glu Arg Ala Pro Leu Leu Phe Ile Leu Phe Lys Phe Ser Leu Cys
      -20                      -15                      -10
cca tat gca gca gct ctc agc aaa cct ata ttt ggc agt gtg gcc tgt 332
Pro Tyr Ala Ala Ala Leu Ser Lys Pro Ile Phe Gly Ser Val Ala Cys
      -5                      1                      5                      10
atg act aaa gaa atc ctg gcc agg cac ggt ggc tca cgc ctg 374
Met Thr Lys Glu Ile Leu Ala Arg His Gly Gly Ser Arg Leu
      15                      20                      25
taatcccagc actttgggag gccgaggcgg gtggattacg aggtcaggag attgagacca 434
tcctggctaa catggcgaaa ccccatctct acgaaaaata caaaaaaaaaa aattagccgg 494
gcatcatggc gggcgccctgt agtcttagct actcaggagg ctgaggcagg agaatggcgt 554
gaacccggga ggcggagctt gcagtgagcc gagattgcgc cactgcactc cagcctgggg 614
caacagagca agactccgtc tcaaaaaaaaa aaaaaaaaaa 653

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<210> 141
<211> 1490
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 59..274

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<220>
<221> sig_peptide
<222> 59..127
<223> Von Heijne matrix
      score 7.37647149292058
      seq LQLCSLLVGEARA/PS

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<400> 141
agacagaggc agggccttgcg acggaagtgg cctctctgct tctgcagggc tggggaag 58
atg ctg cgt cca cgc tta cgc tgg ctg tac ctt ggc ctc tgc agc ctc 106
Met Leu Arg Pro Ala Leu Pro Trp Leu Tyr Leu Gly Leu Cys Ser Leu
-20 -15
ctg gtg ggg gag gca gag gcc ccg agc ccc gtg gat ccg ctg gag cgg 154
Leu Val Gly Glu Ala Glu Ala Pro Ser Pro Val Asp Pro Leu Glu Arg
-5 1 5
agc cgg ccg tac cgc gtg ctg cga ggg cag aac ctg gtg ttg atg gga 202
Ser Arg Pro Tyr Ala Val Leu Arg Gly Gln Asn Leu Val Leu Met Gly
10 15 20 25
acc att ttc agc atc ctg ctg gtg act gtc atc ctt atg gca ttt tgt 250
Thr Ile Phe Ser Ile Leu Leu Val Thr Val Ile Leu Met Ala Phe Cys
30 35 40
gtc tac aag ccc att cgg cgt cgg tgacagccag acaagttctt caatgagtat 304
Val Tyr Lys Pro Ile Arg Arg Arg
45
ttgggaatag gataagttgt gttgcacaca ggccagtgga gaagttggaa ccaaaacttt 364
cctacttggg aatgaccttt ggtctggaca gttggtaaata gctaaatgaa ttagaagaaa 424
acatgtacta gacattattt tttcctaaca ctgtagcgca aataattggc ccttgagttc 484
gcttctcagt gtttctgact gtactttgta aaagtaagac ctgaaagctc caaaggtcag 544
tgtaaagatg gagtgttcac gagaaagaaa acatggtaac cttgtgagtg cctgtaagaa 604
ccacactgta aagaactcat cattaatgct tgaaaatggt attaagaagg agacttacca 664
tgacagacatt ccctatttaa gaacctattg gttacagtgg gttaaagaac acagattttt 724
ttttttaate tcacctgagt tagcctagaa tgcgctgggt gcaaaagtggt gtcagctgtg 784
gggatccttg gccctcgttc ctcaacctgca tcctgccctg cactcagggt ctccccctga 844
agtcagggtc acatcaggta gacctgttac tatatgcacc ttggcctgtg aatgctctga 904
agttggactg gaaatgttac taggttggcc tgttacaaaa aggaccccat cctgctctaa 964
cacatgtatc tcccttggcc tgcattttagc tcttctagc ccacggctctg aaacttgagg 1024
cagctttcca gtttggaaat gtaaaaggct cagtgggcac tctgttcac cctgggtggg 1084
gagggccagc ccaacgagaat tgcattgtcca ctgtgcgggc cagtggtgtgt ttacacaaat 1144
ttcatctcag ctttggaaaat gctgctatta gtttccactg ttggtgaact ggattttttc 1204
ctcctattga aatgatactt tcatacttat aaagctgtcg tcaatattta tttcaagggtg 1264
ctagatttaa ttttgttatt aaattgaaat gcttatcttg tgttcaagca cagcactgat 1324
tttaacaacc tgcatttaat gtgaagtaac cgaagtagga tactgtaaat gtgtaaggat 1384
tttgtttgta atcttgtaac attgaacat tgaaatgttc agttctttgc ttttgagcaa 1444
aacgtcaatt aaaactaaag taaaatctta aaaaaaaaa aaaaaa 1490

<210> 142
<211> 661
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 158..442

<220>
<221> sig_peptide
<222> 158..301
<223> Von Heijne matrix
score 7.53908709538105
seq FVILLLFIFTVVS/LV

<400> 142
aaaaacagac gataccatcg cttcagcagc atcctctcag acaagagcca ctatttctga 60
ttcagatcac ctgtcatcga agtttaaaga aggggaaaca ggagacagaa atacactgaa 120

ccaaaaagat tcaaaagagc aagtggaatc tctaaga atg gct tcc agc cac tgg 175
Met Ala Ser Ser His Trp
-45

aat gaa acc act acc tct gtt tat cag tac ctt ggt ttt caa gtt caa 223
Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr Leu Gly Phe Gln Val Gln
-40 -35 -30

aaa att tac cct ttc cat gac aac tgg aac act gcc tgc ttt gtc atc 271
Lys Ile Tyr Pro Phe His Asp Asn Trp Asn Thr Ala Cys Phe Val Ile
-25 -20 -15

ctg ctt tta ttt ata ttt aca gtg gta tct tta gtg gtg ctg gct ttc 319
Leu Leu Leu Phe Ile Phe Thr Val Val Ser Leu Val Val Leu Ala Phe
-10 -5 1 5

ctt tat gaa gtg ctt gac tgc tgc tgc tgt gta aaa aac aaa acc gtg 367
Leu Tyr Glu Val Leu Asp Cys Cys Cys Val Lys Asn Lys Thr Val
10 15 20

aaa gac ttg aaa agt gaa ccc aac cct ctt aga agt atg atg gac aac 415
Lys Asp Leu Lys Ser Glu Pro Asn Pro Leu Arg Ser Met Met Asp Asn
25 30 35

atc aga aaa cgt gaa act gaa gtg gtc taacactcta tagaagatga 462
Ile Arg Lys Arg Glu Thr Glu Val Val
40 45

acaaatctc tgaagcagc tcaacctctt ctgagaaaaa aaatatattc tgaggccaac 522
tggtgctaca aaacaaattc tgactgaatg tttaaaacat ttctagtaga aggggaaaaa 582
aaagttaaac atgcactgtt tgtgtgtata gccatttcat taaatataca gtaaaacttc 642
ataaaaaaaaa aaaaaaaaaa 661

<210> 143
<211> 1789
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 5..64
<223> Von Heijne matrix
score 6.64507667657896
seq LLPLLSLLVGAWL/KL

<400> 143
cctg atg gcc cgg cat ggg tta cgg ctg ctg ccc ctg ctg tgg ctc ctg 49
Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu
-20 -15 -10

gtc ggc gcg tgg ctc aag cta gga aat gga cag gct act agc atg gtc 97
Val Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val
-5 1 5 10

caa ctg cag ggt ggg aga ttc ctg atg gga aca aat tct cca gac agc 145
Gln Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser
15 20 25

aga gat ggt gaa ggg cct gtg cgg gag gcg aca gtg aaa ccc ttt gcc 193
Arg Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala
30 35 40

atc gac ata ttt cct gtc acc aac aaa gat ttc agg gat ttt gtc agg 241
Ile Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg
45 50 55

ctg ctg gtg ttg ggg ggt tgt ggc cgg gct gga ctg ccc ctg gac act	384
Leu Leu Val Leu Gly Gly Cys Gly Arg Ala Gly Leu Pro Leu Asp Thr	
35 40 45	
gct gag aca ctg gac atg gcc tcg cac aca tgg ctg gca ctg gca ccc	432
Ala Glu Thr Leu Asp Met Ala Ser His Thr Trp Leu Ala Leu Ala Pro	
50 55 60	
ctg ccc act gcc cgg gct ggt gca gct cgg gta gtt ctg ggc aag cag	480
Leu Pro Thr Ala Arg Ala Gly Ala Ala Ala Val Val Leu Gly Lys Gln	
65 70 75 80	
gtg cta gtg gtg tgt ggt gtg gat gag gtc cag agc ccg gta gct gct	528
Val Leu Val Val Cys Gly Val Asp Glu Val Gln Ser Pro Val Ala Ala	
85 90 95	
gta gag gcc ttc ctg atg gat gag ggc cgc tgg gag cgt cgg gcc acc	576
Val Glu Ala Phe Leu Met Asp Glu Gly Arg Trp Glu Arg Arg Ala Thr	
100 105 110	
ctc cct caa gca gcc atg ggg gtt gca act gtg gag aga gat ggt atg	624
Leu Pro Gln Ala Ala Met Gly Val Ala Thr Val Glu Arg Asp Gly Met	
115 120 125	
gtg tat gct ctg ggg gga atg ggc cct gac acg gcc ccc cag gcc cag	672
Val Tyr Ala Leu Gly Gly Met Gly Pro Asp Thr Ala Pro Gln Ala Gln	
130 135 140	
gta cgt gtg tat gac ccc cgt cgg gac tgc tgg ctt tcg cta ccc tcc	720
Val Arg Val Tyr Asp Pro Arg Arg Asp Cys Trp Leu Ser Leu Pro Ser	
145 150 155 160	
atg ccc aca ccc tgc tat ggg gcc tcc acc ttc ctg cac ggg aac aag	768
Met Pro Thr Pro Cys Tyr Gly Ala Ser Thr Phe Leu His Gly Asn Lys	
165 170 175	
atc tat gtc ctg ggg ggc cgc cag ggc aag ctc ccg gtg act gct ttt	816
Ile Tyr Val Leu Gly Gly Arg Gln Gly Lys Leu Pro Val Thr Ala Phe	
180 185 190	
gaa gcc ttt gat ctg gag gcc cgt aca tgg acc cgg cat cca agc cta	864
Glu Ala Phe Asp Leu Glu Ala Arg Thr Trp Thr Arg His Pro Ser Leu	
195 200 205	
ccc agc cgt cgg gcc ttt gct ggc tgc gcc atg gct gaa ggc agc gtc	912
Pro Ser Arg Arg Ala Phe Ala Gly Cys Ala Met Ala Glu Gly Ser Val	
210 215 220	
ttt agc ctg ggt ggc ctg cag cag cct ggg ccc cac aac ttc tac tct	960
Phe Ser Leu Gly Gly Leu Gln Gln Pro Gly Pro His Asn Phe Tyr Ser	
225 230 235 240	
cgc cca cac ttt gtc aac act gtg gag atg ttt gac ctg gag cat ggg	1008
Arg Pro His Phe Val Asn Thr Val Glu Met Phe Asp Leu Glu His Gly	
245 250 255	
tcc tgg acc aaa ttg ccc cgc agc ctg cgc atg agg gat aag agg gca	1056
Ser Trp Thr Lys Leu Pro Arg Ser Leu Arg Met Arg Asp Lys Arg Ala	
260 265 270 275	
gac ttt gtg gtt ggg tcc ctt ggg ggc cac att gtg gcc att ggg ggc	1104
Asp Phe Val Val Gly Ser Leu Gly Gly His Ile Val Ala Ile Gly Gly	
280 285	
ctt gga aac cag cca tgt cct ttg ggc tct gtg gag agc ttt agc ctt	1152
Leu Gly Asn Gln Pro Cys Pro Leu Gly Ser Val Glu Ser Phe Ser Leu	
290 295 300	
gca cgg cgg cgc tgg gag gca ttg cct gcc atg ccc act gcc cgc tgc	1200
Ala Arg Arg Arg Trp Glu Ala Leu Pro Ala Met Pro Thr Ala Arg Cys	
305 310 315 320	
tcc tgc tct agt ctg cag gct ggg ccc cgg ctg ttt gtt att ggg ggt	1248
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325 330 335	
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Gly	Val																
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Arg	Trp	Gly	Ala	Lys	Arg	Leu	Gly	Val	Ala	Ser	Thr	Glu	Ala	Gln	Arg		
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Gly	Val	Ser	Phe	Lys	Leu	Glu	Glu	Lys	Thr	Ala	His	Ser	Ser	Leu	Ala		
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Leu	Phe	Arg	Asp	Asp	Thr	Gly	Val	Lys	Tyr	Gly	Leu	Val	Gly	Leu	Glu		
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Pro	Thr	Lys	Val	Ala	Leu	Asn	Val	Glu	Arg	Phe	Arg	Glu	Trp	Ala	Val		
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Thr	Val	Lys	Arg	Ser	Gln	Gln	Phe	Arg	Ile	Gly	Val	Ala	Asp	Val	Asp		
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Met	Ser	Arg	Asp	Ser	Cys	Ile	Gly	Val	Asp	Asp	Arg	Ser	Trp	Val	Phe		
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Thr	Tyr	Ala	Gln	Arg	Lys	Trp	Tyr	Thr	Met	Leu	Ala	Asn	Glu	Lys	Ala		
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Pro	Val	Glu	Gly	Ile	Gly	Gln	Pro	Glu	Lys	Val	Gly	Leu	Leu	Glu	Glu		
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Tyr	Glu	Ala	Gln	Lys	Leu	Ser	Leu	Val	Ser	Gln	Val	Ser	Val				

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Val His Thr Leu Gln Thr Asp Phe Arg Gly Pro Val Val Pro Ala Phe				
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Ala Leu Trp Asp Gly Glu Leu Leu Thr His Ser Gly Leu Glu Val Pro				
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gag gcc ctg tagtatgtcc attactggag tcctaatca cgctttggc				675
Glu Gly Leu				
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Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg Phe Ser Val	
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Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp Gln Asn Leu	
	40 45 50
ggt aca ctg cac agg ctg gcc cag gct ggc tac cgg gct gtg gcc att	309
Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala Val Ala Ile	
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Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala Pro Ala Pro	
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Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val Val Asp Ala	
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Leu Glu Leu Gly Pro Val Val Ile Ser Pro Ser Leu Ser Gly Met	
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Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Glu Leu Pro Gly Phe	
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Ala	Ser	Val	Lys	Thr	Pro	Ala	Leu	Ile	Val	Tyr	Gly	Asp	Gln	Asp	Pro		
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Met	Gly	Gln	Thr	Ser	Phe	Glu	His	Leu	Lys	Gln	Leu	Pro	Asn	His	Arg		
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Val	Leu	Ile	Met	Lys	Gly	Ala	Gly	His	Pro	Cys	Tyr	Leu	Asp	Lys	Pro		
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Glu	Glu	Trp	His	Thr	Gly	Leu	Leu	Asp	Phe	Leu	Gln	Gly	Leu	Gln			
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Cys	Pro	Leu	Leu	Leu	Pro	Gln	Asn	Arg	Ser	Lys	Thr	Val	Tyr	Glu	Gly		
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Phe	Ile	Ser	Ala	Gln	Gly	Arg	Arg	Phe	His	Leu	Arg	Ile	Val	Leu	Pro		
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gaa	gat	tta	caa	ctg	aag	aat	gca	aga	tta	tta	tgt	att	tgg	cag	ctg	197	
Glu	Asp	Leu	Gln	Leu	Lys	Asn	Ala	Arg	Leu	Leu	Cys	Ile	Trp	Gln	Leu		
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aga	aca	ata	ctt	agt	gga	tac	cat	cga	ata	gta	caa	cag	aga	atg	cag	245	
Arg	Thr	Ile	Leu	Ser	Gly	Tyr	His	Arg	Ile	Val	Gln	Gln	Arg	Met	Gln		
			60			65				70				75			
cac	tct	cct	gat	cta	atg	agc	ttt	atg	atg	gag	ttg	aag	atg	ctt	ttg	293	
His	Ser	Pro	Asp	Leu	Met	Ser	Phe	Met	Met	Glu	Leu	Lys	Met	Leu	Leu		

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gaa gtt gcc tta aag aat aga caa gag ctg tat gca cta cct cct cct						341
Glu Val Ala Leu Lys Asn Arg Gln Glu Leu Tyr Ala Leu Pro Pro						
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ccc cag ttc tac tca agc ctt att gaa gag ata gga act ctt ggt tgg						389
Pro Gln Phe Tyr Ser Ser Leu Ile Glu Glu Ile Gly Thr Leu Gly Trp						
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gat aaa ctt ttg tat gcg gat acc tgc ttc agt acc atc aag tta aaa						437
Asp Lys Leu Val Tyr Ala Asp Thr Cys Phe Ser Thr Ile Lys Leu Lys						
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Ala Glu Asp Ala Ser Gly Arg Glu His Leu Ile Thr Leu Lys Leu Lys						
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Ala Lys Tyr Pro Ala Glu Ser Pro Asp Tyr Phe Val Asp Phe Pro Val						
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Pro Phe Cys Ala Ser Trp Thr Pro Gln Ser Ser Leu Ile Ser Ile Tyr						
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agt cag ttt ttg gca gca ata gaa tca cta aag gca ttc tgg gat gtt						629
Ser Gln Phe Leu Ala Ala Ile Glu Ser Leu Lys Ala Phe Trp Asp Val						
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Met Asp Glu Ile Asp Glu Lys Thr Trp Val Leu Glu Pro Glu Lys Pro						
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Pro Arg Ser Ala Thr Ala Arg Arg Ile Ala Leu Gly Asn Asn Val Ser						
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Ile Asn Ile Glu Val Asp Pro Arg His Pro Thr Met Leu Pro Glu Cys						
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Phe Phe Leu Gly Ala Asp His Val Val Lys Pro Leu Gly Ile Lys Leu						
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Ser Arg Asn Ile His Leu Trp Asp Pro Glu Asn Ser Val Leu Gln Asn						
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Leu Lys Asp Val Leu Glu Ile Asp Phe Pro Ala Arg Ala Ile Leu Glu						
	285		290		295	
aaa tct gat ttt act atg gat tgt gga att tgt tat gct tat caa ctt						965
Lys Ser Asp Phe Thr Met Asp Cys Gly Ile Cys Tyr Ala Tyr Gln Leu						
	300		305		310	
gac ggt acc att cct gat caa gtg tgt gat aat tcc cag tgt gga caa						1013
Asp Gly Thr Ile Pro Asp Gln Val Cys Asp Asn Ser Gln Cys Gly Gln						
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cct ttc cat caa ata tgc tta tat gag tgg ctg aga gga cta cta act						1061
Pro Phe His Gln Ile Cys Leu Tyr Glu Trp Leu Arg Gly Leu Leu Thr						
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agt aga cag agt ttt aac atc ata ttt ggt gaa tgt cca tat tgt agt						1109
Ser Arg Gln Ser Phe Asn Ile Ile Phe Gly Glu Cys Pro Tyr Cys Ser						
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aag cca att acc tta aaa atg tct gga agg aaa cac tgaaaaaaga						1155
Lys Pro Ile Thr Leu Lys Met Ser Gly Arg Lys His						
	365		370		375	
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atcttcagag aaaaaataaa gcaagraata ctaacatcaa aaggacaggt atgatgatgc						1275
gataataata aacatctcgc ttgtctctt cactaagagt aaactgggaa attgtaggcc						1335

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gtg gcc gtc tat aag gat ggc cgg gct ggt gtt gca aat gat gcc 159
Val Ala Val Tyr Lys Asp Gly Arg Ala Gly Val Val Ala Asn Asp Ala
15      20      25      30
ggg gac cga gtt act cca gct gtt gtt gct tac tca gaa aat gaa gag 207
Gly Asp Arg Val Thr Pro Ala Val Val Ala Tyr Ser Glu Asn Glu Glu
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Ile Val Gly Leu Ala Ala Lys Gln Ser Arg Ile Arg Asn Ile Ser Asn
50      55      60
aca gta atg aaa gta aag cag atc ctg ggc aga agc tcc agt gat cca 303
Thr Val Met Lys Val Lys Gln Ile Leu Gly Arg Ser Ser Ser Asp Pro
65      70      75
caa gct cag aaa tac atc gcg gaa agt aaa tgt tta gtc att gaa aaa 351
Gln Ala Gln Lys Tyr Ile Ala Glu Ser Lys Cys Leu Val Ile Glu Lys
80      85      90
aat ggg aaa tta cga tat gaa ata gat act gga gaa gaa aca aaa ttt 399
Asn Gly Lys Leu Arg Tyr Glu Ile Asp Thr Gly Glu Glu Thr Lys Phe
95      100      105      110
gtt aac cca gaa gat gtt gcc aga ctg ata ttt agt aaa atg aaa gaa 447
Val Asn Pro Glu Asp Val Ala Arg Leu Ile Phe Ser Lys Met Lys Glu
115      120      125
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Thr Ala His Ser Val Leu Gly Ser Asp Ala Asn Asp Val Val Ile Thr
130      135      140
gtc ccg ttt gat ttt gga gaa aag caa aaa aat gct ctt gga gaa gca 543
Val Pro Phe Asp Phe Gly Glu Lys Gln Lys Asn Ala Leu Gly Glu Ala
145      150      155
gct aga gct gct gga ttt aat gtt ttg cga tta att cac gaa ccg tct 591
Ala Arg Ala Ala Gly Phe Asn Val Leu Arg Leu Ile His Glu Pro Ser
160      165      170
gca gct ctt ctt gct tat gga att gga caa gac tcc cct act gga aaa 639
Ala Ala Leu Leu Ala Tyr Gly Ile Gly Gln Asp Ser Pro Thr Gly Lys
175      180      185      190
agc aat att ttg gtg ttt aag ctt gga gga aca tcc tta tct ctc agc 687
Ser Asn Ile Leu Val Phe Lys Leu Gly Gly Thr Ser Leu Ser Leu Ser
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Asp Asp Asn Ile Gly Gly Ala His Phe Thr Glu Thr Leu Ala Gln Tyr	
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Leu Ala Ser Glu Phe Gln Arg Ser Phe Lys His Asp Val Arg Gly Asn	
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gcg cga gcc atg atg aaa tta acg aac agt gct gaa gta gcg aaa cat	879
Ala Arg Ala Met Met Lys Leu Thr Asn Ser Ala Glu Val Ala Lys His	
255 260 265 270	
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Ser Leu Ser Thr Leu Gly Ser Ala Asn Cys Phe Leu Asp Ser Leu Tyr	
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290 295 300	
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Leu Phe Pro Ser Gly Thr Pro Leu Pro Ala Arg Arg Gln His Thr Leu	
415 420 425 430	
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Gln Ala Pro Gly Ser Ile Ser Ser Val Cys Leu Glu Leu Tyr Glu Ser	
435 440 445	
gat ggg aag aac tct gcc aaa gag gaa acc aag ttt gca cag gtt gta	1455
Asp Gly Lys Asn Ser Ala Lys Glu Glu Thr Lys Phe Ala Gln Val Val	
450 455 460	
ctc cag gat tta gat aaa aaa gaa aat gga tta cgt gat ata tta gct	1503
Leu Gln Asp Leu Asp Lys Lys Glu Asn Gly Leu Arg Asp Ile Leu Ala	
465 470 475	
gtt ctt act atg aaa agg gat gga tct tta cat gtg aca tgc aca gat	1551
Val Leu Thr Met Lys Arg Asp Gly Ser Leu His Val Thr Cys Thr Asp	
480 485 490	
caa gaa act gga aaa tgt gaa gca atc tct att gag ata gca tct	1596
Gln Glu Thr Gly Lys Cys Glu Ala Ile Ser Ile Glu Ile Ala Ser	
495 500 505	
tagtggtttta gagaaatcaa gaatttttaa aaacaagaat atcaacattt ggttttgtgt	1656
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1747

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gtggggacc atg tac aac act gga aga cac gta tcc ctt cgc ctg gac aag 170
Met Tyr Asn Thr Gly Arg His Val Ser Leu Arg Leu Asp Lys
1 5 10
gag cac ttg gtc aac ata tct gga ggg ccc atg aca tac agc cac cgg 218
Glu His Leu Val Asn Ile Ser Gly Gly Pro Met Thr Tyr Ser His Arg
15 20 25 30
ctg gag gag atc cga cta cac ttt ggg agt gag gac agc caa ggg tcg 266
Leu Glu Glu Ile Arg Leu His Phe Gly Ser Glu Asp Ser Gln Gly Ser
35 40 45
gag cac ctc ctc aat gga cag gcc ttc tct ggg gag ctt caa gag agg 314
Glu His Leu Leu Asn Gly Gln Ala Phe Ser Gly Glu Leu Gln Glu Arg
50 55 60
gat ttg ttc atc ttg ttg act tct gta tca gga cat ctg ccc gat aca 362
Asp Leu Phe Ile Leu Leu Thr Ser Val Ser Gly His Leu Pro Asp Thr
65 70 75
tagaaaaagt ctgtgcacc ctgaattaca gtatgagcca ttcggaatgc atttctcttt 422
aaaagtcttc gcctcattca gtgtctggaa cacagtgggt gctccccaat aggtgacacc 482
ttcctcaagt ttccttggga gaacagactc aatgtcggat ccacaaagga gacctgcaca 542
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Met Ala Thr
1
cat gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg gtg 165
His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met Val
5 10 15
ggc aca gtg gct gtc act gtc atg cct cag tgg ata atg tgc gcc ttc 213
Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Ile Val Ser Ala Phe
20 25 30 35
att gaa aac aac atc gtg gtt ttt gaa aac ttc tgg gaa gga ctg tgg 261
Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu Gly Leu Trp
40 45 50

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Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile Tyr	
55 60 65	
gat tcc ctg ctg gct ctt tct ccg gac cta cag gca gcc aga gga ctg	357
Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly Leu	
70 75 80	
atg tgt gct gct tcc gtg atg tcc ttc ttg gct ttc atg atg gcc atc	405
Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met Ala Ile	
85 90 95	
ctt ggc atg aaa tgc acc agg tgc acg ggg gac aat gag aag gtg aag	453
Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu Lys Val Lys	
100 105 110 115	
gct cac att ctg ctg acg gct gga atc atc ttc atc atc acg ggc atg	501
Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met	
120 125 130	
gtg gtg ctc atc cct gtg agc tgg gtt gcc aat gcc atc atc aga gat	549
Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp	
135 140 145	
ttc tat aac cca ata gtg aat gtt gcc caa aaa cgt gag ctt gga	594
Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly	
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cagtatgtgt agttgtgtat gtttttttaa ctttactata aagccatgca aatgacaaaa	834
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gaatgagata ttaaatccaa tgcctttgatt gttctagaaa gtatagtaat ttgtttctta	1014
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gacattttcac aaatccaaaa ttgccgtgg atg aac tct tta ctt cac ttc ggg 173
Met Asn Ser Leu Leu His Phe Gly
1 5
ata ttg ctg gag ctg agt ctc ctg aaa cag ttt aag tct gta tat gtt 221
Ile Leu Leu Glu Leu Ser Leu Leu Lys Gln Phe Lys Ser Val Tyr Val
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cct gga aat cat acc cac cag gca tct tat aag cca ttg ttg aag caa 269
Pro Gly Asn His Thr His Gln Ala Ser Tyr Lys Pro Leu Leu Lys Gln
25 30 35 40
gtt gtg gag gaa ata ttt cat ccc gag agg cca gat tcc gtt gat att 317
Val Val Glu Glu Ile Phe His Pro Glu Arg Pro Asp Ser Val Asp Ile
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gaa cac atg tct tca ggc ctc act gat ctc ctt aaa act gga ttt agc 365
Glu His Met Ser Ser Gly Leu Thr Asp Leu Leu Lys Thr Gly Phe Ser
60 65 70
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Met Phe Met Lys Val Ser Arg Pro His Pro Ser Asp Tyr Pro Leu Leu
75 80 85
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Ile Leu Phe Val Val Gly Gly Val Thr Val Ser Glu Val Lys Met Val
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Lys Asp Leu Val Ala Ser Leu Lys Pro Gly Thr Gln Val Ile Val Leu
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Ser Thr Arg Leu Leu Lys Pro Leu Asn Ile Pro Glu Leu Leu Phe Ala
125 130 135
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Thr Arg Leu Leu His Pro Asp Leu Gly Phe
140 145
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gcagaagtag cagttccgga gtccagctgg ctaaaaactca tcccagagga ta atg gca 178
Met Ala
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acc cat gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg 226
Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met
5 10 15
gtg ggc aca gtg gct gtc act gtc atg cct cag tgg aga gtg tgc gcc 274
Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val Ser Ala
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ttc att gaa aac aac atc gtg gtt ttt gaa aac ttc tgg gaa gga ctg 322

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Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile	
55 60 65	
tat gat tcc ctg ctg gct ctt tct ccg gac cta cag gca gcc aga gga	418
Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly	
70 75 80	
ctg atg tgt gct gct tcc gtg atg tcc ttc ttg gct ttc atg atg gcc	466
Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met Ala	
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Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu Lys Val	
100 105 110	
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Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ala Gly	
115 120 125	
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Asp Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly	
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Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Val Gly	
165 170 175	
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Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser	
180 185 190	
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Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His	
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Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val	
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                               Met Arg Leu Gln Asp
                               1           5
cgc atc gcc acg ttc ttc ttc cca aaa ggc atg atg ctc acc acg gct 162
Arg Ile Ala Thr Phe Phe Phe Pro Lys Gly Met Met Leu Thr Thr Ala
                               10           15           20
gcg ctg atg ctc ttc tta cac ctg ggc atc ttc atc aga gac gtg 210
Ala Leu Met Leu Phe Phe Leu His Leu Gly Ile Phe Ile Arg Asp Val
                               25           30           35
cac aac ttc tgc atc acc tac cac tat gac cac atg agc ttt cac tac 258
His Asn Phe Cys Ile Thr Tyr His Tyr Asp His Met Ser Phe His Tyr
                               40           45           50
acg gtc gtc ctg atg ttc tcc cag gtg atc agc atc tgc tgg gct gcc 306
Thr Val Val Leu Met Phe Ser Gln Val Ile Ser Ile Cys Trp Ala Ala
                               55           60           65
atg ggg tca ctc tat gct gag atg aca gaa aac aat gct caa cgg agc 354
Met Gly Ser Leu Tyr Ala Glu Met Thr Glu Asn Asn Ala Gln Arg Ser
                               70           75           80           85
cat gtt ctt caa ccg cct gtc ctt gga gtt tct ggc cat cga gta ccg 402
His Val Leu Gln Pro Pro Val Leu Gly Val Ser Gly His Arg Val Pro
                               90           95           100
gga gga gca cca ctg agg cct ggg gag tgc gaa cag gcc taaggagggg 451
Gly Gly Ala Pro Leu Arg Pro Gly Glu Ser Glu Gln Gly
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<211> 1183

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Thr Pro Thr Asn Cys Ser Trp Trp Pro Ile Ser Ala Leu Glu Ser Asp
                               10           15           20
gcg gcc aag cca gcg gag gcc ccc gac gct ccc gag gcg gcc agc ccc 148
Ala Ala Lys Pro Ala Glu Ala Pro Asp Ala Pro Glu Ala Ala Ser Pro
                               25           30           35
gcc cat tgg ccc agg gag agc ctg gtt ctg tac cac tgg acc cag tcc 196
Ala His Trp Pro Arg Glu Ser Leu Val Leu Tyr His Trp Thr Gln Ser
                               40           45           50           55
ttc agc tgc cag aag gtg cgg ctg gtg atc gcc gag aag ggc ctg gtg 244
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Cys	Glu	Glu	Arg	Asp	Val	Ser	Leu	Pro	Gln	Ser	Glu	His	Lys	Glu	Pro	
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tgg	ttc	atg	cg	ctc	aac	ctg	ggc	gag	gtg	ccc	gtc	atc	atc	cac		340
Trp	Phe	Met	Arg	Leu	Asn	Leu	Gly	Glu	Glu	Val	Pro	Val	Ile	Ile	His	
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cgc	gac	aac	atc	atc	agt	gac	tat	gac	cag	atc	att	gac	tat	gtg	gag	388
Arg	Asp	Asn	Ile	Ile	Ser	Asp	Tyr	Asp	Gln	Ile	Ile	Asp	Tyr	Val	Glu	
	105					110					115					
cgc	acc	ttc	aca	gga	gag	cac	gtg	gtg	gcc	ctg	atg	ccc	gag	gtg	ggc	436
Arg	Thr	Phe	Thr	Gly	Glu	His	Val	Val	Ala	Leu	Met	Pro	Glu	Val	Gly	
	120				125				130					135		
agc	ctg	cag	cac	gca	cg	gtg	ctg	cag	tac	cg	gag	ctg	ctg	gac	gca	484
Ser	Leu	Gln	His	Ala	Arg	Val	Leu	Gln	Tyr	Arg	Glu	Leu	Leu	Asp	Ala	
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ctg	ccc	atg	gat	gcc	tac	acg	cat	ggc	tgc	atc	ctg	cat	ccc	gag	ctc	532
Leu	Pro	Met	Asp	Ala	Tyr	Thr	His	Gly	Cys	Ile	Leu	His	Pro	Glu	Leu	
			155					160					165			
acc	acc	gac	tcc	atg	atc	ccc	aag	tac	gcc	acg	gcc	gag	atc	cgc	aga	580
Thr	Thr	Asp	Ser	Met	Ile	Pro	Lys	Tyr	Ala	Thr	Ala	Glu	Ile	Arg	Arg	
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cat	tta	gcc	aat	gcc	acc	acg	gac	ctc	atg	aaa	ctg	gac	cat	gaa	gag	628
His	Leu	Ala	Asn	Ala	Thr	Thr	Asp	Leu	Met	Lys	Leu	Asp	His	Glu	Glu	
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Glu	Pro	Gln	Leu	Ser	Glu	Pro	Tyr	Leu	Ser	Lys	Gln	Lys	Lys	Leu	Met	
	200			205					210				215			
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Val	Lys	Ile	Leu	Glu	His	Asp	Asp	Val	Ser	Tyr	Leu	Lys	Lys	Ile	Leu	
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ggg	gaa	ctg	gcc	atg	gtg	ctg	gac	cag	att	gag	gcg	gag	ctg	gag	aag	772
Gly	Glu	Leu	Ala	Met	Val	Leu	Asp	Gln	Ile	Glu	Ala	Glu	Leu	Glu	Lys	
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agg	aag	ctg	gag	aac	gag	ggg	cag	aaa	tgc	gag	ctg	tgg	ctc	tgt	ggc	820
Arg	Lys	Leu	Glu	Asn	Glu	Gly	Gln	Lys	Cys	Glu	Leu	Trp	Leu	Cys	Gly	
		250				255						260				
tgt	gcc	ttc	acc	ctc	gct	gat	gtc	ctc	ctg	gga	gcc	acc	ctg	cac	cgc	868
Cys	Ala	Phe	Thr	Leu	Ala	Asp	Val	Leu	Leu	Gly	Ala	Thr	Leu	His	Arg	
	265				270					275						
ctc	aag	ttc	ctg	gga	ctg	tcc	aag	aaa	tac	tgg	gaa	gat	ggc	agc	cgg	916
Leu	Lys	Phe	Leu	Gly	Leu	Ser	Lys	Lys	Tyr	Trp	Glu	Asp	Gly	Ser	Arg	
	280				285				290				295			
ccc	aac	ctg	cag	tcc	ttc	ttt	gag	agg	gtc	cag	aga	cgc	ttt	gcc	ttc	964
Pro	Asn	Leu	Gln	Ser	Phe	Phe	Glu	Arg	Val	Gln	Arg	Arg	Phe	Ala	Phe	
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cgg	aaa	gtc	ctg	ggt	gac	atc	cac	acc	acc	ctg	ctg	tcg	gcc	gtc	atc	1012
Arg	Lys	Val	Leu	Gly	Asp	Ile	His	Thr	Thr	Leu	Leu	Ser	Ala	Val	Ile	
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ccc	aat	gct	ttc	cg	ctg	gtc	aag	agg	aaa	ccc	cca	tcc	ttc	ttc	ggg	1060
Pro	Asn	Ala	Phe	Arg	Leu	Val	Lys	Arg	Lys	Pro	Pro	Ser	Phe	Phe	Gly	
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gcg	tcc	ttc	ctc	atg	ggc	tcc	ctg	ggt	ggg	atg	ggc	tac	ttt	gcc	tac	1108
Ala	Ser	Phe	Leu	Met	Gly	Ser	Leu	Gly	Gly	Met	Gly	Tyr	Phe	Ala	Tyr	
	345					350				355						
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Trp	Tyr	Leu	Lys	Lys	Lys	Tyr	Ile									

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gcctcttttg ttcagcatga ttacccagag gcgcacccgt gccctggcct gcccgctgctc 120
tatgcacccg tgcgtgtggcg tgcccgtcgt ctgtgtggc atg cct gtc tgt gca 174
Met Pro Val Cys Ala

1 5
ccc gtg ctg tgg cgt gcc cgt cgt ctg tgt ggc atg cct gtc tgt gca 222
Pro Val Leu Trp Arg Ala Arg Arg Leu Cys Gly Met Pro Val Cys Ala
10 15 20
ccc gtg cgg tgg cgt gcc cgt cgt ctg tgc acc cgt gct gtg gtg tgc 270
Pro Val Pro Trp Arg Ala Arg Arg Leu Cys Thr Arg Ala Val Val Cys
25 30 35
cct tcg tct gtt cct ttt att gcc ggg cag ggt tgc acc cac atg tgc 318
Pro Ser Ser Val Pro Phe Ile Ala Gly Gln Gly Cys Thr His Met Cys
40 45 50
aag cca gcg acg gac ccc agg ttc acc cgt tca ccg ctg gct gga ggc 366
Lys Pro Ala Thr Asp Pro Arg Phe Thr Arg Ser Pro Leu Ala Gly Gly
55 60 65
gtg atc ctg ggt gtg gcc ctg tgg ctg cgc cat gac ccg cag acc acc 414
Val Ile Leu Gly Val Ala Leu Trp Leu Arg His Asp Pro Gln Thr Thr
70 75 80 85
aac ctg ctg tat ctg gag ctg gga gac aag ccc gcg ccc aac acc ttc 462
Asn Leu Leu Tyr Leu Glu Leu Gly Asp Lys Pro Ala Pro Asn Thr Phe
90 95 100
tat gta ggc atc tac atc ctg atc gct gtg ggc gct gtc atg atg ttc 510
Tyr Val Gly Ile Tyr Ile Leu Ile Ala Val Gly Ala Val Met Met Phe
105 110 115
gtt ggc ttc ctg ggc tgc tac ggg gcc atc cag gaa tcc cag tgc ctg 558
Val Gly Phe Leu Gly Cys Tyr Gly Ala Ile Gln Glu Ser Gln Cys Leu
120 125 130
ctg ggg acg ttc ttc act tgc ctg gtc atc ctg ttt gcc tgt gag gtg 606
Leu Gly Thr Phe Phe Thr Cys Leu Val Ile Leu Phe Ala Cys Glu Val
135 140 145
gcc gcc gcc atc tgg ggc ttt gtc aac aag gac cag atc gcc aag gat 654
Ala Ala Gly Ile Trp Gly Phe Val Asn Lys Asp Gln Ile Ala Lys Asp
150 155 160 165
gtg aag cag ttc tat gac cag gcc cta cag cag gcc gtg gtg gat gat 702
Val Lys Gln Phe Tyr Asp Gln Ala Leu Gln Gln Ala Val Val Asp Asp
170 175 180
gac gcc aac aac gcc aag gct gtg gtg aag acc ttc cac gag acg ctt 750
Asp Ala Asn Asn Ala Lys Ala Val Val Lys Thr Phe His Glu Thr Leu
185 190 195
gac tgc tgt ggc tcc agc aca ctg act gct ttg acc acc tca gtg ctg 798
Asp Cys Cys Gly Ser Ser Thr Leu Thr Ala Leu Thr Ser Val Leu
200 205 210
aag aac aat ttg tgt ccc tcg ggc agc aac atc atc agc aac ctg ttc 846

Lys Asn Asn Leu Cys Pro Ser Gly Ser Asn Ile Ile Ser Asn Leu Phe
 215 220 225
 aag gag gac tgc cac cag aag atc gat gac ctc ttc tcc ggg aag ctg 894
 Lys Glu Asp Cys His Gln Lys Ile Asp Asp Leu Phe Ser Gly Lys Leu
 230 235 240 245
 tac ctc atc ggc att gct gcc atc gtg gtc gct gtg atc atg atc ttc 942
 Tyr Leu Ile Gly Ile Ala Ala Ile Val Val Ala Val Ile Met Ile Phe
 250 255 260
 gag atg atc ctg agc atg gtg ctg tgc tgt ggc atc cgg aac agc tcc 990
 Glu Met Ile Leu Ser Met Val Leu Cys Cys Gly Ile Arg Asn Ser Ser
 265 270 275
 gtg tac tgaggccccc cagctctggc cacagggacc tctgcagtgc ccctaagtg 1046
 Val Tyr
 acccgagcac ttccgagggg gccatcaccc cctgtgtata taacgtttcc ggtattactc 1106
 tgctacacgt agccttttta cttttgggggt tttgtttttg ttctgaactt tctgtttacc 1166
 ttttcagggc tgacgtcaca tgtagggtggc gtgtatgagt ggagacgggc ctgggtcttg 1226
 gggactggag ggcaggggtc cttctgcccc ggggtcccag ggtgctctgc ctgctcagcc 1286
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 ccacccagcc cgcccgtcct gtgggtgcga cagctcacct tgttccctcc tgccccggtt 1406
 cgagagccga gtctgtgggc actctctgcc ttcatgcacc tgtcctttct aacacgtcgc 1466
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 gcaaaaaaaaa aaaaaaaaaa 1545

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 <213> Homo sapiens

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 <222> 11..529

 <400> 156
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 1 5 10
 ctg ctg gtg aaa cgg ctg cag gag gtg agc tcc cgg gat ggg aaa ggc 97
 Leu Leu Val Lys Arg Leu Gln Glu Val Ser Ser Arg Asp Gly Lys Gly
 15 20 25
 gac ctg ggg gag ccg ccc ccg aca cgg ccc acg gtg ggc acc aat ctt 145
 Asp Leu Gly Glu Pro Pro Thr Arg Pro Thr Val Gly Thr Asn Leu
 30 35 40 45
 act gac atc gtg gca cag aga aag atc acc atc cgg gag ctt ggg ggg 193
 Thr Asp Ile Val Ala Gln Arg Lys Ile Thr Ile Arg Glu Leu Gly Gly
 50 55 60
 tgc atg ggc ccc atc tgg tcc agt tac tat gga aac tgc cgt tct ctc 241
 Cys Met Gly Pro Ile Trp Ser Ser Tyr Tyr Gly Asn Cys Arg Ser Leu
 65 70 75
 ctg ttt gtg atg gac gcc tct gac ccc acc cag ctc tct gca tcc tgt 289
 Leu Phe Val Met Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Ser Cys
 80 85 90
 gtg cag ctc tta ggt ctc ctt tct gca gaa caa ctt gca gaa gca tgc 337
 Val Gln Leu Leu Gly Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser
 95 100 105
 gtg ctg ata ctc ttc aat aaa atc gac cta ccc tgt tac atg tcc acg 385
 Val Leu Ile Leu Phe Asn Lys Ile Asp Leu Pro Cys Tyr Met Ser Thr
 110 115 120 125
 gag gag atg aag tca tta atc agg ctt cca gac atc att gct tgt gcc 433

Glu	Glu	Met	Lys	Ser	Leu	Ile	Arg	Leu	Pro	Asp	Ile	Ile	Ala	Cys	Ala		
			130						135					140			
aag	cag	aac	atc	acc	acg	gca	gaa	atc	agc	gcc	cgt	gaa	ggc	act	ggc	481	
Lys	Gln	Asn	Ile	Thr	Thr	Ala	Glu	Ile	Ser	Ala	Arg	Glu	Gly	Thr	Gly		
			145						150					155			
tta	gca	ggg	gtg	ctg	gcc	tgg	ctc	cag	gcc	acc	cac	aga	gcc	aac	gat	529	
Leu	Ala	Gly	Val	Leu	Ala	Trp	Leu	Gln	Ala	Thr	His	Arg	Ala	Asn	Asp		
			160					165						170			
tgactgcacg	gcagaggcgc	agctggccctg	agctgggggag	aggtggcaga	gggcagtatg	589											
gctttgctgc	caatagtttc	ttctcacagg	ggcagaataa	cccaaagtaa	ccctacatga	649											
tggggctctg	tgctgggatg	caatgatgtg	taaactgagg	catgtggaga	tgggaagtga	709											
catctggcct	ctgaaaaaag	tgctcccagg	ggctaggcat	gggtggctcac	acctgtaatc	769											
ccagcacttt	gagagggcga	ggcgggtgta	tcacctgagg	tcgggagtgc	gagactagcc	829											
tgaccaacat	ggagaaaccc	tgtctctact	aaaaatacaa	aattagctgg	gtgtgctggg	889											
gcattgctgt	aatctcagct	acttggggagg	ctgagacagg	agaatccctt	gaacctggga	949											
ggtaggggtt	gcagtgagtc	gagatcatgc	cattgcactg	cacctgggga	acaagagtga	1009											
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<210> 157
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 <212> DNA
 <213> Homo sapiens

<220>
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gcaccttcgc	gaaa atg	gcg gct	gcc agg	ccc agc	ctg ggc	mga	gtc	ctc									170
	Met	Ala	Ala	Ala	Arg	Pro	Ser	Leu	Gly	Arg	Val	Leu					
	1				5					10							
cca gga tcc	tct gtc	ctg ttc	ctg tgt	gac atg	cag gag	aag ttc	cgc										218
Pro Gly Ser	Ser Val	Leu Phe	Leu Cys	Asp Met	Gln Glu	Lys Phe	Arg										
	15			20			25										
cac aac atc	gcc tac	ttc cca	cag atc	gtc tca	gtg gct	gcc cgc	atg										266
His Asn Ile	Ala Tyr	Phe Pro	Gln Ile	Val Ser	Val Ala	Ala Arg	Met										
	30		35		40												
ctc aag gtg	gcc cgg	ctg ctt	gag gtg	cca gtc	atg ctg	acg gag	cag										314
Leu Lys Val	Ala Arg	Leu Leu	Glu Val	Pro Val	Met Leu	Thr Glu	Gln										
	45		50		55		60										
tac cca caa	ggc ctg	ggc ccc	acg gtg	ccc gag	ctg ggg	act gag	ggc										362
Tyr Pro Gln	Gly Leu	Gly Pro	Gly Val	Pro Glu	Gly Thr	Glu Gly											
	65		70		75												
ctt cgg ccg	ctg gcc	aag acc	tgc ttc	agc atg	gtg cct	gcc ctg	cag										410
Leu Arg Pro	Leu Ala	Lys Thr	Cys Phe	Ser Met	Val Pro	Ala Leu	Gln										
	80		85		90												
cag gag ctg	gac agt	cgg ccc	cag ctg	cgc tct	gtg ctg	ctc tgt	ggc										458
Gln Glu Leu	Asp Ser	Arg Pro	Gln Leu	Arg Ser	Val Leu	Leu Cys	Gly										
	95		100		105												
att gag gca	cag gcc	tgc atc	ttg aac	acg acc	ctg gac	ctc cta	gac										506
Ile Glu Ala	Gln Ala	Cys Ile	Leu Asn	Thr Thr	Leu Asp	Leu Leu	Asp										
	110		115		120												
cgg ggg ctg	cag gtc	cat gtg	gtg gtg	gtg gac	gcc tgc	tcc tca	cgc agc										554
Arg Gly Leu	Gln Val	His Val	Val Val	Val Asp	Ala Cys	Ser Ser	Arg Ser										
	125		130		135		140										
cag gtg gac	cgt ctg	gct ctg	gcc cgc	atg aga	cag agt	ggg gcc											602


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Gln Val Asp Arg Leu Val Ala Leu Ala Arg Met Arg Gln Ser Gly Ala
      145      150      155
ttc ctc tcc acc agc gaa ggg ctc att ctg cag ctt gtg ggc gat gcc      650
Phe Leu Ser Thr Ser Glu Gly Leu Ile Leu Gln Leu Val Gly Asp Ala
      160      165      170
gtc cac ccc cag ttc aag gag atc cag aaa ctc atc aag gag ccc gcc      698
Val His Pro Gln Phe Lys Glu Ile Gln Lys Leu Ile Lys Glu Pro Ala
      175      180      185
cca gac agc gga ctg ctg ggc ctc ttc caa ggc cag aac tcc ctc ctc      746
Pro Asp Ser Gly Leu Leu Gly Leu Phe Gln Gly Gln Asn Ser Leu Leu
      190      195      200
cac tgaactccaa ccctgccttg agggaagacc accctcctgt caccgccacc      799
His
205
tcagtggaa cccgttcccc ccatccctgg atcccaagag tgggtgcgat caccaggagt      859
gccgccccct tgtggggggg ggcaggggtgc tgccttccca ttggacagct gctcccgaa      919
atgcaaatga gactcctgga aactgggtgg gaattggctg agccaagatg gaggcggggc      979
tcggccccgg gccacttcac ggggcgggaa ggggagggga agaagatct cagactgttg      1039
gacacggact cgcagaataa acatatatgt ggctgtggac caaaaaaaaa aaaaaaaaaa      1097

<210> 158
<211> 894
<212> DNA
<213> Homo sapiens

<220>
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<222> 98..637

<400> 158
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gtcctccccg ttccagagac tcattccagc ggaggag atg tgg ctc tac cgg aac      115
Met Trp Leu Tyr Arg Asn
      1      5
ccc tac gtg gag gcg gag tat ttc ccc acc aag ccg atg ttt gtt att      163
Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr Lys Pro Met Phe Val Ile
      10      15      20
gca ttt ctc tct cca ctg tct ctg atc ttc ctg gcc aaa ttt ctc aag      211
Ala Phe Leu Ser Pro Leu Ser Leu Ile Phe Leu Ala Lys Phe Leu Lys
      25      30      35
aag gca gac aca aga gac agc aga caa gcc tgc ctg gct gcc agc ctt      259
Lys Ala Asp Thr Arg Asp Ser Arg Gln Ala Cys Leu Ala Ala Ser Leu
      40      45      50
gcc ctg gct ctg aat ggc gtc ttt acc aac aca ata aaa ctg atc gta      307
Ala Leu Ala Leu Asn Gly Val Phe Thr Asn Thr Ile Lys Leu Ile Val
      55      60      65      70
ggg agg cca cgc cca gat ttc ttc tac cgc tgc ttc cct gat ggg cta      355
Gly Arg Pro Arg Pro Asp Phe Phe Tyr Arg Cys Phe Pro Asp Gly Leu
      75      80      85
gcc cat tct gac ttg atg tgt aca ggg gat aag gac gtg gtg aat gag      403
Ala His Ser Asp Leu Met Cys Thr Gly Asp Lys Asp Val Val Asn Glu
      90      95      100
ggc cga aag agc ttc ccc agt gga cat tct tcc ttt gca ttt gct ggt      451
Gly Arg Lys Ser Phe Pro Ser Gly His Ser Ser Phe Ala Phe Ala Gly
      105      110      115
ctg gcc ttt gcg tcc ttc tac ctg gca ggg aag tta cac tgc ttc aca      499
Leu Ala Phe Ala Ser Phe Tyr Leu Ala Gly Lys Leu His Cys Phe Thr
      120      125      130

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cca caa ggc cgt ggg aaa tct tgg agg ttc tgt gcc ttt ctg tca cct 547
Pro Gln Gly Arg Gly Lys Ser Trp Arg Phe Cys Ala Phe Leu Ser Pro
135 140 145 150
cta ctt ttt gca gct gtg att gca ctg tcc cgc aca tgt gac tac aag 595
Leu Leu Phe Ala Ala Val Ile Ala Leu Ser Arg Thr Cys Asp Tyr Lys
155 160 165
cat cac tgg caa gat ctg ctc aaa tgc acc aac act gcc aag 637
His His Trp Gln Asp Leu Leu Lys Cys Thr Asn Thr Ala Lys
170 175 180
tgactaagg agaaaaagaaa aatgacagg atcgtcatct gaaggacaga tgaatctttt 697
tctgccctt cttcacaaatg gaatataagg aacaattatg ggatgtcatc agaatggatg 757
ccataggacc tacagctccc tttctcttta ttgtgattat actttaaata tgacattgtc 817
ttttatgtgt atgttcttat attttcaatg tatctttttc cttcagtaaa cctgatattc 877
aaaaaaaa aaaaaa 894

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<212> DNA
<213> Homo sapiens

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<222> 221..670

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atctgcttag ttctacaaag tggagtttct ggcatcatt ctctatttct gtacacaaaag 180
tgctgtgaag ctcaagaaga aatagctctg cacaggaacg atg tgc act gcc cta 235
Met Cys Thr Ala Leu
1 5
ctg ctt ctt tat cta aga tgg tgt ttc aac tta aaa ctt gtg aat gtg 283
Leu Leu Leu Tyr Leu Arg Trp Cys Phe Asn Leu Lys Leu Val Asn Val
10 15 20
aaa tat gag cca aaa gac tct ctc ggc cct gaa atg acc ttt gta gca 331
Lys Tyr Glu Pro Lys Asp Ser Leu Gly Pro Glu Met Thr Phe Val Ala
25 30 35
gat gct gcc aga ggc ccc ctg tta tcc tcc ctg gac tct cca gct aac 379
Asp Ala Ala Arg Gly Pro Leu Leu Ser Ser Leu Asp Ser Pro Ala Asn
40 45 50
ctg atg tca act gcc agt gtg tgc atc tcc tta cct gag ggc tgt tct 427
Leu Met Ser Thr Ala Ser Val Cys Ile Ser Leu Pro Glu Gly Cys Ser
55 60 65
ggg ggc agg agt cct tgc tac tca cag aaa tgg cca cca gaa gtg cca 475
Gly Gly Arg Ser Pro Cys Tyr Ser Gln Lys Trp Pro Pro Glu Val Pro
70 75 80 85
gaa aaa tta acc tcc ctt ggc cag cag tcc tca acc agc tcc ctc act 523
Glu Lys Leu Thr Ser Leu Gly Gln Gln Ser Ser Thr Ser Ser Leu Thr
90 95 100
gac act gat gtg cag gtg tct cct atg ctg gtt gct gga gtc aac cac 571
Asp Thr Asp Val Gln Val Ser Pro Met Leu Val Ala Gly Val Asn His
105 110 115
agc agc agc ctt ctt gac aac ata ccc ttc act ggc tgc ctt cct ttc 619
Ser Ser Ser Leu Leu Asp Asn Ile Pro Phe Thr Gly Cys Leu Pro Phe
120 125 130
cat ctc tct tct tca ctc ccc tac cta tgt ctc cta ggc tct ccc ttc 667
His Leu Ser Ser Ser Leu Pro Tyr Leu Cys Leu Leu Gly Ser Pro Phe
135 140 145

aaa taaacagctt gcacttgaaa aaaaaaaaaa aaa 703
 Lys
 150

<210> 160
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 <212> DNA
 <213> Homo sapiens

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 <222> 165..674

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 atgtttcccg ggaagaactg ggataaagga aggggtcccg cacc atg gag gac ccg 176
 Met Glu Asp Pro
 1
 aac cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt 224
 Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser
 5 10 15 20
 ccc cag agc cca gga ggc aac atc tgc cac ctg ggg gcc ccg aag tgc 272
 Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly Ala Pro Lys Cys
 25 30 35
 acc cgc tgc ctc atc acc ttc gca gat tcc aag ttc cag gag cgt cac 320
 Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe Gln Glu Arg His
 40 45 50
 atg aag cgg gag cac cca gcg gac ttc gtg gcc cag aag ctg cag ggg 368
 Met Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln Lys Leu Gln Gly
 55 60 65
 gtc ctc ttc atc tgc ttc acc tgc gcc cgc tcc ttc ccc tcc tcc aaa 416
 Val Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe Pro Ser Ser Lys
 70 75 80
 gcc cta atc acc cac cag cgc agc cac ggt cca gcc gcc aag ccc acc 464
 Ala Leu Ile Thr His Gln Arg Ser His Gly Pro Ala Ala Lys Pro Thr
 85 90 95 100
 ctg ccg gtt gca acc act act gcc cag ccc acc ttc cct tgt cct gac 512
 Leu Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp
 105 110 115
 tgt ggc aag acc ttt ggg cag gct gtt tct ctg agg cgg cac cgc cag 560
 Cys Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Arg Arg His Arg Gln
 120 125 130
 atg cat gag gtc cgt gcc cct cct gcc acc ttc gcc tgc aca gag tgc 608
 Met His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys Thr Glu Cys
 135 140 145
 ggt cag gac ttt gct cag gaa gca ggg ctg cat caa cac tac att cgg 656
 Gly Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln His Tyr Ile Arg
 150 155 160
 cat gcc cgg ggg gag ctc tgagtgcagc ttaagcctct ccacggtagc 704
 His Ala Arg Gly Glu Leu
 165 170
 ggggtggtct gtggctggta ggactcacc atgatatggg gtgcaggaac tctgggggcc 764
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 <211> 846

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Met Glu Asp Pro 1															
aac cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt 224															
Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser															
5 10 15 20															
ccc cag ccc agg agg caa cat ctg cca cct ggg ggc ccc gaa gtg cac 272															
Pro Gln Pro Arg Arg Gln His Leu Pro Pro Gly Gly Pro Glu Val His															
25 30 35															
ccg ctg cct cat hac cct cgc aga ttc caa gtt cca gya gcg tca cat 320															
Pro Leu Pro Cys His Leu Arg Phe Gln Val Pro Gly Ala Ser His															
40 45 50															
gaa gcg gga gca ccc agc gga ctt cgt ggc cca gaa get gca ggg ggt 368															
Glu Ala Gly Ala Pro Ser Gly Leu Arg Gly Pro Glu Ala Ala Gly Gly															
55 60 65															
cct ctt cat ctg ctt cac ctg cgc ccg ctc ctt ccc ctc ctc caa agc 416															
Pro Leu His Leu Leu His Leu Arg Pro Leu Leu Pro Leu Leu Gln Ser															
70 75 80															
cct aat cac cca cca gcg cag cac ggt cca gcc gcc aag ccc acc ctg 464															
Pro Asn His Pro Pro Ala Gln His Gly Pro Ala Ala Lys Pro Thr Leu															
85 90 95 100															
ccg gtt gca acc act act alc gca ccc acc ttc cct tct cct gac tgt 512															
Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp Cys															
105 110 115															
ggc aag acc ttt ggg cag gct gtt tct ctg agg cgg cac cgc cag atg 560															
Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Arg Arg His Arg Gln Met															
120 125 130															
cat gag gtc cgt gcc cct cct gcc acc ttc gcc tgc aca gag tgc ggt 608															
His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys Thr Glu Cys Gly															
135 140 145															
cag gac ttt gct cag gaa gca ggg ctg cat caa cac tac att cgg cat 656															
Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln His Tyr Ile Arg His															
150 155 160															
gcc cgg ggg gag ctc tgagtgcagc ttaagcctct ccacggtgac gggtggctct 711															
Ala Arg Gly Glu Leu															
165															
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<211> 1176
<212> DNA
<213> Homo sapiens
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<222> 28..1128
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<400> 162

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Thr Asn Cys Ser Trp Trp Pro Ile Ser Ala Leu Glu Ser Asp Ala Ala	
10 15 20 25	
aag cca gcg gag gcc ccc gac gct ccc gag gcg gcc agc ccc gcc cat	150
Lys Pro Ala Glu Ala Pro Asp Ala Pro Glu Ala Ala Ser Pro Ala His	
30 35 40	
tgg ccc agg gag agc ctg gtt ctg tac cac tgg acc cag tcc ttc agc	198
Trp Pro Arg Glu Ser Leu Val Leu Tyr His Trp Thr Gln Ser Phe Ser	
45 50 55	
tcg cag aag gtg cgg ctg gtg atc gcc gag aag ggc ctg gtg tgc gag	246
Ser Gln Lys Val Arg Leu Val Ile Ala Glu Lys Gly Leu Val Cys Glu	
60 65 70	
gag cgg gac gtg agc ctg cca cag agc gag cac aag gag ccc tgg ttc	294
Glu Arg Asp Val Ser Leu Pro Gln Ser Glu His Lys Glu Pro Trp Phe	
75 80 85	
atg cgg ctc aac ctg ggc gag gag gtg ccc gtc atc atc cac cgc gac	342
Met Arg Leu Asn Leu Gly Glu Glu Val Pro Val Ile Ile His Arg Asp	
90 95 100 105	
aac atc atc agt gac tat gac cag atc att gac tat gtg gag cgc acc	390
Asn Ile Ile Ser Asp Tyr Asp Gln Ile Ile Asp Tyr Val Glu Arg Thr	
110 115 120	
ttc aca gga gag cac gtg gtg gcc ctg atg ccc gag gtg ggc agc ctg	438
Phe Thr Gly Glu His Val Val Ala Leu Met Pro Glu Val Gly Ser Leu	
125 130 135	
cag cac gca cgg gtg ctg cag tac cgg gag ctg ctg gac gca ctg ccc	486
Gln His Ala Arg Val Leu Gln Tyr Arg Glu Leu Leu Asp Ala Leu Pro	
140 145 150	
atg gat gcc tac acg cat ggc tgc atc ctg cat ctc gag ctc acc acc	534
Met Asp Ala Tyr Thr His Gly Cys Ile Leu His Leu Glu Leu Thr Thr	
155 160 165	
gac tcc atg atc ccc aag tac gcc acg gcc gag atc cgc aga cat tta	582
Asp Ser Met Ile Pro Lys Tyr Ala Thr Ala Glu Ile Arg Arg His Leu	
170 175 180 185	
gcc aat gcc acc acg gac ctc atg aaa ctg gac cat gaa gag gag ccc	630
Ala Asn Ala Thr Thr Asp Leu Met Lys Leu Asp His Glu Glu Glu Pro	
190 195 200	
cag ctc tcc gag ccc tac ctt tct aaa caa aag aag ctc atg gcc aag	678
Gln Leu Ser Glu Pro Tyr Leu Ser Lys Gln Lys Lys Leu Met Ala Lys	
205 210 215	
atc ttg gag cat gat gat gtg agc tac ctg aag aag atc ctc ggg gaa	726
Ile Leu Glu His Asp Asp Val Ser Tyr Leu Lys Lys Ile Leu Gly Glu	
220 225 230	
ctg gcc atg gtg ctg gac cag att gag gcg gag ctg gag aag agg aag	774
Leu Ala Met Val Leu Asp Asp Gln Ile Glu Ala Glu Leu Glu Lys Arg Lys	
235 240 245	
ctg gag aac gag ggg cag aaa tgc gag ctg tgg ctc tgt ggc tgt gcc	822
Leu Glu Asn Glu Gly Gln Lys Cys Glu Leu Trp Leu Cys Gly Cys Ala	
250 255 260 265	
ttc acc ctc gct gat gtc ctc ctg gga gcc acc ctg cac cgc ctc aag	870
Phe Thr Leu Ala Asp Val Leu Leu Gly Ala Thr Leu His Arg Leu Lys	
270 275 280	
ttc ctg gga ctg tcc aag aaa tac tgg gaa gat ggc agc cgg ccc aac	918
Phe Leu Gly Leu Ser Lys Lys Tyr Trp Glu Asp Gly Ser Arg Pro Asn	

	285	290	295	
ctg cag tcc ttc ttt gag agg gtc cag aga cgc ttt gcc ttc cgg aaa				966
Leu Gln Ser Phe Phe Glu Arg Val Gln Arg Arg Phe Ala Phe Arg Lys				
	300	305	310	
gtc ctg ggt gac atc cac acc acc ctg ctg tcg gcc gtc atc ccc aat				1014
Val Leu Gly Asp Ile His Thr Thr Leu Leu Ser Ala Val Ile Pro Asn				
	315	320	325	
gct ttc cgg ctg gtc aag agg aaa ccc cca tcc ttc ttc ggg gcg tcc				1062
Ala Phe Arg Leu Val Lys Arg Lys Pro Pro Ser Phe Phe Gly Ala Ser				
	330	335	340	345
ttc ctc atg ggc tcc ctg ggt ggg atg ggc tac ttt gcc tac tgg tac				1110
Phe Leu Met Gly Ser Leu Gly Gly Met Gly Tyr Phe Ala Tyr Trp Tyr				
	350	355	360	
ctc aag aaa aaa tac atc tagggccagg cctggggcctt ggtgtctgac				1158
Leu Lys Lys Lys Tyr Ile				
	365			
aaaaaaaaa aaaaaaaaaa				1176

<210> 163
 <211> 1084
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 135..194

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 gccgagaggt gagggtgcc ccgcctcacc tcgagagggg ccgttccggg ctgaaacccg 120
 gcaccttcgg gaaa atg gcg gct gcc agg ccc agc ctg ggc cga gtc ctc 170
 Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu
 1 5 10
 cca gga tcc tct cct gtt cct gtg tgacatgcag gagaagttcc gccacaacat 224
 Pro Gly Ser Ser Pro Val Pro Val
 15 20
 cgcctacttc ccacagatcg tctcagtggc tgcccgcgat ctcaaggtgg ccggtcgtgt 284
 tgaggtgcca gtcagtctga cggagcagta cccacaaggc ctggggcccca cggtgcccca 344
 gctggggact gagggccttc ggccgctggc caagacctgc ttcagcatgg tgcctgcctc 404
 gcagcaggag ctggacagtc ggccccagct gcgctctgtg ctgctctgtg gcattgaggc 464
 acaggcctgc atcttgaaca cgacctgga cctcctagac cgggggctgc aggtccatgt 524
 ggtggtggag gcctgctcct caccgagcca ggtggaccgg ctggtggctc tggcccgcac 584
 gagacagagt ggtgccttcc tctccaccag cgaagggtc atctctgacg ttgtgggcga 644
 tgccgtccac cccagttca aggagatcca gaaactcatc aaggagcccg cccagacag 704
 cggactgcgt ggccctcttcc aaggccagaa ctccctcctc cactgaactc caacctgtgc 764
 ttgagggaa accaccctcc tgtcaccgg acctcagtgg aagcccgctc ccccatccc 824
 tggatcccaa gagtgggtgc atccaccagg agtgccgccc ccttgggggg ggcaggggtgc 884
 tgccctccca ttggacagct gctcccggaa atgcaaatga gactcctgga aactgggtgg 944
 gaattggctg agcccaagat gagggcgggc tcggcccggg gccacttcac ggggcgggaa 1004
 ggggagggga agaagagtct cagactgtgt gacacggact cgcagaataa acatatatgt 1064
 ggcaaaaaaa aaaaaaaaaa 1084

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 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 173..847

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cgatgttcatt actacaggaa aaactgttct cttctgtggc acagagaacc ctgcttcaaa      120
gcagaagtag cagttccgga gtccagctggt ctaaaactca tcccagagga ta atg gca      178
                                   Met Ala
                                   1
acc cat gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg      226
Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met
                                   5
                                   10
                                   15
gtg ggc aca gtg gct gtc act gtc atg cct cag tgg aga gtg tcg gcc      274
Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val Ser Ala
                                   20
                                   25
                                   30
ttc att gaa aac aac atc gtg gtt ttt gaa aac ttc tgg gaa gga ctg      322
Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu Gly Leu
                                   35
                                   40
                                   45
tgg atg aat tgc gtg agg cag gct aac atc agg atg cag tgc aaa atc      370
Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile
                                   55
                                   60
                                   65
tat gat tcc ctg ctg gct ctt tct ccg gac cta cag gca gcc aga gga      418
Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly
                                   70
                                   75
                                   80
ctg atg tgt gct gct tcc gtg atg tcc ttc ttg gct ttc atg atg gcc      466
Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met Ala
                                   85
                                   90
                                   95
atc ctt ggc atg aaa tgc acc agg tgc acg ggg gac aat gag aag gtg      514
Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu Lys Val
                                   100
                                   105
                                   110
aag gct cac att ctg ctg acg gct gga atc atc ttc atc atc acg ggc      562
Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly
                                   115
                                   120
                                   125
atg gtg gtg ctg atc cct gtg agc tgg gtt gcc aat gcc atc atc aga      610
Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg
                                   135
                                   140
                                   145
gat ttc tat aac tca ata gtg aat gtt gcc caa aaa cgt gag ctt gga      658
Asp Phe Tyr Asn Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly
                                   150
                                   155
                                   160
gaa gct ctg tac tta gga tgg acc acg gca ctg gtg ctg att gtt gga      706
Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly
                                   165
                                   170
                                   175
gga gct ctg ttc tgc tgc gtt ttt tgt tgc aac gaa aag agc agt agc      754
Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser
                                   180
                                   185
                                   190
tac aga tac tcg ata cct tcc cat cgc aca acc caa aaa agt tat cac      802
Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
                                   195
                                   200
                                   205
acc gga aag aag tca ccg agc gtc tac tcc aga agt cag tat gtg      847
Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
                                   215
                                   220
                                   225
tagttgtgta tggttttttta accttactat aaagccatgc aaatgacaaa aatctatatt      907
accttctcaa aatggacccc aaagaaactt tgatttactg ttcttaactg cctaactcta      967
attacaggaa ctgtgcatca gctatttatg attctataag ctatttcagc agaatgagat      1027
attaaaccca atgctttgat tgttctagaa agtattgttaa tttgttttct aaggtgtgtc      1087
aagcatctac tctttttatc atttacttca aaatgacatt gctaaagact gcattattct      1147
actactgtaa tttctccacg acatagcatt atgtacatag atgagtgtaa catttatatc      1207
tcacatagag acatgcttat atgggttttat ttaaaaatgaa atgccagtc attacactga      1267

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agt gac agt gag gag ctg agt agc ctg cag gtc cta gat gcg gac acc 577
 Ser Asp Ser Glu Glu Leu Ser Ser Leu Gln Val Leu Asp Ala Asp Thr
 175 180 185 190
 ttt gcc ttc tgc tgt gct tcg ggc cgg ctg ggg ctt gtt gac acc cgg 625
 Phe Ala Phe Cys Cys Ala Ser Gly Arg Leu Gly Leu Val Asp Thr Arg
 195 200 205
 cag aag tgg gca ccg ttg gag aat cgc agc cct ggc cct ggg tct ggt 673
 Gln Lys Trp Ala Pro Leu Glu Asn Arg Ser Pro Gly Pro Gly Ser Gly
 210 215 220
 gga gag aga tgg tgt gct gaa gtt ggg agc tgg ggc cag ggc cct ggg 721
 Gly Glu Arg Trp Cys Ala Glu Val Gly Ser Trp Gly Gln Gly Pro Gly
 225 230 235
 ccc agc att gcc agc ctt agc tca gat ggg cgt ctt tgt ctt ctt gac 769
 Pro Ser Ile Ala Ser Leu Ser Ser Asp Gly Arg Leu Cys Leu Leu Asp
 240 245 250
 ccc cgg gat ctc tgc cat cct ctg agc tca gtc cag tgc cca gta tcc 817
 Pro Arg Asp Leu Cys His Pro Val Ser Ser Val Gln Cys Pro Val Ser
 255 260 265 270
 gta cct agc cct gac cca gag ctg ctg cga gtg act tgg gcc cca ggc 865
 Val Pro Ser Pro Asp Pro Glu Leu Leu Arg Val Thr Trp Ala Pro Gly
 275 280 285
 ctg aag aat tgc ttg gcc atc tca ggt ttt gat ggt aca gtc cag gtc 913
 Leu Lys Asn Cys Leu Ala Ile Ser Gly Phe Asp Gly Thr Val Gln Val
 290 295 300
 tat gat gcc aca tct tgg gat gga aca cgg agc caa gat gga aca cgg 961
 Tyr Asp Ala Thr Ser Trp Asp Gly Thr Arg Ser Gln Asp Gly Thr Arg
 305 310 315
 agc caa gta gaa cct ctc ttc act cac aga ggt cac atc ttc cta gat 1009
 Ser Gln Val Glu Pro Leu Phe Thr His Arg Gly His Ile Phe Leu Asp
 320 325 330
 gga aat ggg atg gac cct gct cct ttg gtc acc acc cac acc tgg cat 1057
 Gly Asn Gly Met Asp Pro Ala Pro Leu Val Thr Thr His Thr Thr His
 335 340 345 350
 ccc tgc aga cca agg act ttg tta tca gca aca aat gat gcc tct ctg 1105
 Pro Cys Arg Pro Arg Thr Leu Leu Ser Ala Thr Asn Asp Ala Ser Leu
 355 360 365
 cat gtg tgg gac tgg gtg gac ctt tgt gcc ccc cgc tgacaccagc 1151
 His Val Trp Asp Trp Val Asp Leu Cys Ala Pro Arg
 370 375
 atctttccat ctaggcctct agaaaagggga ggagctgctg tagtagcaag ggtgctgatg 1211
 taggactcaa gtgactacca gtccctgtta ccagctgtgt ggccttgggc aagtctgcca 1271
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 tgatattgag aaggttagaa gaaacgcgat gcataattac ttggttagcta ttggttagatc 1391
 tgggagtgtg aaatggtagc gttttgtccc tgtcttcaca ctatcatagg gagaatcaaa 1451
 agagctaaaca aatataaaca tgctttgtga atttttttaa agaaaaaaat gtagggggggc 1511
 caataaacat gaaaaaatcc cagccctagt agcaattaa gaaatagcaa aacaggattt 1571
 ctgctcctct tgaggggggc tcatgggaac acaggtgcac tttccacac ttgtccccc 1631
 aggtgactag gtccaagaga catttgcttt tgggtggccc acaaacattt ccttttgagg 1691
 gcccatagt aatatntaaa gtgtgctgga catggtggct catgctgta atcccagcac 1751
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 catagcaaga tcccttcccc aaaaaaaaaa aaaaaaaa 1849

<210> 166
 <211> 1748
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 136..264

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ggcacagaga accctgcttc aaagcagaag tagcagttcc ggagttccagc tggctaaaaac      120
tcatcccaga ggata atg gca acc cat gcc tta gaa atc gct ggg ctg ttt      171
                Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe
                1                5                10
ctt ggt ggt gtt gga atg gtg ggc aca gtg gct gtc act gtc atg cct      219
Leu Gly Gly Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro
                15                20                25
cag tgg aga gtg tgc gcc ttc att gaa aac aac atc gtg gtt ttt      264
Gln Trp Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe
                30                35                40
taaaactctt gggaaggact gtggatgaat tgcgtgaggc aggctaacat caggatgcag      324
tgcaaaatct atgattccct gctggctctt tctccggacc tacaggcagc cagaggactg      384
atgtgtgtcgt ctcccgctgat gtcttctctg gctttcatga tggccatcct tggcatgaaa      444
tgcaccagggt gcacggggga caatgagaag gtgaaggctc acattctgct gacggctgga      504
atcatcttca tcatcacggg catggtggtg ctcatccctg tgagctgggt tgcgaatgcc      564
atcatcagag atttctataa ctcaatagtg aatgttgccc aaaaacgtga gcttggagaa      624
gctctctact taggatggac cacggcactg gtgctgattg ttggaggagc tctgttctgc      684
tgcgtttttt gtgtcaacga aaagagcagt agctacagat actcgatacc ttcccatcgc      744
acaacccaaa aaagttaatc caccggaag aagtcacoga gcgtctactc cagaagtacg      804
tatgtgtagt tgtgtatggt tttttaactt tactataaag ccatgaaatc gacaaaaatc      864
tatattactt tctcaaaatg gaccccaag aacttttgat ttaactgtct taactgccta      924
atcttaatta caggaactgt gcatacgcta tttatgattc tataagctat ttcagcagaa      984
tgagatatta aaccgaatgc tttgattggt ctagaaagta tagtaatttg ttttctaagg      1044
tgggtkcaagc atctactcct tttatcattt acttcaaaat gacattgcta aagactgcatt      1104
tattttacta ctgtaatttc tccacgcagt agcattatct acatagatga gtgtaacatt      1164
tatattctac atagagacat gcttatatgg ttkcatttaa aatgaaatgc cagtccatta      1224
cactgaactaa atagaactca actattgctt ttcagggaat tcattgtagg ggttgaagaa      1284
ggttactatt aattgtttaa aaacagctta gggattaatg tctctccatt ataatgaaga      1344
ttaaaatgaa ggcttttaact agcattgtta aggaaattga atggctttct gatatgctgt      1404
tttttagcct agggagttaga aatcctaact tctttatcct ctctctccag aggctttttt      1464
tttctgtgtt attaaattaa catttttaaa aagcagatat tttgtcaagg ggctttgcat      1524
tcaaaactgct ttccaggggc tatactcaga agaaagataa aagtgtgata taagaaaaag      1584
tgatggtttt aggaaagtga aatatTTTT gtttttgatg ttgaagaaga atgatgcatt      1644
ttgacaagaa atcatatatg tatggatata ttttaataag tatttgagta cagactttga      1704
ggtttcatca atataataaa aagagcaaaa aaaaaaaaaa aaaa      1748

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<210> 167
<211> 1275
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 14..1048

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<400> 167
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                Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly
                1                5                10
tgc ggc cag gcg tgg ggt gcg tgc gtg ggc ggc cgc agc tgc gag gag      97
Cys Gly Gln Ala Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Gly
                15                20                25
ctc act gcg gtc cta acc ccg ccg cag ctc ctc gga cgc agg ttt aac      145

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Leu Thr Ala Val Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn	
30 35 40	
ttc ttt att caa caa aaa tgc gga ttc aga aaa gca ccc agg aag gtt	193
Phe Phe Ile Gln Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val	
45 50 55 60	
gaa cct cga aga tca gac cca ggg aca agt ggt gaa gca tac aag aga	241
Glu Pro Arg Arg Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg	
65 70 75	
agt gct ttg att cct cct gtg gaa gaa aca gtc ttt tat cct tct ccc	289
Ser Ala Leu Ile Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro	
80 85 90	
tat cct ata agg agt ctc ata aaa cct tta ttt ttt act gtt ggg ttt	337
Tyr Pro Ile Arg Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe	
95 100 105	
aca ggc tgt gca ttt gga tca gct gct att tgg caa tat gaa tca ctg	385
Thr Gly Cys Ala Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu	
110 115 120	
aaa tcc agg gtc cag agt tat ttt gat ggt ata aaa gct gat tgg ttg	433
Lys Ser Arg Val Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu	
125 130 135 140	
gat agc ata aga cca caa aaa gaa gga gac ttc aga aag gag att aac	481
Asp Ser Ile Arg Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn	
145 150 155	
aag tgg tgg aat aac cta agt gat ggc cag cgg act gtg aca ggt att	529
Lys Trp Trp Asn Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile	
160 165 170	
ata gct gca aat gtc ctt gta ttc tgt tta tgg aga gta cct tct ctg	577
Ile Ala Ala Asn Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu	
175 180 185	
cag cgg aca atg atc aga tat ttc aca tcg aat cca gcc tca aag gtc	625
Gln Arg Thr Met Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val	
190 195 200	
ctt tgt tct cca atg ttg ctg tca aca ttc agt cat ttc tcc tta ttt	673
Leu Cys Ser Pro Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe	
205 210 215 220	
cac atg gca gca aat atg tat gtt ttg tgg agc ttc tct tcc agc ata	721
His Met Ala Ala Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile	
225 230 235	
gtg aac att ctg ggt caa gag cag ttc atg gca gtg tac cta tct gca	769
Val Asn Ile Leu Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala	
240 245 250	
ggt gtt att tcc aat ttt gtc agt tac gtg ggt aaa gtt gcc aca gga	817
Gly Val Ile Ser Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly	
255 260 265	
aga tat gga cca tca ctt ggt gca gcc ctg aaa gcc att atc gcc atg	865
Arg Tyr Gly Pro Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met	
270 275 280	
gat aca gca gga atg atc ctg gga tgg aaa ttt ttt gat cat gcg gca	913
Asp Thr Ala Gly Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala	
285 290 295 300	
cat ctt ggg gga gct ctt ttt gga ata tgg tat gtt act tac ggt cat	961
His Leu Gly Gly Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His	
305 310 315	
gaa ctg att tgg aag aac agg gag ccg cta gtg aaa atc tgg cat gaa	1009
Glu Leu Ile Trp Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu	
320 325 330	
ata agg act aat ggc ccc aaa aaa gga ggt ggc tct aag taaaactggg	1058
Ile Arg Thr Asn Gly Pro Lys Lys Gly Gly Ser Lys	

00771072 120700

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      335              340              345
attggacagt agtggtgcat ctggtccttg cgcctgaga gccccaggag acatcggcta 1118
gagtgaccat ggctatgctc ccgtctggaa gatgccagca tctggccctcc cacttttttc 1178
agctgtgtcc ccagctcgt gtcctttttag aatgtgaatg atgataaagt tgtgaaataa 1238
aggtttctat ctagtttgca aaaaaaaaaa aaaaaaa
<210> 168
<211> 1023
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 70..777

<400> 168
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ggcccccggg atg aag aga tct ggg aac ccg gga gcc gag gta acg aac agc 111
      Met Lys Arg Ser Gly Asn Pro Gly Ala Glu Val Thr Asn Ser
      1              5              10
tcg gtg gca ggg cct gac tgc tgc gga ggc ctc ggc aat att gat ttt 159
Ser Val Ala Gly Pro Asp Cys Cys Gly Gly Leu Gly Asn Ile Asp Phe
15              20              25              30
aga cag gca gac ttc tgc gtt atg acc cgg ctg ctg ggc tac gtg gac 207
Arg Gln Ala Asp Phe Cys Val Met Thr Arg Leu Leu Gly Tyr Val Asp
      35              40              45
ccc ctg gat ccc agc ttt gtg gct gcc gtc atc acc atc acc ttc aat 255
Pro Leu Asp Pro Ser Phe Val Ala Ala Val Ile Thr Ile Thr Phe Asn
50              55              60
ccg ctc tac tgg aat gtg gtt gca cga tgg gaa cac aag acc cgc aag 303
Pro Leu Tyr Trp Asn Val Val Ala Arg Trp Glu His Lys Thr Arg Lys
65              70              75
ctg agc agg gcc ttc gga tcc ccc tac ctg gcc tgc tac tct cta agc 351
Leu Ser Arg Ala Phe Gly Ser Pro Tyr Leu Ala Cys Tyr Ser Leu Ser
80              85              90
atc acc atc ctg ctc ctg aac ttc ctg cgc tgc cac tgc ttc acg cag 399
Ile Thr Ile Leu Leu Leu Asn Phe Leu Arg Ser His Cys Phe Thr Gln
95              100              105              110
gcc atg ctg agc cag ccc agg atg gag agc ctg gac acc ccc gcg gcc 447
Ala Met Leu Ser Gln Pro Arg Met Glu Ser Leu Asp Thr Pro Ala Ala
115              120              125
tac agc ctg gtc ctc gca ctc ctg gga ctg ggc gtc gtg ctc gtg ctc 495
Tyr Ser Leu Val Leu Ala Leu Leu Gly Leu Gly Val Val Leu Val Leu
130              135              140
tcc agc ttc ttt gca ctg ggg ttc gct gga act ttc cta ggt gat tac 543
Ser Ser Phe Phe Ala Leu Gly Phe Ala Gly Thr Phe Leu Gly Asp Tyr
145              150              155
ttc ggg atc ctc aag gag gcg aga gtg acc gtg ttc ccc ttc aac atc 591
Phe Gly Ile Leu Lys Glu Ala Arg Val Thr Val Phe Pro Phe Asn Ile
160              165              170
ctg gac aac ccc atg tac tgg gga agc aca gcc aac tac ctg ggc tgg 639
Leu Asp Asn Pro Met Tyr Trp Gly Ser Thr Ala Asn Tyr Leu Gly Trp
175              180              185              190
gcc atc atg cac gcc agc ccc acg ggc ctg ctc ctg acg gtg ctg gtg 687
Ala Ile Met His Ala Ser Pro Thr Gly Leu Leu Leu Thr Val Leu Val
195              200              205
gcc ctc acc tac ata gtg gct ctc cta tac gaa gag ccc ttc acc gct 735
Ala Leu Thr Tyr Ile Val Ala Leu Leu Tyr Glu Glu Pro Phe Thr Ala

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210 215 220
 gag atc tac cgg cag aaa gcc tcc ggg tcc cac aag agg agc 777
 Glu Ile Tyr Arg Gln Lys Ala Ser Gly Ser His Lys Arg Ser
 225 230 235
 tgattgagct gcaacagctt tgctgaaggc ctggccagcc tcttggcctg ccccaagtgg 837
 caggccctgc gcagggcgag aatggtgcct gctgctcagg gctcgccccc ggcgtgggct 897
 gccccagtgc cttggaacct gctgccttgg ggaccctgga cgtgcgcgaca tatggccatt 957
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 aaaaaa 1023

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 <212> DNA
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 <222> 38..400

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 Met Asn Thr Glu Ala Glu
 1 5
 caa cag ctt ctc cat cac gcc aga aat ggc aat gct gaa gaa gta aga 103
 Gln Gln Leu Leu His His Ala Arg Asn Gly Asn Ala Glu Glu Val Arg
 10 15 20
 caa cta tta gag acc atg gcg agt aat gaa gtg att gct gac att aat 151
 Gln Leu Leu Glu Thr Met Ala Ser Asn Glu Val Ile Ala Asp Ile Asn
 25 30 35
 tgc aaa gga aga agt aag tct aac ttg ggc tgg aca ccc cta cat ctg 199
 Cys Lys Gly Arg Ser Lys Ser Asn Leu Gly Trp Thr Pro Leu His Leu
 40 45 50
 gca tgc tat ttt gga cac aga caa gtg gtc cag gat ctg ttg aag gct 247
 Ala Cys Tyr Phe Gly His Arg Gln Val Val Gln Asp Leu Leu Lys Ala
 55 60 65 70
 ggt gca gaa gtg aat gtg ttg aat gac atg gga gac acg ccg ctt cat 295
 Gly Ala Glu Val Asn Val Leu Asn Asp Met Gly Asp Thr Pro Leu His
 75 80 85
 cga gct gcc ttt aca gga cga aag gtg aaa atc att cta tgt tca atg 343
 Arg Ala Ala Phe Thr Gly Arg Lys Val Lys Ile Ile Leu Cys Ser Met
 90 95 100
 ttt gta agt gag gta ttt gga gga gta gtt acc att gtt ttc tct gtt 391
 Phe Val Ser Glu Val Phe Gly Gly Val Val Thr Ile Val Phe Ser Val
 105 110 115
 ata acc atc tgaccagcaa ccgaagaaa ccacacaaaa aaatgtatac 440
 Ile Thr Ile
 120
 accagcactt tgggtcaaaa ggccacagga tctttttagt ctgacagtga ggtccagtac 500
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 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..572

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ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg      107
    Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
      1          5          10          15
ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt      155
Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys
      20          25          30
gag ggc cgg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg      203
Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
      35          40          45
ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg      251
Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
      50          55          60
gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct      299
Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
      65          70          75
ctt ggc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt      347
Leu Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
      80          85          90          95
ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg      395
Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
      100          105          110
ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc      443
Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
      115          120          125
aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc      491
Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
      130          135          140
gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca      539
Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
      145          150          155
gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga      592
Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
      160          165          170
gaggagggac gccagggtg gggaggaaga gtctgcaagc agggctgtgg agttagggtt      652
caccccaatg ggaccacct cctgggtccc ctgggtgccgt ttttccttag aaatcagaga      712
aatgggaaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagcaaaaaa      772
aaaaa                                                                776

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 <222> 160..867

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ggtttccgga ggacagccaa caagcgatgc tgccgccgcc gtttctctgat tggttgtggg 120
tgggtacctc ttcgttctga ttggccgcta gtgagcaag atg ctg agc aag ggt 174
Met Leu Ser Lys Gly
1 5

ctg aag cgg aaa cgg gag gag gag gag gag aag gaa cct ctg gca gtc 222
Leu Lys Arg Lys Arg Glu Glu Glu Glu Glu Lys Glu Pro Leu Ala Val
10 15 20

gac tcc tgg tgg cta gat cct ggc cac aca gcg gtg gca cag gca ccc 270
Asp Ser Trp Trp Leu Asp Pro Gly His Thr Ala Val Ala Gln Ala Pro
25 30 35

ccg gcc gtg gcc tct agc tcc ctc ttt gac ctc tca gtg ctc aag ctc 318
Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu Ser Val Leu Lys Leu
40 45 50

cac cac agc ctg cag cag agt gag ccg gac ctg cgg cac ctg gtg ctg 366
His His Ser Leu Gln Gln Ser Glu Pro Asp Leu Arg His Leu Val Leu
55 60 65

gtc gtg aac act ctg cgg cgc atc cag gcg tcc atg gca ccc gcg gct 414
Val Val Asn Thr Leu Arg Arg Ile Gln Ala Ser Met Ala Pro Ala Ala
70 75 80 85

gcc ctg cca cct gtg cct agc cca cct gca gcc ccc agt gtg gct gac 462
Ala Leu Pro Pro Val Pro Ser Pro Pro Ala Ala Pro Ser Val Ala Asp
90 95 100

aac tta ctg gca agc tcg gac gct gcc ctt tca gcc tcc atg gcc agc 510
Asn Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser Ala Ser Met Ala Ser
105 110 115

ctc ctg gag gac ctc agc cac att gag ggc ctg agt cag gct ccc caa 558
Leu Glu Asp Leu Ser His Ile Glu Gly Leu Ser Gln Ala Pro Gln
120 125 130

ccc ttg gca gac gag ggg cca cca ggc cgt agc atc ggg gga gca gcg 606
Pro Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser Ile Gly Gly Ala Ala
135 140 145

ccc agc ctg ggt gcc ttg gac ctg ctg ggc cca gcc act ggc tgt cta 654
Pro Ser Leu Gly Ala Leu Asp Leu Leu Gly Pro Ala Thr Gly Cys Leu
150 155 160 165

ctg gac gat ggg ctt gag ggc ctg ttt gag gat att gac acc tct atg 702
Leu Asp Asp Gly Leu Glu Gly Leu Phe Glu Asp Ile Asp Thr Ser Met
170 175 180

tat gac aat gaa ctt tgg gca cca gcc tct gag ggc ctc aaa cca ggc 750
Tyr Asp Asn Glu Leu Trp Ala Pro Ala Ser Glu Gly Leu Lys Pro Gly
185 190 195

cct gag gat ggg ccg ggc aag gag gaa gct ccg gag ctg gac gag gcc 798
Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro Glu Leu Asp Glu Ala
200 205 210

gaa ttg gac tac ctc atg gat gtg ctg gtg ggc aca cag gca ctg gag 846
Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly Thr Gln Ala Leu Glu
215 220 225

cga ccg ccg ggg cca ggg cgc tgagccctcg tgctggaatg gttgtctggt 897
Arg Pro Pro Gly Pro Gly Arg
230 235

atctgaactg agcctgctgg ctggaccaac tgtcctcgaa aagacacagc tggcttcctt 957
agtacagaga acagggcttg ggccaacttg gagagacaga atctagtctt gggcaacttc 1017
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aatgacaggg tctggtgggg acttaattcc ctggccctgg ggtcatagct tgggctgttc 1137
cttctctgat acggaagag accccaatca gatttttcaa attaaagcca gtcctgggaa 1197
atctcaaaaa aaaaaaaaaa aa 1219

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 <212> DNA
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<220>
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 <222> 68..640

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      Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu
      1          5          10
ata aca ttt gta ttt caa gaa aag gaa gat ctt cct gtt aca gag gat      157
Ile Thr Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp
15          20          25          30
aac ttt gtg aaa ctt caa gtt aaa gct tgt gct ctg agc cag ata aat      205
Asn Phe Val Lys Leu Ala Glu Met Lys Ala Cys Ala Leu Ser Gln Ile Asn
      35          40          45
aca aag ctt ctg gca gaa atg aag atg aaa aag gat tta ttt cct gtt      253
Thr Lys Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val
      50          55          60
ggg aga gaa att gct gga att gta tta gat gtt gga agc aag gta tca      301
Gly Arg Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser
      65          70          75
ttc ttt caa cca gat gat gaa gta gtt gga att ttg ccc ctg gac tct      349
Phe Phe Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser
      80          85          90
gaa gac cct gga ctt tgt gaa gtt gtt aga gta cat gag cat tac ttg      397
Glu Asp Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu
      95          100          105          110
gtt cat aaa cca gaa aag gtc aca tgg acg gaa gca gca gga agc att      445
Val His Lys Pro Glu Lys Val Thr Trp Thr Glu Ala Ala Gly Ser Ile
      115          120          125
cgg gat gga gtg cgt gcc tat aca gct ctg cat tat ctt tct cat ctc      493
Arg Asp Gly Val Arg Ala Tyr Thr Ala Leu His Tyr Leu Ser His Leu
      130          135          140
tct cct gga aaa tca gtg ctg ata atg gat gga gca agt gca ttt ggt      541
Ser Pro Gly Lys Ser Val Leu Ile Met Asp Gly Ala Ser Ala Phe Gly
      145          150          155
aca ata gct att cag tta gca cat cat aga gga gcc aaa gta ttt caa      589
Thr Ile Ala Ile Gln Leu Ala His His Arg Gly Ala Lys Val Phe Gln
      160          165          170
cag cat gca gcc ttg aag ata agc agt gcc ttg aaa gat tca gac ctc      637
Gln His Ala Ala Leu Lys Ile Ser Ser Ala Leu Lys Asp Ser Asp Leu
      175          180          185          190
cca tagcccgagt gattgatgta tctaattggga aagttcatgt tgctgaaagc      690
Pro
tgtttggaaag aaacaggtgg cctggggagta gatattgtcc tagatgctgg agtgagatta      750
tatagtaaaag atgatgaacc agctgtaaaa ctacaactac taccacataa acatgatatc      810
atcacacttc ttggtgttgg aggccactgg gtaacaacag aagaaaaact tcagttggat      870
cctccagata gccactgcct ttctctcaag ggagcaacgt tagctttcct gaatgatgaa      930
gttttggaaatt tgtcaaatgt acaacaggga aaatatcttt gtatctttaa ggtatggatg      990
gagaagtatt caactgggtt ttccagacct cagttggatg aaccatctcc actgtatgag      1050
gcaaaagtatt ccatgggaagc tgttcagaaa aatcaaggaa gaaaaagca agttgttcaa      1110
ttttaatttt cttcttttctc agacctcagt cggatgaaca tattccagta tttgaagcca      1170

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gaatttttctt	tggaatttgt	tgagaaaaac	caaggaagat	aaaacaagtt	gcatttttaa	1230
gcacgtttct	ctgctaagac	aagatgctca	gttgacacat	ttgaaaagtg	tttgaataat	1290
tcttgtgcga	atgatcaaga	taattctata	attaacatct	taagggaatt	tttctaaaaa	1350
ccttttcatt	gtttctatat	attttgcccc	tgctataaaa	ttccttccat	gaagaaaact	1410
gctgttttca	gcaaaagtca	cactactctt	gataaaagct	gttgccagcc	tttgctaagc	1470
aaaaaaaaaa	aaaaaaaa					1487

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gcaccgcgcc	c atg gca gag cca gac ccc tct cac cct ctg gag acc cag	170
	Met Ala Glu Pro Asp Pro Ser His Pro Leu Glu Thr Gln	
	1 5 10	
gca ggg aag gtg cag gag gct cag gac tca gat tca gac tct gag gga		218
Ala Gly Lys Val Gln Glu Ala Gln Asp Ser Asp Ser Asp Ser Glu Gly		
	15 20 25	
gga gcc gct ggt gga gaa gca gac atg gac ttc ctg cgg aac tta ttc		266
Gly Ala Ala Gly Gly Glu Ala Asp Met Asp Leu Arg Asn Leu Phe		
	30 35 40 45	
tcc cag acg ctc agc ctg ggc agc cag aag gag cgt ctg ctg gag gag		314
Ser Glu Thr Leu Ser Leu Gly Ser Gln Lys Glu Arg Leu Leu Asp Glu		
	50 55 60	
ctg acc ttg gaa ggg gtg gcc cgg tac atg cag agc gaa cgc tgt cgc		362
Leu Thr Leu Glu Gly Val Ala Arg Tyr Met Gln Ser Glu Arg Cys Arg		
	65 70 75	
aga gtc atc tgt ttg gtg gga gct gga atc tcc aca tcc gca ggc atc		410
Arg Val Ile Cys Leu Val Gly Ala Gly Ile Ser Thr Ser Ala Gly Ile		
	80 85 90	
ccc gac ttt cgc tct cca tcc acc ggc ctc tat gac aac cta gag aag		458
Pro Asp Phe Arg Ser Pro Ser Thr Gly Leu Tyr Asp Asn Leu Glu Lys		
	95 100 105	
tac cat ctt ccc tac cca gag gcc atc ttt gag atc agc tat ttc aag		506
Tyr His Leu Pro Tyr Pro Glu Ala Ile Phe Glu Ile Ser Tyr Phe Lys		
	110 115 120 125	
aaa cat ccg gaa ccc ttc gcc ctc gcc aag gaa ctc tat cct ggg		554
Lys His Pro Glu Pro Phe Phe Ala Leu Ala Lys Glu Leu Tyr Pro Gly		
	130 135 140	
cag ttc aag cca acc atc tgt cac tac ttc atg cgc ctg ctg aag gac		602
Gln Phe Lys Pro Thr Ile Cys His Tyr Phe Met Arg Leu Leu Lys Asp		
	145 150 155	
aag ggg cta ctc ctg cgc tgc tac acg cag aac ata gat acc ctg gag		650
Lys Gly Leu Leu Leu Arg Cys Tyr Thr Gln Asn Ile Asp Thr Leu Glu		
	160 165 170	
cga ata gcc ggg ctg gaa cag gag gac ttg gtg gag gcg cac ggc acc		698
Arg Ile Ala Gly Leu Glu Gln Glu Asp Leu Val Glu Ala His Gly Thr		
	175 180 185	
ttc tac aca tca cac tgc gtc agc gcc agc tgc cgg cac gaa tac ccg		746
Phe Tyr Thr Ser His Cys Val Ser Ala Ser Cys Arg His Glu Tyr Pro		
	190 195 200 205	

cta agc tgg atg aaa gag aag atc ttc tct gag gtg acg ccc aag tgt	794
Leu Ser Trp Met Lys Glu Lys Ile Phe Ser Glu Val Thr Pro Lys Cys	
210 215 220	
gaa gac tgt cag agc ctg gtg aag cct gat atc gtc ttt ttt ggt gag	842
Glu Asp Cys Gln Ser Leu Val Lys Pro Asp Ile Val Phe Phe Gly Glu	
225 230 235	
agc ctc cca gcg cgt ttc ttc tcc tgt atg cag tca gac ttc ctg aag	890
Ser Leu Pro Ala Arg Phe Phe Ser Cys Met Gln Ser Asp Phe Leu Lys	
240 245 250	
gtg gac ctc ctc ctg gtc atg ggt acc tcc ttg cag gtg cag ccc ttt	938
Val Asp Leu Leu Val Met Gly Thr Ser Leu Gln Val Gln Pro Phe	
255 260 265	
gcc tcc ctc atc agc aag gca ccc ctc tcc acc cct cgc ctg ctc atc	986
Ala Ser Leu Ile Ser Lys Ala Pro Leu Ser Thr Pro Arg Leu Leu Ile	
270 275 280	
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Asn Lys Glu Lys Ala Gly Gln Ser Asp Pro Phe Leu Gly Met Ile Met	
290 295 300	
ggc ctc gga gga ggc atg gac ttt gac tcc aag aag gcc tac agg gac	1082
Gly Leu Gly Gly Met Asp Phe Asp Ser Lys Lys Ala Tyr Arg Asp	
305 310 315	
gtg gcc tgg ctg ggt gaa tgc gac cag ggc tgc ctg gcc ctt gct gag	1130
Val Ala Trp Leu Gly Glu Cys Asp Gln Gly Cys Leu Ala Leu Ala Glu	
320 325 330	
ctc ctt gga tgg aag aag gag ctg gag gac ctt gtc cgg agg gag cac	1178
Leu Leu Gly Trp Lys Lys Glu Leu Glu Asp Leu Val Arg Arg Glu His	
335 340 345	
gcc agc ata gat gcc cag tgc ggg gcg ggg gtc ccc aac ccc agc act	1226
Ala Ser Ile Asp Ala Gln Ser Gly Ala Gly Val Pro Asn Pro Ser Thr	
350 355 360	
tca gct tcc ccc aag aag tcc ccg cca cct gcc aag gac gag gcc agg	1274
Ser Ala Ser Pro Lys Lys Ser Pro Pro Pro Ala Lys Asp Glu Ala Arg	
370 375 380	
aca aca gag agg gag aaa ccc cag tgacagctgc atctcccagg cgggatgccg	1328
Thr Thr Glu Arg Glu Lys Pro Gln	
385	
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ggtatctaggt	caacaggg	atg agc ctg aac ctc cct	gag gcc agc tta ctt			291
	Met Ser Leu Asn Leu Pro	Glu Ala Ser Leu Leu				
	1	5	10			
agc aga gca tcc tgg cca gaa caa gcc aag gag cca aga cga gag gga	339					
Ser Arg Ala Ser Trp Pro Glu Gln Ala Lys Glu Pro Arg Arg Glu Gly						
	15	20	25			
cac acg gac aaa caa cag aca gaa gac gta ctg gcc gct gga ctc cgc	387					
His Thr Asp Lys Gln Gln Thr Glu Asp Val Leu Ala Ala Gly Leu Arg						
	30	35	40			
tgc ctc ccc cat ctc ccc gcc atc tgc gcc cgg agg atg agc cca gcc	435					
Cys Leu Pro His Leu Pro Ala Ile Cys Ala Arg Arg Met Ser Pro Ala						
	45	50	55			
ttc agg gcc atg gat gtg gag ccc cgc gca aaa ggc gtc ctt ctg gag	483					
Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu Leu Glu						
	60	65	70			
ccc ttt gtc cac cag gtc ggg ggg cac tca tgc gtg ctc cgc ttc aat	531					
Pro Phe Val His Gln Val Gly Gly His Ser Cys Val Leu Arg Phe Asn						
	80	85	90			
gag aca acc ctg tgc aag ccc ctg gtc cca agg gaa cat cag ttc tac	579					
Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu His Gln Phe Tyr						
	95	100	105			
gag acc ctc cct gct gag atg cgc aaa ttc act ccc cag tac aaa ggt	627					
Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro Gln Tyr Lys Gly						
	110	115	120			
gtg gta tct gtg cgc ttt gaa gaa gat gaa gac agg aac ttg tgt cta	675					
Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg Asn Leu Cys Leu						
	125	130	135			
ata gca tat cca ttg aaa ggg gac cat gga att gtg gac att gta gat	723					
Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val Asp Ile Val Asp						
	140	145	150			
aat tca gac tgt gaa cca aaa agt aag ctc cta agg tgg aca aca aac	771					
Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg Trp Thr Thr Asn						
	160	165	170			
aaa aaa cat cat gtc tta gaa aca gaa aag acc cct aag gac tgg gtg	819					
Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro Lys Asp Trp Val						
	175	180	185			
cgt cag cac cgt aaa gag gag aaa atg aag agc cat aag tta gaa gaa	867					
Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His Lys Leu Glu Glu						
	190	195	200			
gaa ttt gag tgg cta aag aaa tct gaa gtc ttg tac tac act gta gag	915					
Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr Thr Val Glu						
	205	210	215			
aag aag ggg aat ata agt tcc cag ctt aaa cac tat aac cct tgg agc	963					
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His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn Leu Thr Ser Arg						
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Ala	Ala	Ala	Val	Val	Leu	Gly	Lys	Gln	Val	Leu	Val	Val	Gly	Gly	Val	
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Asp	Glu	Val	Gln	Ser	Pro	Val	Ala	Ala	Val	Glu	Ala	Phe	Leu	Met	Asp	
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Glu	Gly	Arg	Trp	Glu	Arg	Arg	Ala	Thr	Leu	Pro	Gln	Ala	Ala	Met	Gly	
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Val	Ala	Thr	Val	Glu	Arg	Asp	Gly	Met	Val	Tyr	Ala	Leu	Gly	Gly	Met	
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Ala Thr Ile Val Met Leu Leu Cys Phe Ile Phe Thr Leu Cys Ala Ala			
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ttggccattg ggaagtttgg tgctccctcag agccatccgg tcaagcagat ggtctgttct 1837
atctcacaga aaagtctttt cttccatgag ttctgtctga actgaacatg taaaaagtat 1897
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Ser Thr Val Leu Ser Ser Val Pro Leu Gln Met Leu Phe Tyr Leu Ser
15 20 25
gga acg tac tac gcc ctg tat ttc ctg gcc acg ctg ctg atg atc acg 148
Gly Thr Tyr Tyr Ala Leu Tyr Phe Leu Ala Thr Leu Leu Met Ile Thr
30 35 40

tat aaa agt cag gtg ttc agc tat cct cac cgc tac ctg gtc ctc gat	196
Tyr Lys Ser Gln Val Phe Ser Tyr Pro His Arg Tyr Leu Val Leu Asp	
45 50 55	
ctt gct ctg ctg ttt ctg atg ggg att cta gaa gca gtt cgg tta tac	244
Leu Ala Leu Leu Phe Leu Met Gly Ile Leu Glu Ala Val Arg Leu Tyr	
60 65 70	
ctg ggc acc agg ggc aac ctg aca gag gct gag agg ccg ctg gcc gcc	292
Leu Gly Thr Arg Gly Asn Leu Thr Glu Ala Glu Arg Pro Leu Ala Ala	
75 80 85 90	
agc ctg gcc ctc acg gct ggc acc gcc ctc ctc tct gcc cac ttc ctg	340
Ser Leu Ala Leu Thr Ala Gly Thr Ala Leu Leu Ser Ala His Phe Leu	
95 100 105	
ctt tgg cag gcc cta gtg ttg tgg gcg gac tgg gcc ctc agc gcc acg	388
Leu Trp Gln Ala Leu Val Leu Trp Ala Asp Trp Ala Leu Ser Ala Thr	
110 115 120	
ctc ctg gcc ctt cac ggc ctg gag gcc gtc ctg cag gtg gtt gcc atc	436
Leu Leu Ala Leu His Gly Leu Glu Ala Val Leu Gln Val Val Ala Ile	
125 130 135	
gcg gcc ttc acc agg tagctacgga caccgggat accccacat ggggccctcc	491
Ala Ala Phe Thr Arg	
140	
tctctgggacct gaccagctccc ccagctgtca cctcccatt cctggacagg aaggggcaact	551
tctctagtga ctggcccatag atgggttttgg atggttccat ctgttctggc agggagtggga	611
gcaggagcca gggcagaaca aactgctgga ggccctgggtg ttgggaacag ctgcggggag	671
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gaggggaggac agagcccttc agaacagagg cctcatctca ctgcattcccc catcaccccc	851
tagttcccca atgggtcctaa tttgtgttct gagatcccag tttactctgt ggccaggccc	911
caactgtggt tccaaagtcgg gctggagacg caggatgggg taggccttgt gctctgagca	971
accccgctc tgcctcacag gcaggcaggg ccggtgcaag agtggactct gggttcctaa	1031
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ttctcccttc aggggcttcg gaggagaggt cagggtctaa gccggggatg atactgcagg	1151
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ctattgtgtg ttttctatgt ttggaataat tacacccaaa tatctagata ttttctcttc	1391
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<222> 232..450	
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ccaaaactta caggcttaaa acaacaaaca tgtatcattt cttatgattc tgtgggttg	180
ctgggtgtgtt ctctagctg aggcaggatg gctataggata gctacatcca c atg tct	237
Met Ser	
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ggg gtc cca gct gag atg act ggg gct gtt gag gcc ttt ctc cct gtc	285
Gly Val Pro Ala Glu Met Thr Gly Ala Val Glu Ala Phe Leu Pro Val	
5 10 15	
gtg tca tcc tcc aga agg ctg ccc aga ttt gtc cat atg gta gca gga	333

Val Ser Ser Ser Arg Arg Leu Pro Arg Phe Val His Met Val Ala Gly
20 25 30
gtt tcc tgc aag caa gag agg gca aga tcc aac aca gaa gca ctt ttc 381
Val Ser Ser Lys Gln Glu Arg Ala Arg Ser Asn Thr Glu Ala Leu Phe
35 40 45 50
aag ctc tgt ttc cat cac att tgc caa tgt ctc act gat gaa cac aag 429
Lys Leu Cys Phe His His Ile Cys Gln Cys Leu Thr Asp Glu His Lys
55 60 65
ttc cat ggc caa gtc cag ttt taagaaatgg agaaataggg cttggctcag 480
Phe His Gly Gln Val Gln Phe
70
tggctcatgt ctgtaatccc agcactttgg gaggccaaagg catgcggatc atttgaggtc 540
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aaaaa 605

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<211> 1724
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 758..1183

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ccagcccccc accatggttaa gtccctcaag ggtgggatct ggaagaggaa agaggaggga 180
caccagccag gtggagggtgt cctaaaaaat accatcagaa attgggggtga ggggaggggc 240
atggtggact tctgtggggg tggggtgtct ctcagtgcag ctcaggtgcc tccagcatcc 300
cttaccaggg agcaagctcc catctgtagg tgggtgggat gccagggtgg tatccctgga 360
tccaaggata gggcaggacc tggaagacag aaggtggccc agggagaatc acagagtctg 420
cagggacaag gacatagcct cctttgcttg caaattaagg gagcccttcc ccagtccagc 480
ccagtctctc gtctccctgt gtagccttgg gctagtcaact tcccctctct tggccccggt 540
tcccacagat gtcatatttg gaaatccgtc tagatgcgga agttgctctt caggggtctt 600
tcagttgcaa cattctcaag gtctgtgggt tctgccacag agtcctcggc tgagatggga 660
agctatgtct aacaagcgat ggggtggatt gacgcccctc ctgtgccggg gacgggcggg 720
atggctgcag cagaggcagg agaggctgaa tacgtccc atg cca ccc ttt ggt ggg 775
Met Pro Phe Gly Gly
1 5
cat ccc tta tcc caa gag gag gat ggc agc cag agg tgt tgc tgc ctg 823
His Pro Leu Ser Gln Glu Glu Asp Gly Ser Gln Arg Cys Cys Leu
10 15 20
tca agt ctg agg tct gtc gat gat agc aac ggg gag act gtc gtc atc 871
Ser Ser Leu Arg Ser Val Asp Asp Ser Asn Gly Glu Thr Val Val Ile
25 30 35
atg gcg cta ttc cta gca gta tgc tac cac cat aag acg caa agt aag 919
Met Ala Leu Phe Leu Ala Val Ser Tyr His His Lys Thr Gln Ser Lys
40 45 50
agg tgg cca ggg ctg acc cca ccc cac agc tct ctg ctg tgt aga cca 967
Arg Trp Pro Gly Leu Thr Pro His Ser Ser Leu Leu Cys Arg Pro
55 60 65 70
ctt cag ctt tca ttt ctc gtc att cag tca gtg agg atg aga gca tgt 1015
Leu Gln Leu Ser Phe Leu Val Ile Gln Ser Val Arg Met Arg Ala Cys
75 80 85
ggc tgt gac agc ggc cac tgc agg att ctt ggc agg tac agc tta cta 1063
Gly Cys Asp Ser Gly His Cys Arg Ile Leu Gly Arg Tyr Ser Leu Leu
90 95 100

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ggg tgg agt cag gga cat agg gca aga ggc aga ggt ggt gtt agt ctg      1111
Gly Trp Ser Gln Gly His Arg Ala Arg Gly Arg Gly Gly Val Ser Leu
      105      110      115
aga gac aac acc ttc ttt cag gaa gcc agt gag ggc cag gga cag tgg      1159
Arg Asp Asn Thr Phe Phe Gln Glu Ala Ser Glu Gly Gln Gly Gln Trp
      120      125      130
ctc atg cct gta atc cca gca ttt taggaggctg agacaggtag atcacttgag      1213
Leu Met Pro Val Ile Pro Ala Phe
      135      140
gtcagggtgt cgagaccagc ctggccaacg tggtgaaacc tcgtctctac taaaaaatac      1273
aaaaaattaa ctgggcgtgg tggcacacgc ctgtaatccc agctacatat gaggctgagg      1333
caagagaata acttgaaccc agggaggcga ggggtgcagt agctgagatc ctgccgctgc      1393
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ttcttccaag atgagaagca agccaggagg gctcagggtc tgggatgggc agggctttga      1573
tcaaaagaac acaggaagtg atttgtact tgaaagaaag gcaaccctcc cccaaggaag      1633
ccctctgaaa atgcttagtc aacagtcggc ttggcagaca aggtctggga ggggccaccc      1693
gtatcgaga ggacaaaaaa aaaaaaaaaa a      1724

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<210> 183
<211> 1686
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 486..932

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<400> 183
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atgggggttt accatgttgg ccaggctggc cttgaactcc tgacctcagg tgatccgcc      180
gcctcggcct cccaaagtgc tggggttaca ggcattgagcc accgcaccgc gcccccctcc      240
ttcgtcttag tcaatcctat cccacctctt ctccaccag tccctcacc tgatgggtcc      300
aacacttcct catccaccac ctccctggag gggtagcccg aggtgctccg ctgggggactc      360
tgctcattct gggggtgcag ttgacggctg gtcgtgatct ttcccgtaat ctgtcccctc      420
ttacgggaac tagtctccgt tctgtccatg gcctctctct ggacctgct aggatccaga      480
agagt atg tta tca att ctc aag cct agg aga agt cag gag tgg aga aca      530
      Met Leu Ser Ile      Leu Lys Pro Arg Arg Ser Gln Glu Trp Arg Thr
      1      5      10      15
gct ctg aga aga tac tgt tgt cca act gat ctc cag gca cca cgg agt      578
Ala Leu Arg Arg Tyr Cys Cys Pro Thr Asp Leu Gln Ala Pro Arg Ser
      20      25      30
ccg gtc cct cca atc agg aag gtc gga atc tct gat gtc atc gtt cat      626
Pro Val Pro Pro Ile Arg Lys Val Gly Ile Ser Asp Val Ile Val His
      35      40      45
gcc aac ctg gca acc agt ttg aaa aaa aac aca tgt aac tgc cag gct      674
Ala Asn Leu Ala Thr Ser Leu Lys Lys Asn Thr Cys Asn Cys Gln Ala
      50      55      60
gat ctc ttg tcc tgg aga tcc tgg gtg aat ggt atc tcc tgc cac tgt      722
Asp Leu Leu Ser Trp Arg Ser Trp Val Asn Gly Ile Ser Cys His Cys
      65      70      75
ccc aac ctc aga cca ttg tcc aaa agc atc ttc agg gac tcc aca tcc      770
Pro Asn Leu Arg Pro Leu Ser Lys Ser Ile Phe Arg Asp Ser Thr Ser
      80      85      90      95
ctc tgt tcc ctg tcc cag cag agg ctg tgt cct ctc cac tca aag cct      818
Leu Cys Ser Leu Ser Gln Gln Arg Leu Cys Pro Leu His Ser Lys Pro
      100      105      110

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gaa gca tgt tgg ggt ctc ttt gtc tct gta cat gcc cat ttc aga gtc      866
Glu Ala Cys Trp Gly Leu Phe Val Ser Val His Ala His Phe Arg Val
      115      120      125
cag gct ggt ggg aga ggg aac aga gtg gga aag aaa act agg gta agc      914
Gln Ala Gly Gly Arg Gly Asn Arg Val Gly Lys Lys Thr Arg Val Ser
      130      135      140
aga aac gat gaa acc tta taagagtggag attatcatgt gcaagagtga      962
Arg Asn Asp Glu Thr Leu
      145
gattatcatg tacaagagat cccaggaaat actgactttg atgaaaaagt cacatcagag      1022
cactcagttt tggcagagct ttttctgccg aatgtttact cacattcact gtccgagatt      1082
ctatactggg ggtacacacg tctctgtccc taaggcaatt ttgagtcctaa gagacatttt      1142
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agactcatgt gacaggaaga tcacttgagc ccgggggtta gaggctgcag tgagctatga      1622
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<211> 463
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> 80..304

<400> 184
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ccattagatc atttcacaa atg tat ctg cca cca aac agg tca gag ctt tgc      112
      1      5      10
aac ttt gct ttg tct ctt aac ctc tat ggc aaa ggg ttt ttt agc ctg      160
Asn Phe Ala Leu Ser Leu Asn Leu Tyr Gly Lys Phe Ser Leu
      15      20      25
gtg gaa aag cat aac agc agg gat tta gaa gat aga gct agt tct ggc      208
Val Glu Lys His Asn Ser Arg Asp Leu Glu Asp Arg Ala Ser Ser Gly
      30      35      40
cca tca ctt tca tct cca tca cac ccg gac tgg ggt tat ata gtt ctg      256
Pro Ser Leu Ser Ser Pro Ser His Pro Asp Trp Gly Tyr Ile Val Leu
      45      50      55
att tta gtg gca acc ctg ggg gaa ctt gat acc cag gta ggt ggt cac      304
Ile Leu Val Ala Thr Leu Gly Glu Leu Asp Thr Gln Val Gly Gly His
      60      65      70      75
tgatcagtag ttgggagagg taggaattgg tgagtacagg taattagagg aaagtcttgt      364
gtccgtgttc ccccttttta attttatccc ttgctagaat taagatacta tatgcctcac      424
tatacaatta cagtctaaat ccaaaagaaa aaaaaaaaaa      463

<210> 185
<211> 773
<212> DNA
<213> Homo sapiens

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 <222> 188..691

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 aaaggactct ggattgggtg gcagtctgct ttttttttcc caagggtgac actttactgt 180
 agaagaa atg agg tta aca gaa aag agt gag gga gaa caa caa ctc aag 229
 Met Arg Leu Thr Glu Lys Ser Glu Gly Glu Gln Gln Leu Lys
 1 5 10
 ccc aac aac tct aat gca ccc aat gaa gat caa gaa gaa gaa atc caa 277
 Pro Asn Asn Ser Asn Ala Pro Asn Glu Asp Gln Glu Glu Glu Ile Gln
 15 20 25 30
 cag tca gaa cag cat act cca gca agg cag cga aca caa aga gca gac 325
 Gln Ser Glu Gln His Thr Pro Ala Arg Gln Arg Thr Gln Arg Ala Asp
 35 40 45
 aca cag cca tcc aga tgt cga ttg cct tca cgt agg aca cct aca aca 373
 Thr Gln Pro Ser Arg Cys Arg Leu Pro Ser Arg Arg Thr Pro Thr Thr
 50 55 60
 tcc agc gac aga acg atc aac ctt ctt gaa gtc ctt ccg tgg cct act 421
 Ser Ser Asp Arg Thr Ile Asn Leu Leu Glu Val Leu Pro Trp Pro Thr
 65 70 75
 gag tgg att ttc aac ccc tat cga ttg cct gct ctt ttt gag ctt tat 469
 Glu Trp Ile Phe Asn Pro Tyr Arg Leu Pro Ala Leu Phe Glu Leu Tyr
 80 85 90
 cct gaa ttt ctt ctg gtg ttt aaa gaa gcc ttc cat gac ata tcc cat 517
 Pro Glu Phe Leu Leu Val Phe Lys Glu Ala Phe His Asp Ile Ser His
 95 100 105 110
 tgt ctg aaa gcc cag atg gaa aag atc gga ctg ccc atc ata ctc cac 565
 Cys Leu Lys Ala Gln Met Glu Lys Ile Gly Leu Pro Ile Ile Leu His
 115 120 125
 ctc ttc gca ctc tcc acc ctc tac ttc tac aag ttt ttc ctt cct aca 613
 Leu Phe Ala Leu Ser Thr Leu Tyr Phe Tyr Lys Phe Phe Leu Pro Thr
 130 135 140
 att ctt tcc ctt tct ttc ttt att ctt ctt gta ctt ctg ctt ctg ctt 661
 Ile Leu Ser Leu Ser Phe Phe Ile Leu Leu Val Leu Leu Leu Leu Leu
 145 150 155
 ttt att att gtc ttc att ctg atc ttc ttc tgattctttt gtttcaataa 711
 Phe Ile Ile Val Phe Ile Leu Ile Phe Phe
 160 165
 acagcaatga gcatgaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 771
 aa 773

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 <211> 753
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 94..573

<400> 186
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 catctccatc cccaatccta aagaaggaaa tcg atg cca cgg tcc tca agg agc 114
 Met Pro Arg Ser Ser Arg Ser
 1 5

cct ggg gac cca ggc gcc cta ctc gaa gat gtg gcc cac aat ccc aga	162
Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Val Ala Asn Pro Arg	
10 15 20	
ccc cgg agg att gcc cag cga ggc cgg aac acc agc agg atg gca gag	210
Pro Arg Arg Ile Ala Gln Arg Gly Arg Asn Thr Ser Arg Met Ala Glu	
25 30 35	
gac acc tcc cca aac atg aat gac aac atc ctg ttg cct gtc cgc aac	258
Asp Thr Ser Pro Asn Met Asn Asp Asn Ile Leu Leu Pro Val Arg Asn	
40 45 50 55	
aat gac caa gcc cta ggc ctg act cag tgc atg ctg gga tgt gtg tcc	306
Asn Asp Gln Ala Leu Gly Leu Thr Gln Cys Met Leu Gly Cys Val Ser	
60 65 70	
tgg ttc acc tgt ttt gcc tgc tcc ctg aga act cag gcc cag cag gtt	354
Trp Phe Thr Cys Phe Ala Cys Ser Leu Arg Thr Gln Ala Gln Gln Val	
75 80 85	
ctg ttt aac acg tgc aga gac aga gtt tca cca tgt tgc cca ggc tgg	402
Leu Phe Asn Thr Cys Arg Asp Arg Val Ser Pro Cys Cys Pro Gly Trp	
90 95 100	
tct caa act cca gtg atc ctc cca cct cag cct tcc gaa gtg ctg gga	450
Ser Gln Thr Pro Val Ile Leu Pro Gln Pro Ser Glu Val Leu Gly	
105 110 115	
tta cag atg caa gct gct gtg cca gaa gct cat gga gaa gac agg cat	498
Leu Gln Met Gln Ala Ala Val Pro Glu Ala His Gly Glu Asp Arg His	
120 125 130 135	
tct gct cct ctg tgc ttt cgg tgt gtc cca ggg ccc tgc cca gtc cca	546
Ser Ala Pro Leu Cys Phe Arg Cys Val Pro Gly Pro Cys Pro Val Pro	
140 145 150	
ggt gga ggt atc cct ggg ccc tgg cac tgattatagg acactgggca	593
Gly Gly Gly Ile Pro Gly Pro Trp His	
155 160	
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attatgaaat gaaatgatga ccatgaaaat attgtagaag ccaagaaatg cttcagaagt	713
tataaagctc tccccaacc gtgttaaaaa aaaaaaaaaa	753
<210> 187	
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attgagttat tacatatcaa ttgaacaagg tagttttaa atgaaagaaa atcttgcaac	180
atg aat aaa gag ata gac tct ttg aat ctg gca tac agc ttt ccc ttc	228
Met Asn Lys Glu Ile Asp Ser Leu Asn Leu Ala Tyr Ser Phe Pro Phe	
1 5 10 15	
ctt ctt cct gct ttc ctg gac aca ccg tgg aca gac cca ttt ccc tct	276
Leu Leu Pro Ala Phe Leu Asp Thr Pro Trp Thr Asp Pro Phe Pro Ser	
20 25 30	
gga ttc atg gta agg tcc cga gtg ctt ctg ata cag ctg ctg agc aga	324
Gly Phe Met Val Arg Ser Arg Val Leu Leu Ile Gln Leu Leu Ser Arg	
35 40 45	
ccc cgc tca tct cag gag tcc cga gga cac tcg ctt ccc tgc agc ccg	372
Pro Arg Ser Ser Gln Glu Ser Arg Gly His Ser Leu Pro Cys Ser Pro	

50	55	60	
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Ser Ala Leu His Lys Pro Gly Gly Ile Cys Pro Ala Ala Leu Gly Arg			
65 70 75 80			
agc cac ctc ctt gtc tgg gaa cag cca agc ctc cgt gac agc	462		
Ser His Leu Leu Val Trp Glu Gln Pro Ser Leu Arg Asp Ser			
85 90			
tgaggattct tgtggattgt tctttctgta actggacagc acatccggaa ttccttgcca	522		
tagctctgtg ccttgctggg gtctgaggtt cacaggtcag atgtgctgtg ctggctcttc	582		
ccaattgcgg cgtgaattcc ttcattctca ccagtagctt cttgctctcc ccaagggagg	642		
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 <222> 871
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Ser Leu Ile Arg His Leu Arg Thr Phe Ser Ala Ala Ala Leu Ala	
20 25 30	
cca aga tac cca acc aga ctt ccc agt tca ctg ctt cta tgg cac ctc	146
Pro Arg Tyr Pro Thr Arg Leu Pro Ser Ser Leu Leu Leu Trp His Leu	
35 40 45	
tgc cag tgc ctc cat ctc ctc tat gca gtt tct acc tca tgc aac agc	194
Cys Gln Cys Leu His Leu Leu Tyr Ala Val Ser Thr Ser Cys Asn Ser	
50 55 60	
cat ggg aag aga tcg gct gcc tgg gca atg acc aga aca gaa gac aca	242
His Gly Lys Arg Ser Ala Ala Trp Ala Met Thr Arg Thr Glu Asp Thr	
65 70 75	
gat gcg cta aca gat tcc ttc gat gac agt ttc atc agt tct gca gat	290
Asp Ala Leu Thr Asp Ser Phe Asp Asp Ser Phe Ile Ser Ser Ala Asp	
80 85 90 95	
taaagacttt caccagaaaa aaaaattacc tgattttgcc ctgaggcagc cagggaggggc	350
tttgcctctg acaatccccc tgacttattt aacaggtagc tcaaaaccca acaaaaactg	410
gaggagcgtg cttccactgca gggatggttt caattcggta actggagtat tgtactctcc	470
ttgcaccctg gctcatcccc acaaaagacc ttccaagaaa aacacttaat tacctccttg	530
cacaagccct gtaagcccta aggtgaaaag aaactcagca gacaaggctc acagagaagg	590
agaaggcaca attcagtagg gacctacgct cagcaccagg ataaagaaac tgtccattcc	650
tgccactctc taggaagcta aaagaattaa ggggaggccg ggcacggtgg ctcacgcctg	710
taatcccagc actttgggag gccgaggcgg gtggatcatg aggtcaggag atcgagacca	770
tcttggtctaa catggtgaaa ccccatctct actaaaaata caaaaaatta gccggcgctg	830
gtggcgggcg cctctagctc ccagctactc gggaggctga nggcaggaga atggtgtgaa	890
cctgggaggc ggagcttgca gtgagccgag attgcgccct gctccactcc agcctgagcg	950
acagagcgag actccgtctc aaaaaaaaaa argaaaaaaaaa aaaaaaaaaa	998

<210> 189
 <211> 605
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 115..411

<400> 189
 aagaaagggg tgaggcctaa gggacaatca ggaatgtttt cagagagaag tgtggatgct 60
 ggacaggaag aaccacagat accagatacgg ggtactgttg taactctggt cccc atg 117
 Met
 1
 aaa aaa aag gaa gaa aca aca ett tca gag atg gag cct gtt gag cca 165
 Lys Lys Lys Glu Glu Thr Thr Leu Ser Glu Met Glu Pro Val Glu Pro
 5 10 15
 cag tac caa cta gtc aat gct gaa tcg act tct ccc ttt cta cat tgc 213
 Gln Tyr Gln Leu Val Asn Ala Glu Ser Thr Ser Pro Phe Leu His Cys
 20 25 30
 ctg aga gaa gtc att ggg gaa tac tct gta cac gaa ttt tca ctg ttg 261
 Leu Arg Glu Val Ile Gly Glu Tyr Ser Val His Glu Phe Ser Leu Leu
 35 40 45
 ggg aaa aca gag agt caa ggg att gga ttg tgg att gca ttg gtg gtt 309
 Gly Lys Thr Glu Ser Gln Gly Ile Gly Leu Trp Ile Ala Leu Val Val
 50 55 60 65
 ttc ctc agt ttc ctc atc ttc tcc aca agt ttc tac ata tcg aat gca 357
 Phe Leu Ser Phe Leu Ile Phe Ser Thr Ser Phe Tyr Ile Ser Asn Ala
 70 75 80
 gag cag ccc ttc ttc aaa gaa cct cct acg gaa gct gct aag gaa ctc 405
 Glu Gln Pro Phe Phe Lys Glu Pro Pro Thr Glu Ala Ala Lys Glu Leu
 85 90 95
 agt ctg tagctctgcg tggagccatg tgtaaacact gaactgagac ctgccacctc 461
 Ser Leu
 ctactaccta agggcccatt ttcatctgat atcatccccc agaaacaaac tcatgatgac 521
 ttccatgttt ttttttagatt agatacatgg agaattttcc tttcccttag aattaaaatc 581
 ctgcattcta aaaaaaaaaa aaaa 605

<210> 190
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 3..368

<400> 190
 ag atc cga gcg acc atg gtg gcc cgg gtg tgg tcg ctg atg agg ttc 47
 Ile Arg Ala Thr Met Val Ala Arg Val Trp Ser Leu Met Arg Phe
 1 5 10 15
 ctc atc aag gga agt gtg gct ggg ggc gcc gtc tac ctg gtg tac gac 95
 Leu Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr Asp
 20 25 30
 cag gag ctg ctg ggg ccc agc gac aag agc cag gca gcc cta cag aag 143
 Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln Lys
 35 40 45

gct ggg gag gtg gtc ccc ccc gcc atg tac cag ttc agc cag tac gtg	191
Ala Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr Val	
50 55 60	
tgt cag cag aca ggc ctg cag ata ccc cag ctc cca gcc cct cca aag	239
Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro Lys	
65 70 75	
att tac ttt ccc atc cgt gac tcc tgg aat gca ggc atc atg acg gtg	287
Ile Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr Val	
80 85 90 95	
atg tca gct ctg tgc gtg gcc ccc tcc aag gcc cgc gag tac tcc aag	335
Met Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser Lys	
100 105 110	
gag ggc tgg gag tat gtg aag gcg cgc acc aag tagcgcagtcga gcaggggccc	388
Glu Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys	
115 120	
cctgcccccgc ccagaaacggg caggggctgcc actgacctga agactccgga ctggggacccc	448
actccgagggc cagctcccgc ccttgccggcg ccaataaagg acttcagaag tgaaaaaaa	508
ataaaaaaaa aaaaaaaa	526

<210> 191
 <211> 910
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 174..527

<400> 191	
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tcccttgctt gtgggcatat gtgggtcata ttccctcc atcaccctct gcacgccacc	120
cccatcaccg ccacagacc ccagcccttc agttgccctg caccctcttg gtg atg	176
Met	
1	
cag ccg tcc ttg tta agg tca tac agg ttg aag gcc caa tta agc ctg	224
Gln Pro Ser Leu Leu Arg Ser Tyr Arg Leu Lys Ala Gln Leu Ser Leu	
5 10 15	
tca tct aca gtt ccc cga aga atc acg gac aaa cca gcc aca aag tcc	272
Ser Ser Thr Val Pro Arg Arg Ile Thr Asp Lys Pro Ala Thr Lys Ser	
20 25 30	
tgg gaa gga ggc agg agg gag ctg tgt cct cgg gta ctc ttc acc caa	320
Trp Glu Gly Gly Arg Arg Glu Leu Cys Pro Arg Val Leu Phe Thr Gln	
35 40 45	
ctc ctt ctc tgg gtt tgg cct gga gat cct gcc cct gaa ctc cag gaa	368
Leu Leu Leu Trp Val Trp Pro Gly Asp Pro Gly Pro Glu Leu Gln Glu	
50 55 60 65	
aca ggc ttc cct gcc cca cct cgc cca gct cac ctc aaa act gac cga	416
Thr Gly Phe Pro Gly Pro Pro Arg Pro Ala His Leu Lys Thr Asp Arg	
70 75 80	
gcc atc atg gtt ggt gtc aaa ggc att gaa gag aaa agt gcc ata ggt	464
Ala Ile Met Val Gly Val Lys Gly Ile Glu Glu Lys Ser Gly Ile Gly	
85 90 95	
gct gga gtc tgc agg gtg agt gtg gag aag ttg gct tcc aca cag gag	512
Ala Gly Val Cys Arg Val Ser Val Glu Lys Leu Ala Ser Thr Gln Glu	
100 105 110	
agg act tcc tcc ctc taaggagctc ccataacccc ccatacactt ggcattecca	567
Arg Thr Ser Ser Leu	
115	

gctectccag	aatccctccc	tccctcagcc	tagagaagga	caactgcttc	cccttggggc	627
ttgtcccttc	acctccttga	ggaaagaact	gggagtaa	ctgcttgaag	ttctcctcat	687
tgacaatttc	gctgggacat	tcttggaag	agagggcacc	aggctgagg	cagagacaaa	747
atcccccttc	gttcaccgcc	cccaccttc	atggcccaag	actcccagg	agggggataa	807
tcttcaagcc	tccagaggac	tcaccactg	gctcatgtga	tgggagggaa	gactttcttc	867
ccagtgcaca	aataaaaaac	atggaacgaa	aaaaaaaaaa	aaa		910

<210> 192
 <211> 668
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 57..203

<400> 192	tctctgtcgac	gtgttctcttc	ggtggcggag	cggcggatta	gccttcgcgg	ggcaaa	atg	59									
							Met										
							1										
	gag	ctc	gag	gcc	atg	agc	aga	tat	acc	agc	cca	gtg	aac	cca	cct	gtc	107
	Glu	Leu	Glu	Ala	Met	Ser	Arg	Tyr	Thr	Ser	Pro	Val	Asn	Pro	Pro	Val	
				5													
	ttc	ccc	cat	ctg	acc	gtg	gtg	ctt	ttg	gcc	att	ggc	atg	ttc	ttc	acc	155
	Phe	Pro	His	Leu	Thr	Val	Val	Leu	Leu	Ala	Ile	Gly	Met	Phe	Phe	Thr	
				20													
	gcc	tgg	ttc	ttc	gtg	tat	cct	ttc	act	gag	cag	cca	gag	gac	cag	cat	203
	Ala	Trp	Phe	Phe	Val	Tyr	Pro	Phe	Thr	Glu	Gln	Pro	Glu	Asp	Gln	His	
				35													
	tagt	gat	gtg	gga	agct	cag	ggagaaa	acca	cgct	taggt	ac	atgg	accccg	ccggt	ttttgt		263
	acatt	ggatt	gggg	ctg	aga	gaagatt	gcc	gtggg	ctggg	ctctct	gcac	tcac	cag	tcc		323	
	accc	cttgc	tttg	ccttaa	ctgct	gtgccc	cagtt	acgag	gtc	acctcta	cca	agt	atcac		383		
	tcgt	gata	atc	tata	aagagc	tctct	catctc	attag	tggcc	tcact	cttca	tggg	ctttg		443		
	agtc	ctcttc	ctgct	gctct	gggtt	ggcat	ctacg	tgtga	gcaccca	aagg	gta	aca	acca		503		
	gatg	ggtcca	ctg	aaacctg	ctttt	gtaaaa	ttact	ttttt	ttact	gtgtgc	tgg	aagt	gtc		563		
	ccacct	gctg	ctcata	ataa	atgc	agatgt	atag	caaaaa	aaaaaaaa	aaaa	aaaa	aaaa		623			
	aaaaaaaa		aaaaaaaa		aaaaaaaa		aaaaaaaa		aaaa					668			

<210> 193
 <211> 637
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..334

<400> 193	agttatgaag	ttctaaaagc	aagtcttaat	caggaagtgt	ccttgatcac	caacggctcg	60										
	cccaggc	atg	ctg	gct	ctc	ttc	cac	ttc	cac	ctt	cca	cca	tgg	gat	gac	109	
		Met	Leu	Ala	Leu	Phe	His	Phe	His	Leu	Pro	Pro	Trp	Asp	Asp		
		1															
	gca	gta	aga	agg	cca	tca	gta	gat	gcc	agt	ccc	tca	acc	ttg	aac	ttt	157
	Ala	Val	Arg	Arg	Pro	Ser	Val	Asp	Ala	Ser	Pro	Ser	Thr	Leu	Asn	Phe	
	cca	gac	gca	gaa	ctt	tat	gcc	tcg	att	ttc	etc	tgc	tgc	atg	gcc	cca	205
	Pro	Asp	Ala	Glu	Leu	Tyr	Ala	Ser	Ile	Phe	Leu	Cys	Cys	Met	Ala	Pro	

<222> 94..228

<400> 195

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acttttcagg ggacattcag aggcattcagc cccttctctcc tcaccagctc ccagagttcc      60
catctccatc cccaatccta aagaaggaaa tcg atg cca cgg tcc tca agg agc      114
                               Met Pro Arg Ser Ser Arg Ser
                               1           5
cct ggg gac cca ggc gcc cta ctc gaa gat ggc cca caa tcc cag acc      162
Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Gly Pro Gln Ser Gln Thr
    10           15           20
ccg gag gat tgc cca gcg agg ccg gaa cac cag cag gat ggc aga gga      210
Pro Glu Asp Cys Pro Ala Arg Pro Glu His Gln Gln Asp Gly Arg Gly
    25           30           35
cac ctc ccc aaa cat gaa tgacaacatc ctgttgctgt tccgcaacaa      258
His Leu Pro Lys His Glu
    40           45
tgaccaagcc ctaggcctga ctacgtgcat gctgggatgt gtgtcctggt tcacctgttt      318
tgectgtctc ctgagaactc aggccccagca ggttctgttt aacacgtgca gatgcaagct      378
gctgtgccag aagctcatgg agaagacagg cattctgctc ctctgtgctt tcggtgtgtc      438
ccagggccct gcccagtcctc aggtggaagg tatccctggg ccctggcaact gattatagga      498
cactggggcaa gacactgcac gcgccagtga ctacgtttcc ccactgtgctc gatgggtgtt      558
gctgtgagaa ttatgaaatg aaatgatgac catgaaaaata ttgtagaagc caagaaatgc      618
ttcagaagtt ataaagctct ccccaaaccg tgttatgaaa aaaaaaaaaa aa      670
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<210> 196

<211> 510

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 133..327

<400> 196

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aacctcaagg agccctgttg tgctaccgac tgcagagctc atggacatcc atcaggaagc      60
ctccaatacc caaaccaggg gtatgtgcct aatccatatc catgtggata gctctttact      120
taggaaacct tg atg gct tat ttg gat gac aaa ggt tcc ctt ttg gcg ata      171
                               Met Ala Tyr Leu Asp Asp Lys Gly Ser Leu Leu Ala Ile
                               1           5           10
cat agc cat gcg aga caa cat agc cat gaa aca aac caa gtc cac cag      219
His Ser His Ala Arg Gln His Ser His Glu Thr Asn Gln Val His Gln
    15           20           25
tgg ctt cct agg aac aca ttt gct ttc ctg ata aaa gag gac aga tgc      267
Trp Leu Pro Arg Asn Thr Phe Ala Phe Leu Ile Lys Glu Asp Arg Cys
    30           35           40           45
agt tgc aga agt acc tgt gcc tct ttt tct ttt tct tct ttt tct      315
Ser Cys Arg Ser Thr Cys Ala Ser Phe Ser Phe Ser Ser Ser Phe Ser
    50           55           60
ttt tta atc tct taaatgcaga tataagaact ggtactgaag cagccatctt      367
Phe Leu Ile Ser
    65
gtgaccataa ggaagaagcc aagaacatca gaaccagtgg cctagccatt gcacagtcac      427
ctaaacacac ctctggactt gttattatgt aaaaaaaaaa aaacacctgc tctgtgtatt      487
tgcaatccaa aaaaaaaaaa aaa      510
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<210> 197

<211> 500

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 22..357

<400> 197

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atagaatata cacaaaagga a atg aga aag aaa tgt aaa tgc ttc act ata      51
                        Met Arg Lys Lys Cys Lys Cys Phe Thr Ile
                        1          5          10
aaa aaa aca aat aca tac gaa gaa agt aat gca gga aat gaa gga caa      99
Lys Lys Thr Asn Thr Tyr Glu Glu Ser Asn Ala Gly Asn Glu Gly Gln
                        15          20          25
aaa gaa gct ata agc att tgt att tgc aga aga gat ggt tta ctt cct      147
Lys Glu Ala Ile Ser Ile Cys Ile Cys Arg Arg Asp Gly Leu Leu Pro
                        30          35          40
ctg tgg gta acc agg tta tca gat ttg gtg ttt tcc aaa gaa aag gca      195
Leu Trp Val Thr Arg Leu Ser Asp Leu Val Phe Ser Lys Glu Lys Ala
                        45          50          55
cat ggc atg att cca ctt ctt ggc tcc cat agg gaa aag aca agt      243
His Gly Met Ile Pro Leu Leu Gly Ser His Arg Glu Lys Lys Thr Ser
                        60          65          70
aaa gag atg aag act tct tcc agg aac ctg agg tac ttc att gtc tgc      291
Lys Glu Met Lys Thr Ser Ser Arg Asn Leu Arg Tyr Phe Ile Val Cys
                        75          80          85          90
aga gat gcc tca tcc tac acc cct cag tca ctc ata tct gga tac att      339
Arg Asp Ala Ser Ser Tyr Thr Pro Gln Ser Leu Ile Ser Gly Tyr Ile
                        95          100          105
gga cct tgt caa cat caa taatggacat acctctgata ttggaactct      387
Gly Pro Cys Gln His Gln
                        110
gaatctcact ctgtgaccac aactttgtat ctttctaagt ctttaactct caacctcaca      447
gaactcttca taccctaaaa tatagtattt tcacctggaa aaaaaaaaaa aaa      500
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<210> 198

<211> 667

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 4..333

<400> 198

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aaa atg gtg ttt gga gcc atg gtc ctt ctt gtg gga ctt gaa gaa ctg      48
      Met Val Phe Gly Ala Met Val Leu Leu Val Gly Leu Glu Leu
      1          5          10          15
acc aat atc cgc aac gtg gag aga ctg aag aag gac ttg agg gcc agt      96
Thr Asn Ile Arg Asn Val Glu Arg Leu Lys Lys Asp Leu Arg Ala Ser
      20          25          30
tat tgc ctc atc gac agc ttc ctg ggg gac tgc gag ctc atc ggg gac      144
Tyr Cys Leu Ile Asp Ser Phe Leu Gly Asp Ser Glu Leu Ile Gly Asp
      35          40          45
ctg acc cag tgt gtg gac tgc gtg att cct cca gag ggg tcc ctc ttg      192
Leu Thr Gln Cys Val Asp Cys Val Ile Pro Pro Glu Gly Ser Leu Leu
      50          55          60
cag atc tct agc tac ctc tac tta aat act gct ctt gtg gac ttg cct      240
Gln Ile Ser Ser Tyr Leu Tyr Leu Asn Thr Ala Leu Val Asp Leu Pro
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65	70	75	
ggt gtg gcg gcc tcc cag gca tgt gac tct cag cag gtg act tgg ctt			288
gly Val Ala Ala Ser Gln Ala Cys Asp Ser Gln Val Thr Trp Leu			
80	85	90	95
ctc tac gtt gct aat ggt gcc tac tcg gca tgt aac agg cct gga			333
Leu Tyr Val Ala Asn Gly Ala Tyr Ser Ala Cys Asn Arg Pro Gly			
100	105	110	
tgaacggtag ctgctcggt tacattatta gcttcagttt gcccgcccag gctagatgtt			393
taatcagatt tcacagactt cacagtgtga gttggggatg tgacttcgta tgaagtga			453
ggaactcagg ctcagagagg gtgagacgta ggagcatggc cactgcgcga gctcggggct			513
ggctgtgggt ttctcccat tccctgccca tctgggaagt cgctgccacc ccctacgctt			573
gtctgctgac tcccagtcct cctaaccctc cagaatgtaa acagcagcag atgaacaaaa			633
ataaaaaatac aaaagccga aaaaaaaaaa aaaa			667

<210> 199
 <211> 514
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 1..363

<400> 199	
acg agt tct tcc ggg gcg gag gtc acc atg gca gct gcc ttg gct cgg	48
Thr Ser Ser Ser Gly Ala Glu Val Thr Met Ala Ala Ala Leu Ala Arg	
1 5 10 15	
ctt ggt ctg cgg cct gtc aaa cag gtt cgg gtt cag ttc tgt ccc ttc	96
Leu Gly Leu Arg Pro Val Lys Gln Val Arg Val Gln Phe Cys Pro Phe	
20 25 30	
gag aaa aac gtg gaa tcg acg agg acc ttc ctg cag acg gtg agc agt	144
Glu Lys Asn Val Glu Ser Thr Arg Thr Phe Leu Gln Thr Val Ser Ser	
35 40 45	
gag aag gtc cgc tcc act aat ctc aac tgc tca gtg att gcg gac gtg	192
Glu Lys Val Arg Ser Thr Asn Leu Asn Cys Ser Val Ile Ala Asp Val	
50 55 60	
agg cat gac ggc tcc gag ccc tgc gtg gac gtg ctg ttc gga gac ggg	240
Arg His Asp Gly Ser Glu Pro Cys Val Asp Val Leu Phe Gly Asp Gly	
65 70 75 80	
cat cgc ctg att atg cgc ggc gct cat ctc acc gct ctg gaa atg ctc	288
His Arg Leu Ile Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu	
85 90 95	
acc gcc ttc gcc tcc cac atc cgg gcc agg gac gcg gcg ggc agc ggg	336
Thr Ala Phe Ala Ser His Ile Arg Ala Arg Asp Ala Ala Gly Ser Gly	
100 105 110	
gac aag ccg ggc gct gat act ggt cgc tgacagcgcc aaagagacca	383
Asp Lys Pro Gly Ala Asp Thr Gly Arg	
115 120	
acaagatgat ttgcgtggac taggacactt aacctaaaga gagtttctact taatcattca	443
aatcactatc tgaagggtca cggagcgcaa aataaagttt aaaaccctgc taccacaaaa	503
aaaaaaaaa a	514

<210> 200
 <211> 462
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 41..337

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<400> 200
cttcaccacc aaaactctcc actccaccag cacagccaaa atg ctc gca cgt gct      55
                                     Met Leu Ala Arg Ala
                                     1       5
act ttc cgc gcc gcc tgc gcc cca act ctc gtc gcc cgc cgc ggc ttc      103
Thr Phe Arg Ala Ala Ser Ala Pro Thr Leu Val Ala Arg Arg Gly Phe
                                     10      15      20
cag tgc acc cgc gcg caa atg gcc agc cca tac cac tac ccc gag ggt      151
Gln Ser Thr Arg Ala Gln Met Ala Ser Pro Tyr His Tyr Pro Glu Gly
                                     25      30      35
cct cgc agc aac ttg cca ttc gac ccg ctg aag aag ggc ttt gct ttc      199
Pro Arg Ser Asn Leu Pro Phe Asp Pro Leu Lys Lys Gly Phe Ala Phe
                                     40      45      50
aag tac tgg ggc ttt atg ggc acc gga ttc gcc ett ccc ttc ctc ctt      247
Lys Tyr Trp Gly Phe Met Gly Thr Gly Phe Ala Leu Pro Phe Leu Leu
                                     55      60      65
gct gtc tgg caa aca gaa caa gcc gta aat gcg ctg aga cac ggc gtg      295
Ala Val Trp Gln Thr Glu Gln Ala Val Asn Ala Leu Arg His Gly Val
                                     70      75      80      85
gac atg cgt atc ggg atc ccg ggg aac acg gca ttt gta gat      337
Asp Met Arg Ile Gly Ile Pro Gly Asn Thr Ala Phe Val Asp
                                     90      95
taggtggagg gccgcatac ggctatacta gacatcacag catcaatttc attgtctgtc      397
ccccaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
aaaaaa      457
aaaaa      462

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<210> 201
<211> 551
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 1..549

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<400> 201
aga gag gga gcc cga gcc agg cca tct cca acc atg tcc gac gag gcc      48
Arg Glu Gly Ala Arg Ala Arg Pro Ser Pro Thr Met Ser Asp Glu Ala
1       5       10      15
tcg gcc atc act tcc tac gag aag ttt cta acc ccc gag gag ccc ttc      96
Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe
20      25      30
cca ctc ctg gga cct cct cgc ggg gtg ggc acc tgc ccg agc gag gag      144
Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu
35      40      45
ccg ggc tgc ctg gac atc agc gac ttc ggc tgc cag ctg tcc tcc tgc      192
Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys
50      55      60
cat cgc acc gac ccg ctc cac cgc ttc cac acc aac agg tgg aac cta      240
His Arg Thr Asp Pro Leu His Arg Phe His Asn Arg Trp Asn Leu
65      70      75      80
act tct tgt gga aca agt gtt gcc agc tca gaa ggc agt gag gag ctg      288
Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu
85      90      95
ttt tca tct gtg tct gtt gga gat caa gat gat tgc tat tcc ctg tta      336

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```

Phe Ser Ser Val Ser Val Gly Asp Gln Asp Asp Cys Tyr Ser Leu Leu
      100      105      110
gat gat cag gac ttc act tct ttt gat tta ttt cct gag ggg agt gtc      384
Asp Asp Gln Asp Phe Thr Ser Phe Asp Leu Phe Pro Glu Gly Ser Val
      115      120      125
tgc agt gat gtc tct tct tct att agc act tac tgg gat tgg tca gat      432
Cys Ser Asp Val Ser Ser Ser Ile Ser Thr Tyr Trp Asp Trp Ser Asp
      130      135      140
agc gag ttt gaa tgg cag tta cca ggc agt gac att gcc agt ggg agt      480
Ser Glu Phe Glu Trp Gln Leu Pro Gly Ser Asp Ile Ala Ser Gly Ser
      145      150      155      160
gat gta ctt tct gat gtc ata ccc agt att cca agt tca cct tgc ctg      528
Asp Val Leu Ser Asp Val Ile Pro Ser Ile Pro Ser Ser Pro Cys Leu
      165      170      175
ctt cct aaa aaa aaa aaa aa
Leu Pro Lys Lys Lys Lys
      180

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<210> 202
<211> 550
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 34..315

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<220>
<221> misc_feature
<222> 483
<223> n=a, g, c or t

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<400> 202
agagaggagg cccgagccag gccatctcca acc atg tcc gac gag gcc tgc gcc      54
      1      5
Met Ser Asp Glu Ala Ser Ala

atc act tcc tac gag aag ttt cta acc ccc gag gag ccc ttc cca ctc      102
Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe Pro Leu
      10      15      20

ctg gga cct cct cgc ggg gtg ggc acc tgc ccg agc gag gag ccg ggc      150
Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu Pro Gly
      25      30      35

tgc ctg gac atc agc gac ttc ggc tgc cag ctg tcc tcc tgc cat cgc      198
Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys His Arg
      40      45      50      55

acc gac ccg ctc cac cgc ttc cac acc aac agg tgg aac cta act tct      246
Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu Thr Ser
      60      65      70

tgt gga aca agt gtt gcc agc tca gaa ggc agt gag gag ctg ttt tca      294
Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu Phe Ser
      75      80      85

tct gtc tgt tgg aga tca aga tgattgctat tcctgttag atgatcagga      345
Ser Val Cys Trp Arg Ser Arg
      90

cttcactctct ttgtatattt ttctgaggg gagtgtctgc agtgaagtct cttctcttat      405
tagcacttac tgggattgtt cagatagcga gtttgaatgg cagttaccag gcagtgacat      465
tgccagtggg agtgaatgnta ctttctgatg tcataccccag tattccaagt tcaccttgcc      525
tgcttccctaa aaaaaaaaaa aaaaaa      550

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<210> 203
 <211> 408
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 1..315

<400> 203
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 Ile Gly Pro Arg Ala Pro Ser Pro Ser Phe Ser Val Arg Asp Val Glu
 1 5 10 15
 ctg agc gac cca gcc cgc gag cga ggt gag atg ccg gtg gcc gtg ggt 96
 Leu Ser Asp Pro Ala Arg Glu Arg Gly Glu Met Pro Val Ala Val Gly
 20 25 30
 ccc tac gga cag tcc cag cca agc tgc ttc gac cgt gtc aaa atg ggc 144
 Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly
 35 40 45
 ttc gtg atg ggt tgc gcc gtg ggc atg gcg gcc ggg gcg ctc ttc ggc 192
 Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly
 50 55 60
 acc ttt tcc tgt ctc agg atc gga atg ccg ggt cga gag ctg atg ggc 240
 Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly
 65 70 75 80
 ggc att ggg aaa acc atg atg cag agt ggc gcc acc ttt ggc aca ttc 288
 Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe
 85 90 95
 atg gcc att ggg atg ggc atc cga tgc taaccatggt tgccaactac 335
 Met Ala Ile Gly Met Gly Ile Arg Cys
 100 105
 atctgtccct tcccatcaat ccagcccat gtactaataa aagaagtct ttgagcaaaa 395
 aaaaaaaaaa aaa 408

<210> 204
 <211> 665
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 94..582

<400> 204
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 catctccatc cccaatccta aagaaggaaa tcg atg cca cgg tcc tca agg agc 114
 Met Pro Arg Ser Ser Arg Ser
 1 5
 cct ggg gac cca ggc gcc cta ctc gaa gat gtg gcc cac aat ccc aga 162
 Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Val Ala His Asn Pro Arg
 10 15 20
 ccc cgg agg att gcc cag cga ggc cgg aac acc agc agg atg gca gag 210
 Pro Arg Arg Ile Ala Gln Arg Gly Arg Asn Thr Ser Arg Met Ala Glu
 25 30 35
 gac acc tcc cca aac atg aat gac aac atc ctg ttg cct gtc cgc aac 258
 Asp Thr Ser Pro Asn Met Asn Asp Asn Ile Leu Leu Pro Val Arg Asn
 40 45 50 55

aat gac caa gcc cta ggc ctg act cag tgc atg ctg gga tgt gtg tcc	306
Asn Asp Gln Ala Leu Gly Leu Thr Gln Cys Met Leu Gly Cys Val Ser	
60 65 70	
tgg ttc acc tgt ttt gcc tgc tcc ctg aga act cag gcc cag cag gtt	354
Trp Phe Thr Cys Phe Ala Cys Ser Leu Arg Thr Gln Ala Gln Gln Val	
75 80 85	
ctg ttt aac acg tgc aga tgc aag ctg ctg tgc cag aag ctc atg gag	402
Leu Phe Asn Thr Cys Arg Cys Lys Leu Leu Cys Gln Lys Leu Met Glu	
90 95 100	
aag aca ggc att ctg ctc ctc tgt gct ttc ggt gtg tcc cag ggc cct	450
Lys Thr Gly Ile Leu Leu Leu Cys Ala Phe Gly Val Ser Gln Gly Pro	
105 110 115	
gcc cag tcc cag gtg gag gta tcc ctg ggc cct ggc act gat tat agg	498
Ala Gln Ser Gln Val Glu Val Ser Leu Gly Pro Gly Thr Asp Tyr Arg	
120 125 130 135	
aca ctg ggc aag aca ctg cac tgc cac gtg act cag ttt ccc cat ctg	546
Thr Leu Gly Lys Thr Leu His Cys His Val Thr Gln Phe Pro His Leu	
140 145 150	
cct gat ggg tgt tgc tgt gag aat tat gaa atg aaa tgatgaccat	592
Pro Asp Gly Cys Cys Glu Asn Tyr Glu Met Lys	
155 160	
gaaaatatgt tagaagccaa gaaatgcttc agaagttata aagctctccc caaaccgcaa	652
aaaaaaaaaa aaa	665

<210> 205
 <211> 1008
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 540..923

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agactcccgg agccctggtc tctacaccac atggacgtta tccacctcct ctgtgtccctc	120
ccaaggcgac atttcagaag gtgatccacg gcaaagccgt cccttcaaat ccgtctttgt	180
gccactgcc atagtcaacc ccgtgagaag cacagccggc cctgggaatt taggacaagg	240
gtctcttcgg aaaggcgga gcagcatgag aaagagtaag tgggtggcaga gagatggatc	300
ctgtgcagaga cccctccagt ccgggatccc cactctctgt gtagtctccc tcagacgcag	360
ccccaccatg gtccttcggc ctcagcagtt ccaattctac cagccacagg ggatcacctc	420
ctccccctca gcogtgggtg tggagatggg gtccaagcct gccctcacgg gggagcccg	480
cctcactgac atcagcaggg gcagtggagg ggatccactc cgcgccagc tccctcatt	539
atg gaa gac aaa gaa atc ccc atc aag agt gag cct ctg cca aaa ccg	587
Met Glu Asp Lys Glu Ile Pro Ile Lys Ser Glu Pro Leu Pro Lys Pro	
1 5 10 15	
ccc gca tct gcc cca cca tcc atc ctg gtg aaa cca gaa aac tca aga	635
Pro Ala Ser Ala Pro Pro Ser Ile Leu Val Lys Pro Glu Asn Ser Arg	
20 25 30	
aat gga atc gaa aag caa gtc aaa acc gtg aga ttt cag aat tac agc	683
Asn Gly Ile Glu Lys Gln Val Lys Thr Val Arg Phe Gln Asn Tyr Ser	
35 40 45	
cct cct ccc acc aaa cat tac acc tcc cat ccc acc tcc gga aag cct	731
Pro Pro Pro Thr Lys His Tyr Thr Ser His Pro Thr Ser Gly Lys Pro	
50 55 60	
gaa cag cca gcc acc ctc aag gcg tcc cag cct gaa gca gcg tcc ttg	779
Glu Gln Pro Ala Thr Leu Lys Ala Ser Gln Pro Glu Ala Ala Ser Leu	
65 70 75 80	

ggc cca gag atg acc gtc cta ttt gcc cac cga agt ggc tgc cac tcc	827
Gly Pro Glu Met Thr Val Leu Phe Ala His Arg Ser Gly Cys His Ser	
85 90 95	
gga cag cag aca gac ctc cgg aga aag tca gct ctt gcc aag gcc aca	875
Gly Gln Gln Thr Asp Leu Arg Arg Lys Ser Ala Leu Ala Lys Ala Thr	
100 105 110	
acc ctg gtg tcc act gcc tca ggc acg cag acc gtg ttt ccc agc aaa	923
Thr Leu Val Ser Thr Ala Ser Gly Thr Gln Thr Val Phe Pro Ser Lys	
115 120 125	
tgaacctacg ggtggctttt cctagacccc aaagaggtga attgcattta aatacagtct	983
gcctycactg aaaaaaaaaa aaaaaa	1008

<210> 206
 <211> 455
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 77..364

<400> 206	
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tttcaaccaa aacctc atg ctg acc aga gtt gag gaa cag aag aag atg gtg	112
Met Leu Thr Arg Val Glu Glu Gln Lys Lys Met Val	
1 5 10	
aag gcc tgc agg tat agg tgt tca gca tgt cat ctg aaa tat tcc cca	160
Lys Ala Cys Arg Tyr Arg Cys Ser Ala Cys His Leu Lys Tyr Ser Pro	
15 20 25	
cag agg caa aaa gaa agg aaa tta tct ctg aaa agg ggg agg aca agt	208
Gln Arg Gln Lys Glu Arg Lys Leu Ser Leu Lys Arg Gly Arg Thr Ser	
30 35 40	
cag cag aat atg tca atg ttt tgg ttg aag aag ctg ctt gaa tct ggg	256
Gln Gln Asn Met Ser Met Phe Trp Leu Lys Lys Leu Leu Glu Ser Gly	
45 50 55 60	
ctt ttc tgt gcc atg tgt tct ccc agg gcc agc aca aag aag ggc ttt	304
Leu Phe Cys Ala Met Cys Ser Pro Arg Ala Ser Thr Lys Lys Gly Phe	
65 70 75	
tgg tgc agg ccc aag acc acc ata atc atc att gat tat tcc tct cca	352
Trp Cys Arg Pro Lys Thr Thr Ile Ile Ile Asp Tyr Ser Ser Pro	
80 85 90	
cgc cag tgt ctc taaataaact ttctcttctt ttcttgaaaa aaaaaaaaaa	404
Arg Gln Cys Leu	
95	
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaagaaaa aaaaaaaaaa a	455

<210> 207
 <211> 749
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 65..544

<400> 207	
cttttacgac gcgccggaaa gcaacggcaa gggccgcagc cagcaccggg cggagagggc	60
tacc atg ggg aaa atc gcg ctg caa ctc aaa gcc acg ctg gag aac atc	109

Met Gly Lys Ile Ala Leu Gln Leu Lys Ala Thr Leu Glu Asn Ile	
1 5 10 15	
acc aac ctc cgg ccc gtg ggc gag gac ttc cgg tgg tac ctg aag atg	157
Thr Asn Leu Arg Pro Val Gly Glu Asp Phe Arg Trp Tyr Leu Lys Met	
20 25 30	
aaa tgt ggc aac tgt ggt gag att tcg gac aag tgg cag tac atc cgg	205
Lys Cys Gly Asn Cys Gly Glu Ile Ser Asp Lys Trp Gln Tyr Ile Arg	
35 40 45	
ctg atg gac agt gtg gca ctg aag ggg ggc cgt ggc agt gct tcc atg	253
Leu Met Asp Ser Val Ala Leu Lys Gly Gly Arg Gly Ser Ala Ser Met	
50 55 60	
gtc cag aag tgc aag ctg tgt gca aga gaa aat tcc atc gag att tta	301
Val Gln Lys Cys Lys Leu Cys Ala Arg Glu Asn Ser Ile Glu Ile Leu	
65 70 75	
agc agc acc atc aag cct tac aat gct gaa gac aat gag aac ttc aag	349
Ser Ser Thr Ile Lys Pro Tyr Asn Ala Glu Asp Asn Glu Asn Phe Lys	
80 85 90 95	
aca ata gtg gag ttt gag tgc cgg ggc ctt gaa cca gtt gat ttc cag	397
Thr Ile Val Glu Phe Glu Cys Arg Gly Leu Glu Pro Val Asp Phe Gln	
100 105 110	
ccg cas gwg rtw ttg ctg ctg aag gtg tgg agt cag gga cag cct tca	445
Pro Xaa Xaa Xaa Leu Leu Leu Lys Val Trp Ser Gln Gly Gln Pro Ser	
115 120 125	
gtg aca tta atc tgc agg aga agg act ggg act gac tat gat gaa aag	493
Val Thr Leu Ile Cys Arg Arg Arg Thr Gly Thr Asp Tyr Asp Glu Lys	
130 135 140	
gcc cag gag tct gtg gga atc tat gag gtc acc cac cag ttt gtg aag	541
Ala Gln Glu Ser Val Gly Ile Tyr Glu Val Thr His Gln Phe Val Lys	
145 150 155	
tgc tgatccctct tccttcccg ttgcccttaa gaactgagaa aggacaaagt	594
Cys	
160	
actctaagca gcagagccca cagaggctcg ttcctttgac cettgtctcc tgggtgctat	654
acgaaacctt cacaatctgc atgctggact ttattacagc ttcccaagcc ccataataa	714
agccccctgtt cagcgtacaa aaaaaaaaaa aaaaa	749
<210> 208	
<211> 594	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> 117..467	
<400> 208	
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tggggccccc actccccgcc gcaagtctct aggatggcca gcagagaaac aagaaa atg	119
Met	
1	
gac tcc ctg gct gct gga gag ttg aat gcc agc cac cag cca tgg gtg	167
Asp Ser Leu Ala Ala Gly Glu Leu Asn Ala Ser His Gln Pro Trp Val	
5 10 15	
cca gag ttt gta gcc tat tgg agg aaa aca cac caa gat cac ctc tgc	215
Pro Glu Phe Val Ala Tyr Trp Arg Lys Thr His Gln Asp His Leu Cys	
20 25 30	
agc ctg cac agc cgg gcc ttt gga ctc ctg gat gct aga gtg acc tgg	263
Ser Leu His Ser Arg Ala Phe Gly Leu Leu Asp Ala Arg Val Thr Trp	

35	40	45	
gcg ctg agg agg gcc ccc gag cca gta cca gga aag gat aga ctc ctg			311
Ala Leu Arg Arg Ala Pro Glu Pro Val Pro Gly Lys Asp Arg Leu Leu			
50	55	60	65
ctt gca gca ttc cca gca gag gca tgc cct gtg gac acc gcg tct gtg			359
Leu Ala Ala Phe Pro Ala Glu Ala Ser Pro Val Asp Thr Ala Ser Val			
70	75	80	
tct gta tat ggc aga gct ccc aga tat atg cac aag gga gtg aaa aaa			407
Ser Val Tyr Gly Arg Ala Pro Arg Tyr Met His Lys Gly Val Lys Lys			
85	90	95	
tgt gtt tgc acc cca gtc tct aaa aat tca aca gcc tgg tta ctt ctg			455
Cys Val Cys Thr Pro Val Ser Lys Asn Ser Thr Ala Trp Leu Leu Leu			
100	105	110	
ggt ggt ata tgc tagtggtgctt taatacgtgt tatttgctca tctgtatttc			507
Gly Gly Ile Ser			
115			
ttactctttg cacaattaaa ccattgttctt ttactttatg tacattttta ataaaagaaa			567
gttgtaacg aaaaaaaaa aaaaaaa			594
<210> 209			
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<213> Homo sapiens			
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<222> 893..1897			
<400> 209			
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tttcagagtc acccattctg cctcctgctc aagcaacaga cctgccgatc acccccgtcg			120
ggcccgcgtt tctcagggtc ttcttaatcc cctgggtctt ccggcttctg ctgtgcctgg			180
agtcaggccg ccgtgcggca ggctgttaac ctagcctcgg ggagagtggg atggagccac			240
cttctcatgt aacgatctc gccttcctc atctccattg ttttatggct tcacacggac			300
cgtggctttc tgcattggaag cttgggtggc aggggtgctgt cactttggga agcagccaga			360
gaaccacagg atgcgtgaat cggctctcct gtcttcatgg gcactctcgg ccagggtgtgt			420
gtctttgtgct gtgattagtg ggtcactggc aagtgtctga atgaagtggg ggttcgggtg			480
gcaacagtga cggggaaggg ctatgggtcc gcctcaatgt catctgcccc atccctgggc			540
ctccaggaaat ccagggtctc agccccctgct ttagaaggaa gtccctgacg ccacgctgga			600
tctggaggac gtccggagct acaggggcga gatattcatc cgaaacctgg cggccagcag			660
ggcagagccc taacccagag tgaagggtgga ctttgccctc tcgtgccacg aggacttgct			720
ggcaccctac tctgagccca tcgagtggaa ataccacagc cctgaggagg agataagcct			780
tggacctgcc tgctggctct gggatttttt aagacgaagt caacaggcag ggtttttgct			840
gcccttgagt ggcgggggtg acagcgcagc caccgcctgc ctcactact cc atg tgc			898
		Met Cys	
		1	
tgc cag gtc tgc gag gcc gtg agg agt gga aat gag gaa gtg ctg gct			946
Cys Gln Val Cys Glu Ala Val Arg Ser Gly Asn Glu Glu Val Leu Ala			
5	10	15	
gat gtc cgc acc atc gtg aac cag atc agc tac acc ccc cag gat ccc			994
Asp Val Arg Thr Ile Val Asn Gln Ile Ser Tyr			
20	25	30	
cga gac ctc tgt gga cgc ata ctg acc acc tgc tac atg gcc agc aag			1042
Arg Asp Leu Cys Gly Arg Ile Leu Thr Thr Cys Tyr Met Ala Ser Lys			
35	40	45	50
aac tcc tcc cag gag acg tgc acc cgg gcc aga gag ttg gcc cag cag			1090
Asn Ser Ser Gln Glu Thr Cys Thr Arg Ala Arg Glu Leu Ala Gln Gln			
55	60		

att gga agc cac cac atc agt ctc aac atc gat cca gcc gtg aag gcc	1138
Ile Gly Ser His His Ile Ser Leu Asn Ile Asp Pro Ala Val Lys Ala	
70 75 80	
gtc atg ggc atc ttc agc ctg gtg acg ggg aag agc cct ctg ttt gca	1186
Val Met Gly Ile Phe Ser Leu Val Thr Gly Lys Ser Pro Leu Phe Ala	
85 90 95	
gct cat gga gga agc agc agg gaa aac ctg gcg ctg caa aat gtg cag	1234
Ala His Gly Gly Ser Ser Arg Glu Asn Leu Ala Leu Gln Asn Val Gln	
100 105 110	
gct cga ata cgg atg gtc ctc gcc tat ctg ttt gct cag ttg agc ctc	1282
Ala Arg Ile Arg Met Val Leu Ala Tyr Leu Phe Ala Gln Leu Ser Leu	
115 120 125	
tgg tct cgg ggt gtc cac ggt ggg ctc ctc gtg ctg gga tcc gcc aac	1330
Trp Ser Arg Gly Val His Gly Gly Leu Leu Val Leu Gly Ser Ala Asn	
135 140 145	
gtg gat gag agt ctc ctg ggc tac ctg acc aag tac gac tgc tcc agt	1378
Val Asp Glu Ser Ser Leu Leu Gly Tyr Leu Thr Lys Tyr Asp Cys Ser Ser	
150 155 160	
gcg gac atc aac ccc ata ggc ggg atc agc aag acg gac ctc agg gcc	1426
Ala Asp Ile Asn Pro Ile Gly Gly Ile Ser Lys Thr Asp Leu Arg Ala	
165 170 175	
ttc gtc cag ttc tgc atc cag cgc ttc cag ctt cct gcc ctg cag agc	1474
Phe Val Gln Phe Cys Ile Gln Arg Phe Gln Leu Pro Ala Leu Gln Ser	
180 185 190	
atc ctg ttg gcg ccg gcc acc gca gag ctg gag ccc ttg gct gat gga	1522
Ile Leu Leu Ala Pro Ala Thr Ala Glu Leu Glu Pro Leu Ala Asp Gly	
195 200 205	
cag gtg tcc cag acc gac gag gaa gat atg ggg atg aca tat gcg gag	1570
Gln Val Ser Gln Thr Asp Glu Glu Asp Met Gly Met Thr Tyr Ala Glu	
215 220 225	
ctc tcg gtc tat ggg aaa ctc agg aag gtg gcc aag atg ggg ccc tac	1618
Leu Ser Val Tyr Gly Lys Leu Arg Ser Lys Val Ala Lys Met Gly Pro Tyr	
230 235 240	
agc atg ttc tgc aaa ctc ctc ggc atg tgg aga cac atc tgc acc ccg	1666
Ser Met Phe Cys Lys Leu Leu Gly Met Trp Arg His Ile Cys Thr Pro	
245 250 255	
aga cag gtc gct gac aaa gtg aag cgg ttt ttc tcc aag tac tcc atg	1714
Arg Gln Val Ala Asp Lys Val Lys Arg Phe Phe Ser Lys Tyr Ser Met	
260 265 270	
aac aga cac aag atg acc acg ctc aca ccc gcg tac cac gcc gag aac	1762
Asn Arg His Lys Met Thr Thr Leu Thr Pro Ala Tyr His Ala Glu Asn	
275 280 285	
tac agc cct gag gac aac agg ttt gat ctg cga cca ttt ctg tac aac	1810
Tyr Ser Pro Glu Asp Asn Arg Phe Asp Leu Arg Pro Phe Leu Tyr Asn	
295 300 305	
aca agc tgg cct tgg cag ttt cgg tgc ata gaa aat cag gtg cta cag	1858
Thr Ser Trp Pro Trp Gln Phe Arg Cys Ile Glu Asn Gln Val Leu Gln	
310 315 320	
ctc gag agg gca gag cca cag tcc ctg gac ggc gtg gac tgaggccgggt	1907
Leu Glu Arg Ala Glu Pro Gln Ser Leu Asp Gly Val Asp	
325 330 335	
tecttctctgg aggcctctctg tctctgggga cccagcacc tcatcatcag cattgctgga	1967
gccaaagggtg ggagccctac actaggagcc caggatggga cggcgcatca gccgagagg	2027
agggaaacttt tcagtcaaat tectcaaaaa gaggctggaa taaagcctgg gctcaaaaaa	2087
aaaaaaaaa a	2098

<210> 210

<211> 428

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 85..342

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<400> 210
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ctacaattta cagttcctct atcc atg tgc tgg gtt ata aat cat gcc atc      111
               Met Cys Trp Val Ile Asn His Ala Ile
               1               5
ctc cct aga atg aga atg cac agc aag cgg cag aca atc acc cgg cat      159
Leu Pro Arg Met Arg Met His Ser Lys Arg Gln Thr Ile Thr Arg His
10               15               20               25
tcg gca tct ett tct ttt cac gcg ctc cct cgc tcc gcc ttt ctc cag      207
Ser Ala Ser Leu Ser Phe His Ala Leu Pro Arg Ser Ala Phe Leu Gln
               30               35               40
ctc tgc ctt ctc agg cag ata cat cag ata cct tgt tta tcc atc ttc      255
Leu Cys Leu Leu Arg Gln Ile His Gln Ile Pro Cys Leu Ser Ile Phe
               45               50               55
agc tcc act ctg agg gcg cag acg cac gat tcc ggg atc ggg tgc acc      303
Ser Ser Thr Leu Arg Ala Gln Thr His Asp Ser Gly Ile Gly Cys Thr
               60               65               70
acg gcg aas cca gcc ggg aga cgg cag gag cag ctc agg taaccagggg      352
Thr Ala Xaa Pro Gly Gly Arg Arg Gln Glu Gln Leu Arg
               75               80               85
aagcttgctg gccacaggag atgcagccgt ggagctgtga ggaaagacgg tctggcttca      412
aaaaaaaaaa aaaaaa      428

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<210> 211
<211> 769
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 155..433

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<400> 211
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gaatgggtgga tgctgtgggg caccacctcc ttgaggacca aggcactcca gctgccaggga      120
atttggctgc taacctcaca cagctgagcc ttcc atg aaa att gct ctc tgc caa      175
               Met Lys Ile Ala Leu Cys Gln
               1               5
aga gaa ctt cct agt cca agg tca tgt cta ctc tcc aga gat gtg act      223
Arg Glu Leu Pro Ser Pro Arg Ser Cys Leu Leu Ser Arg Asp Val Thr
10               15               20
gga gtg att tgc acc cgg atg cct aga ctc gcc atc tgc tca aag act      271
Gly Val Ile Cys Thr Arg Met Pro Arg Leu Ala Ile Cys Ser Lys Thr
25               30               35
gct cag aaa gcc ctc cca tgc att ccc ctg ctg cat acc agc cca ctc      319
Ala Gln Lys Ala Leu Pro Cys Ile Pro Leu Leu His Thr Ser Pro Leu
40               45               50               55
tgc ctg cag ctg ctg tct gca gga ctt cat atc tat gcc aca ctg tgt      367
Cys Leu Gln Leu Leu Ser Ala Gly Leu His Ile Tyr Ala Thr Leu Cys
               60               65               70
aaa agc tgt gct tca aga aat cac aaa aac att ttc ctg cac cta cta      415

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Lys Ser Cys Ala Ser Arg Asn His Lys Asn Ile Phe Leu His Leu Leu
 75 80 85
 cac agc ctg agt gcg gca taagttgacc ttgcttgcta agaaatgggg 463
 His Ser Leu Ser Ala Ala
 90
 caagaaatgc ttttttgtat gtgtcatgtc tgtttgtttt tcaattaaga gaggaagaca 523
 ttaggcagat ggaatgtaca tgtgaggatg aggagacaga aaacaagtag ccotttccat 583
 caagatagag ggttttctgg gggttgcctggc tattgaatgt cactcctgat ttctctttcc 643
 aaggcactgt accaccagcc tactgagatt gtgtgggagc tttcatgggg gttgtatttc 703
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 aaaaaa 769

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 Met Ala Val Arg Ala Ser Phe Glu Asn Asn Cys Glu Ile Gly Cys
 1 5 10 15
 ttt gcc aag ctg acc aac acc tac tgt ctg gta gcg atc gga ggc tca 155
 Phe Ala Lys Leu Thr Asn Thr Tyr Cys Leu Val Ala Ile Gly Gly Ser
 20 25 30
 gag aac ttc tac agt gtg ttc gag ggc gag ctg tcc gat acc atc ccc 203
 Glu Asn Phe Tyr Ser Val Phe Glu Gly Glu Leu Ser Asp Thr Ile Pro
 35 40 45
 gtg gtg cac gcg tct atc gcc ggc tgc cgc atc atc ggg cgc atg tgt 251
 Val Val His Ala Ser Ile Ala Gly Cys Arg Ile Ile Gly Arg Met Cys
 50 55 60
 gtg gga gac aga aga aat tct ggc aga tgt gct caa ggt gga agt ctt 299
 Val Gly Asp Arg Arg Asn Ser Gly Arg Cys Ala Gln Gly Gly Ser Leu
 65 70 75
 cag aca gac agt ggc cga cca ggt gct agt agg aag cta ctg tgt ctt 347
 Gln Thr Asp Ser Gly Arg Pro Gly Ala Ser Arg Lys Leu Leu Cys Leu
 80 85 90 95
 cag caa tca ggg agg gct ggt gca tcc caa gac ttc aat tgaagaccag 396
 Gln Gln Ser Gly Arg Ala Gly Ala Ser Gln Asp Phe Asn
 100 105
 gatgagctgt cctctcttct tcaagtcccc cttgtggcgg ggaactgtgaa ccgaggcagt 456
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 cattaaagtg cagttccctc caaaaaaaaa aaaaaaaa 914

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ggcttgggatt tggatattct caacagaaag ggttaaaggc tgaatgggtacc taaagccttgg    180
tacttgaatt ttgatcaaga taagctgcct taagtctctt tcattacaca aatgatcccta    240
gataaattgat agatcctgtg gttcaactgg atttctagat agaagctgga ttcatgtgat    300
gccagaggag taaaatttca agagactgaa accagatctg agtttctcgt ttccagctctg    360
gacctctttg gtgctgtaaa tcctggatat actgtagatg agtactgcgt tttttctttta    420
tggactctct tcagcttctg gagacctcac tatcctatt atg tct ttg tgt gaa    474
                                     Met Ser Leu Cys Glu
                                     1           5

gac atg ctg ctt tgt aat tat cga aag tgt cgc atc aaa ctg tct ggc    522
Asp Met Leu Leu Cys Asn Tyr Arg Lys Cys Arg Ile Lys Leu Ser Gly
                                     10           15           20

tat gca tgg gtc act gcc tgc tct cac atc ttc tgt gat cag cat ggc    570
Tyr Ala Trp Val Thr Ala Cys Ser His Ile Phe Cys Asp Gln His Gly
                                     25           30           35

agt ggt gag ttt agt cgc tca cca gct atc tgt cct gcc tgc aac agt    618
Ser Gly Glu Phe Ser Arg Ser Pro Ala Ile Cys Pro Ala Cys Asn Ser
                                     40           45           50

acc ctt tct gga aag cta gat att gtc cgc aca gaa ctg agt cca tca    666
Thr Leu Ser Gly Lys Leu Asp Ile Val Arg Thr Glu Leu Ser Pro Ser
                                     55           60           65

gag gaa tat aaa gct atg gta ttg gca gga ctg cga cca gag atc gtg    714
Glu Glu Tyr Lys Ala Met Val Leu Ala Gly Leu Arg Pro Glu Ile Val
                                     70           75           80           85

ttg gac att agc tcc cga gcg ctg gcc ttc tgg aca tat cag gta cat    762
Leu Asp Ile Ser Ser Arg Ala Leu Ala Phe Trp Thr Tyr Gln Val His
                                     90           95           100

cag gaa cgt ctg tat caa gaa tac aat ttc agc aag gct gag ggc cat    810
Gln Glu Arg Leu Tyr Gln Glu Tyr Asn Phe Ser Lys Ala Glu Gly His
                                     105          110          115

ctg aaa cag atg gag aag ata tat act cag caa ata caa agc aag gat    858
Leu Lys Gln Met Glu Lys Ile Tyr Thr Gln Gln Ile Gln Ser Lys Asp
                                     120          125          130

gta gaa ttg acc tct atg aaa ggg gag gtt acc tcc atg aag aaa gta    906
Val Glu Leu Thr Ser Met Lys Gly Glu Val Thr Ser Met Lys Lys Val
                                     135          140          145

cta gaa gaa tac aag aaa aag ttc agt gac atc tct gag aaa ctt atg    954
Leu Glu Glu Tyr Lys Lys Lys Phe Ser Asp Ile Ser Glu Lys Leu Met
                                     150          155          160          165

gag cgc aat cgt cag tat caa aag ctg caa ggc ctg tat gat agc ctt    1002
Glu Arg Asn Arg Gln Tyr Gln Lys Leu Gln Gly Leu Tyr Asp Ser Leu
                                     170          175          180

agg cta cga aac atc act att gct aac cat gaa ggc acc ctt gaa cca    1050
Arg Leu Arg Asn Ile Thr Ile Ala Asn His Glu Gly Thr Leu Glu Pro
                                     185          190          195

tcc atg att gca cag tct ggt gtt ctt ggc ttc cca tta ggt aac aac    1098
Ser Met Ile Ala Gln Ser Gly Val Leu Gly Phe Pro Leu Gly Asn Asn
                                     200          205          210

tcc aag ttt cct ttg gat aat aca cct gtt cga aat cgg ggc gat gga    1146
Ser Lys Phe Pro Leu Asp Asn Thr Pro Val Arg Asn Arg Gly Asp Gly
                                     215          220          225

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gat gga gat ttt cag ttc aga cca ttt ttt gcg ggt tct ccc aca gca 1194
 Asp Gly Asp Phe Gln Phe Arg Pro Phe Phe Ala Gly Ser Pro Thr Ala
 230 235 240 245
 cct gaa ccc agc aac agc ttt ttt agt ttt gtc tct cca agt cgt gaa 1242
 Pro Glu Pro Ser Asn Ser Phe Phe Ser Phe Val Ser Pro Ser Arg Glu
 250 255 260
 tta gag cag cag caa gtt tct agc agg gcc ttc aaa gta aaa aga att 1290
 Leu Glu Gln Gln Gln Val Ser Ser Arg Ala Phe Lys Val Lys Arg Ile
 265 270 275
 tgagccacgc atagtgtcac gcacctgtga tcccagctac ttaggagggtt gaggctggga 1350
 ggatcacttg agcccaggag tctgaggctt tagtgatcta agatcatgcc actgcactcc 1410
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 Gly Tyr Leu Thr Phe Tyr Gly Glu Val Glu Asp Glu Leu Leu His Ala
 15 20 25
 tac agc aaa gtg tat aca tta gac atc cct ctt ctg atg gtt cgc ctg 149
 Tyr Ser Lys Val Tyr Thr Leu Asp Ile Pro Leu Leu Met Val Arg Leu
 30 35 40
 gca gtc ctt gtg gca gta aca cta act gtg ccc att gtc ctg ttc cca 197
 Ala Val Leu Val Ala Val Thr Leu Thr Val Pro Ile Val Leu Phe Pro
 45 50 55
 att cgt aca tca gtg atc aca ctg tta ttt ccc aaa cga ccc ttc agc 245
 Ile Arg Thr Ser Val Ile Thr Leu Leu Phe Pro Lys Arg Pro Phe Ser
 60 65 70 75
 tgg ata cga cat ttc ctg att gca gct gtg ctt att gca ctt aat aat 293
 Trp Ile Arg His Phe Leu Ile Ala Ala Val Leu Ile Ala Leu Asn Asn
 80 85 90
 gtt ctg gtc atc ctt gtg cca act ata aaa tac atc ttc gga ttc ata 341
 Val Leu Val Ile Leu Val Pro Thr Ile Lys Tyr Ile Phe Gly Phe Ile
 95 100 105
 ggg gct tct tct gcc act atg ctg att ttt att ctt cca gca gtt ttt 389
 Gly Ala Ser Ser Ala Thr Met Leu Ile Phe Ile Leu Pro Ala Val Phe
 110 115 120
 tat ctt aaa ctt gtc aag aaa gaa act ttt agg tca ccc caa aag gtc 437
 Tyr Leu Lys Leu Val Lys Lys Glu Thr Phe Arg Ser Pro Gln Lys Val
 125 130 135
 ggg gct tta att ttc ctt gtg gtt gga ata ttc ttc atg att gga agc 485
 Gly Ala Leu Ile Phe Leu Val Val Gly Ile Phe Phe Met Ile Gly Ser
 140 145 150 155
 atg gca ctg att ata att gac tgg att tat gat cct cca aat tcc aag 533
 Met Ala Leu Ile Ile Ile Asp Trp Ile Tyr Asp Pro Pro Asn Ser Lys
 160 165 170
 cat cac taacacaagg aaaaaactt tctttttcta ttggaaatgg ttacaagtta 589

His His
tactcCaaaa gatatttgaa ttatcttgat tggaaatgtta ttcataaggaa ataacaggaa 649
gattccaaag acgtttacca gtmatatcac caggcacctg cagaagagga aaatcactgt 709
ttttgtcaag gatggttggt tatgtgttta aaataaaacc tgtggtgcac aaaaaaaaaa 769
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<222> 34..1143

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ggg gtc ttc gtg ctg tcc ctc tcg gcc atc ccg gtc acc tat gtc ttc 102
Gly Val Phe Val Leu Ser Leu Ser Ala Ile Pro Val Thr Tyr Val Phe
10 15 20
aac cac ctg gcg gcc cag cat gat tcc tgg act att gta ggg gtt gct 150
Asn His Leu Ala Ala Gln His Asp Ser Trp Thr Ile Val Gly Val Ala
25 30 35
gcc ctc atc ctg ttc ctg gta gca ctg ctg gct cgt gtc ctc gtc aaa 198
Ala Leu Ile Leu Phe Leu Val Ala Leu Leu Ala Arg Val Leu Val Lys
40 45 50 55
aga aaa cca ccc cgg gac cca ctg ttc tat gtg tat gca gtt ttt gga 246
Arg Lys Pro Pro Arg Asp Pro Leu Phe Tyr Val Tyr Ala Val Phe Gly
60 65 70
ttt acc agc gtg gtg aac ctc atc ata gga ctg gag caa gat gga atc 294
Phe Thr Ser Val Val Asn Leu Ile Ile Gly Leu Glu Gln Asp Gly Ile
75 80 85
att gac ggg ttc atg aca cac tac ttg aga gag ggt gaa ccg tat ctg 342
Ile Asp Gly Phe Met Thr His Tyr Leu Arg Glu Gly Glu Pro Tyr Leu
90 95 100
aac acc gca tat ggg cac atg atc tgc tac tgg gat ggc tct gct cat 390
Asn Thr Ala Tyr Gly His Met Ile Cys Tyr Trp Asp Gly Ser Ala His
105 110 115
tat ctg atg tac ctg gtg atg gtg gca gcc ata gca tgg gag gaa act 438
Tyr Leu Met Tyr Leu Val Met Val Ala Ala Ile Ala Trp Glu Glu Thr
120 125 130 135
tat aga acc att ggc cta tat tgg gtt gga tct att att atg agt gtt 486
Tyr Arg Thr Ile Gly Leu Tyr Trp Val Gly Ser Ile Ile Met Ser Val
140 145 150
gtt gtt ttt gtg cca gga aac att gta ggg aag tat gga aca cga att 534
Val Val Phe Val Pro Gly Asn Ile Val Gly Lys Tyr Gly Thr Arg Ile
155 160 165
tgc cct gct ttt ttc tta agc ata cca tat act tgt ctt cct gtc tgg 582
Cys Pro Ala Phe Phe Leu Ser Ile Pro Tyr Thr Cys Leu Pro Val Trp
170 175 180
gtt ggt ttc aga atc tat aat cag cca tca gaa aat tat aat tac ccc 630
Ala Gly Phe Arg Ile Tyr Asn Gln Pro Ser Glu Asn Tyr Asn Tyr Pro
185 190 195
tca aag gtt att caa gaa gcc caa gcg aaa gac ctg ctg aga aga cca 678
Ser Lys Val Ile Gln Glu Ala Gln Ala Lys Asp Leu Leu Arg Arg Pro
200 205 210 215

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Phe Asp Leu Met Leu Val Val Cys Leu Leu Leu Ala Thr Gly Phe Cys
220 225 230
ctg ttc aga ggt ttg att gct ttg gat tgc cca tct gag ctc tgc cga      774
Leu Phe Arg Gly Leu Ile Ala Leu Asp Cys Pro Ser Glu Leu Cys Arg
235 240 245
tta tat acg caa ttt caa gag ccc tat cta aag gat cct gct gct tat      822
Leu Tyr Thr Gln Phe Gln Glu Pro Tyr Leu Lys Asp Pro Ala Ala Tyr
250 255 260
cct aaa att cag atg ctg gca tat atg ttc tat tct gtt cct tac ttt      870
Pro Lys Ile Gln Met Leu Ala Tyr Met Phe Tyr Ser Val Pro Tyr Phe
265 270 275
gtg act gca ctg tat ggc tta gtg gtt cct gga tgt tcc tgg atg cct      918
Val Thr Ala Leu Tyr Gly Leu Val Val Pro Gly Cys Ser Trp Met Pro
280 285 290 295
gac atc aca ttg ata cat gct gga ggt ctg gct cag gct cag ttt tct      966
Asp Ile Thr Leu Ile His Ala Gly Gly Leu Ala Gln Ala Gln Phe Ser
300 305 310
cac att ggt gca tct ctt cat gct aga act gct tat gtc tac aga gtc      1014
His Ile Gly Ala Ser Leu His Ala Arg Thr Ala Tyr Val Tyr Arg Val
315 320 325
cct gaa gaa gca aaa atc ctt ttt tta gca tta aac ata gca tat gga      1062
Pro Glu Glu Ala Lys Ile Leu Phe Leu Ala Leu Asn Ile Ala Tyr Gly
330 335 340
gtt ctt cct cag ctc ttg gcc tat cgt tgt atc tac aaa cca gag ttc      1110
Val Leu Pro Gln Leu Leu Ala Tyr Arg Cys Ile Tyr Lys Pro Glu Phe
345 350 355
ttc ata aaa aca aag gca gaa gaa aaa gtg gaa taataaatatt acttcatggt      1163
Phe Ile Lys Thr Lys Ala Glu Glu Lys Val Glu
360 370
ctctcctttct aaattactaa cttttgttat actggtactg atattttgtc ccatttcact      1223
ctctctcat acgtgagtac ttaagaatat gtacattctt gctctgcact gtatgtgtga      1283
gctatatggt atttgtgtaaa ttttttttga aggaaaatgg aaattcttga gaaacagttt      1343
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<222> 6..1184

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1 5 10 15
gag ccc cgg cca gga ttt cat ggt gtc ttg ggt atc aat tcc atc act      98
Glu Pro Arg Pro Gly Phe His Gly Val Leu Gly Ile Asn Ser Ile Thr
20 25 30
ggg aag gag gag cct ctg tac ccc agc tac aag aga cag ttg cgc att      146
Gly Lys Glu Glu Pro Leu Tyr Pro Ser Tyr Lys Arg Gln Leu Arg Ile
35 40 45
tac ctg gtc tcc ctg cca ttc gtg tgc ctc tgc ctc tat ttc tca ctg      194
Tyr Leu Val Ser Leu Pro Phe Val Cys Leu Cys Leu Tyr Phe Ser Leu
50 55 60

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tat gtc atg atg att tac ttc gac atg gag gtt tgg gcc ttg ggt cta	242
Tyr Val Met Met Ile Tyr Phe Asp Met Glu Val Trp Ala Leu Gly Leu	
65 70 75	
cat gag aac agc ggg tct gag tgg acc agt gtc ctg ttg tat gtg ccc	290
His Glu Asn Ser Gly Ser Glu Trp Thr Ser Val Leu Leu Tyr Val Pro	
80 85 90 95	
agc atc atc tat gcc att gtg att gag atc atg aat cgt ctc tat cga	338
Ser Ile Ile Tyr Ala Ile Val Ile Glu Ile Met Asn Arg Leu Tyr Arg	
100 105 110	
tat gct gcc gag ttt tta act tca tgg gag aat cac aga ttg gaa tct	386
Tyr Ala Ala Glu Phe Leu Thr Ser Trp Glu Asn His Arg Leu Glu Ser	
115 120 125	
gcc tat cag aac cat cta att ctg aaa gtt tta gtg ttc aac ttc ctc	434
Ala Tyr Gln Asn His Leu Ile Leu Lys Val Leu Val Phe Asn Phe Leu	
130 135 140	
aat tgc ttt gcc tca ctc ttc tat att gcc ttt gtc ttg aaa gat atg	482
Asn Cys Phe Ala Ser Leu Phe Tyr Ile Ala Phe Val Leu Lys Asp Met	
145 150 155	
aag ctt ttg cgc cag agc ttg gcc act ctc cta att acc tcc cag atc	530
Lys Leu Leu Arg Gln Ser Leu Ala Thr Leu Leu Ile Thr Ser Gln Ile	
160 165 170 175	
ctc aac caa att atg gaa tct ttt ctt cct tat tgg ctr caa agg aag	578
Leu Asn Gln Ile Met Glu Ser Phe Leu Pro Tyr Trp Leu Gln Arg Lys	
180 185 190	
cat ggt gtg cgg gtg aag agg aag gtg cag gct tta aag gca gac att	626
His Gly Val Arg Val Lys Arg Lys Val Gln Ala Leu Lys Ala Asp Ile	
195 200 205	
gat gct aca tta tat gaa caa gtc atc ctg gaa aaa gaa atg gga act	674
Asp Ala Thr Leu Tyr Glu Gln Val Ile Leu Glu Lys Glu Met Gly Thr	
210 215 220	
tat ttg ggc acc ttt gat gat tac ttg gag tta ttc ctg cag ttt ggt	722
Tyr Leu Gly Thr Phe Asp Asp Tyr Leu Glu Leu Phe Leu Gln Phe Gly	
225 230 235	
tat gtg agc ctt ttc tcc tgt gtt tac cca tta gca gct gcc ttt gct	770
Tyr Val Ser Leu Phe Ser Cys Val Tyr Pro Leu Ala Ala Phe Ala	
240 245 250 255	
gtg tta aat aac ttc act gaa gta aat tca gat gcc tta aaa atg tgc	818
Val Leu Asn Asn Phe Thr Glu Val Asn Ser Asp Ala Leu Lys Met Cys	
260 265 270	
agg gtc ttc aaa cgt cca ttc tca gaa cct tca gcc aat att ggt gtg	866
Arg Val Phe Lys Arg Pro Phe Ser Glu Pro Ser Ala Asn Ile Gly Val	
275 280 285	
tgg cag ttg gct ttt gaa acg atg agt gtt ata tct gtg gtc act aac	914
Trp Gln Leu Ala Phe Glu Thr Met Ser Val Ile Ser Val Val Thr Asn	
290 295 300	
tgt gcg ctg att gga atg tca cca gaa gca gtc ttt cca gaa	962
Cys Ala Leu Ile Gly Met Ser Pro Gln Val Asn Ala Val Phe Pro Glu	
305 310 315	
tca aaa gca gac ctc att ttg att gta gta gca gtg gag cac gca ctc	1010
Ser Lys Ala Asp Leu Ile Leu Ile Val Val Ala Val Glu His Ala Leu	
320 325 330 335	
ctg gct tta aag ttt ata ctt gca ttt gcc ata cct gat aag cca cgg	1058
Leu Ala Leu Lys Phe Ile Leu Ala Phe Ala Ile Pro Asp Lys Pro Arg	
340 345 350	
cat atc cag atg aaa cta gcc aga ctg gaa ttt gag tct ttg gag gca	1106
His Ile Gln Met Lys Leu Ala Arg Leu Glu Phe Glu Leu Glu Ala	
355 360 365	
ctc aag cag cag caa atg aag ctc gtg acc gag aac ctg aag gag gaa	1154

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Leu Lys Gln Gln Gln Met Lys Leu Val Thr Glu Asn Leu Lys Glu Glu
      370                      375                      380
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Pro Met Glu Ser Gly Lys Glu Lys Ala Thr
      385                      390
ctgccctggt gcgacaggcc tgtgtctgtg ccacacctgc caccgtggca gggggggtag      1264
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catgtggcaa gcaccccttc cagtttcgca gtggcttggc tcgggatacct tggcagttcc      1384
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aaaaaaaaaa taaaaaaaaa aaaaaaaaaa

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 Ala Val Glu Glu Leu Val Ser Gly Val Arg Gln Ala Ala Asp Phe Ala
 10 15 20
 gag cag ttc cgc tcc tac tca gag agc gag aag caa tgg aag gcc cgc 148
 Glu Gln Phe Arg Ser Tyr Ser Glu Ser Glu Lys Gln Trp Lys Ala Arg
 25 30 35 40
 atg gaa ttc atc ctg cgc cac ctg ccc gac tac cgc gac ccg ccc gac 196
 Met Glu Phe Ile Leu Arg His Leu Pro Asp Tyr Arg Asp Pro Pro Asp
 45 50 55
 ggc agt ggc cgc ctg gac cag ctg ctc tcc ctc tcc atg gtc tgg gcc 244
 Gly Ser Gly Arg Leu Asp Gln Leu Leu Ser Leu Ser Met Val Trp Ala
 60 65 70
 aac cat ctc ttc cta ggc tgc agt tac aat aaa gac ctt tta gac aag 292
 Asn His Leu Phe Leu Gly Cys Ser Tyr Asn Lys Asp Leu Leu Asp Lys
 75 80 85
 gtg atg gaa atg gcc gat ggg att gaa gtg gaa gac ctg cca caa ttt 340
 Val Met Glu Met Ala Asp Gly Ile Glu Val Glu Asp Leu Pro Gln Phe
 90 95 100
 act acc aga agt gaa tta atg aaa aag cat caa agc taaggcagaa 386
 Thr Thr Arg Ser Glu Leu Met Lys Lys Gln Ser
 105 110 115
 gatttatcac attttcatca tcagctacag gattagaaag gaggctggga tgaatgtgac 446
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<213> Homo sapiens

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<222> 78..566

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acaagacagc aagcagg atg gag cac tac cgg aaa gct ggc tct gta gag 110
Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu
1 5 10
ctc cca gcg cct tcc cca atg ccc cag cta cct cct gat acc ctt gag 158
Leu Pro Ala Pro Ser Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu
15 20 25
atg cgg gtc cga gat ggc agc aaa att cgc aac ctg ctg ggg ttg gct 206
Met Arg Val Arg Asp Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala
30 35 40
ctg ggt cgg ttg gag ggc ggc agt gct cgg cat gta gtg ttc tca ggt 254
Leu Gly Arg Leu Glu Gly Gly Ser Ala Arg His Val Val Phe Ser Gly
45 50 55
tct ggc agg gct gca gga aag gct gtc agc tgc gct gag att gtc aag 302
Ser Gly Arg Ala Ala Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys
60 65 70 75
cgg cgg gtc cca ggc ctg cac cag ctc acc aag cta cgt ttc ctt cag 350
Arg Arg Val Pro Gly Leu His Gln Leu Thr Lys Leu Arg Phe Leu Gln
80 85 90
act gag gac agc tgg gtc cca gcc tca cct gac aca ggg cta gac ccc 398
Thr Glu Asp Ser Trp Val Pro Ala Ser Pro Asp Thr Gly Leu Asp Pro
95 100 105
ctc aca gtg cgc cgc cat gtg cct gca gtg tgg gtg ctg ctc agc cgg 446
Leu Thr Val Arg Arg His Val Pro Ala Val Trp Val Leu Leu Ser Arg
110 115 120
gac ccc ctg gac ccc aat gag tgt ggt tac caa ccc cca gga gca ccc 494
Asp Pro Leu Asp Pro Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro
125 130 135
cct ggc ctg ggt tcc atg ccc agc tcc agc tgt ggc cct cgt tcc cga 542
Pro Gly Leu Gly Ser Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Arg
140 145 150 155
aga agg gct cga gac acc cga tgc tgaagacctg ctgagccagc ctgttctccg 596
Arg Arg Ala Arg Asp Thr Arg Ser
160
ggcctgaatg tctgggggtc ttgtgccttt tctgagaagc gttgtgactg ctcaacatcc 656
ccatcaaggt ttgagtcac aaaaaggagc ctccctatca tgcttccccct tccctctagc 716
atgtgggaaag ggactcgtgt gaagaatgac agatgtgggg cctctcgcaa gtctctgcat 776
gctaataaag ggcttccctt gccttctacc tacagtgcatt ttgaactgcc ttctgaaaga 836
ggtccaggga gggatttagg aaataaagtt tctacctatt taaaaaaaaa aaaaaaaa 894

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<210> 219
 <211> 910
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 16..705

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              1              5              10
agg gat tca ggt gtg gtg ccg gtg gga act gag gaa gcg ccc aag gtt      99
Arg Asp Ser Gly Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys Val
              15              20              25
ttc aag atg gca gca tct atg cat ggt cag ccc agt cct tct cta gaa      147
Phe Lys Met Ala Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu
              30              35              40
gat gca aaa ctc aga aga cca atg gtc ata gaa atc ata gaa aaa aat      195
Asp Ala Lys Leu Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn
              45              50              55              60
ttt gac tat ctt aga aaa gaa atg aca caa aat ata tat caa atg gcg      243
Phe Asp Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala
              65              70              75
aca ttt gga aca aca gct ggt ttc tct gga ata ttc tca aac ttc ctg      291
Thr Phe Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu
              80              85              90
ttc aga cgc tgc ttc aag gtt aaa cat gat gct ttg aag aca tat gca      339
Phe Arg Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala
              95              100              105
tca ttg gct aca ctt cca ttt ttg tct act gtt gtt act gac aag ctt      387
Ser Leu Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu
              110              115              120
ttt gta att gat gct ttg tat tca gat aat ata agc aag gaa aac tgt      435
Phe Val Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys
              125              130              135              140
gtt ttc aga agc tca ctg att ggc ata gtt tgt ggt gtt ttc tat ccc      483
Val Phe Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro
              145              150              155
agt tct ttg gct ttt act aaa aat gga cgc ctg gca acc aag tat cat      531
Ser Ser Leu Ala Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His
              160              165              170
acc gtt cca ctg cca cca aaa gga agg gtt tta atc cat tgg atg acg      579
Thr Val Pro Leu Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr
              175              180              185
ctt tgt caa aca caa atg aaa tta atg gcg att cct cta gtc ttt cag      627
Leu Cys Gln Thr Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln
              190              195              200
att atg ttt gga ata tta aat ggt cta tac cat tat gca gta ttt gaa      675
Ile Met Phe Gly Ile Leu Asn Gly Leu Tyr His Tyr Ala Val Phe Glu
              205              210              215              220
gag aca ctt gag aaa act ata cat gaa gag taacacaaaa aatgaatggt      725
Glu Thr Leu Glu Lys Thr Ile His Glu Glu
              225              230
tgctaaactta gcaaaatgaa gtttctataa agaggactca ggcattgctg aaagagttaa      785
aagtaactgt gaacaaataa tttgttctgt gccttttgcc tggatatag caaatactca      845
aaaaatattc aataattcaa tcaataaata taagtttcat cttacaccaa aaaaaaaaaa      905

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aaaaa 910

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<212> DNA
<213> Homo sapiens

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<222> 103..405

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gccagctcc gccgcgagc gctctgtgcc gcacgbhaca cc atg gag cgc ccg 114
Met Glu Arg Pro
1
gat aag gcg gcg ctg aac gca ctg cag cct cct gag ttc aga aat gaa 162
Asp Lys Ala Ala Leu Asn Ala Leu Gln Pro Pro Glu Phe Arg Asn Glu
5 10 15 20
agc tca tta gca tct aca ctg aag acg ctc ctg ttc ttc aca gct tta 210
Ser Ser Leu Ala Ser Thr Leu Lys Thr Leu Leu Phe Phe Thr Ala Leu
25 30 35
atg atc act gtt cct att ggg tta tat ttc aca act aaa tct tac ata 258
Met Ile Thr Val Pro Ile Gly Leu Tyr Phe Thr Thr Lys Ser Tyr Ile
40 45 50
ttt gaa ggc gcc ctt ggg atg tcc aat agg gac agc tat ttt tac gct 306
Phe Glu Gly Ala Leu Gly Met Ser Asn Arg Asp Ser Tyr Phe Tyr Ala
55 60 65
gct att gtt gca gtg gtc gcc gtc cat gtg gtg ctg gcc ctc ttt gtg 354
Ala Ile Val Ala Val Val Ala Val His Val Val Leu Ala Leu Phe Val
70 75 80
tat gtg gcc tgg aat gaa ggc tca cga cag tgb cgt gaa ggc aaa cag 402
Tyr Val Ala Trp Asn Glu Gly Ser Arg Gln Xaa Arg Glu Gly Lys Gln
85 90 95 100
gat taaagtgaac atcacctttt tatagcatta aattcatttt taaaaatgat 455
Asp
aatgctggag ggggccatct gatttgaata aagttgaaag aacatgtaaa aaaaaaaaaa 515
aaaa 519

<210> 221
<211> 632
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 72..350

<400> 221
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tgcaggcgcc c atg gat tcc ttg cgg aaa atg ctg atc tca gtc gca atg 110
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met
1 5 10
ctg ggc gca ggg gct ggc gtg ggc tac gcg ctc ctc gtt atc gtg acc 158
Leu Gly Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr
15 20 25
ccg gga gag cgg cgg aag cag gaa atg cta aag gag atg cca ctg cag 206
Pro Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln

30 35 40 45
 gac cca agg agc aga gag gag gcg gcc agg acc cag cag cta ttg ctg 254
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu
 50 55 60
 gcc act ctg cag gag gca gcg acc acg cag gag aac gtg gcc tgg agg 302
 Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg
 65 70 75
 aag aac tgg atg gtt ggc ggc gaa ggc gcc ggc ggc ggg agg tca ccg 350
 Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Gly Gly Arg Ser Pro
 80 85 90
 tgagaccgga cttgcctccg tgggcgcgg acccttgctt gggcgagga atccgaggca 410
 gctttctcc ttcgtgggc cagcggagag tccggaccga gataccatgc caggactctc 470
 cggggtcctg tgagctgcg tcgggtgagc acgtttcccc caaacctgg actgactgct 530
 ttaaggctcg caaggcgggc caggccgag acgcgagtcg gatgtggtga actgaaagaa 590
 ccaataaaat catgttctc cacccaaaaa aaaaaaaaaa aa 632

 <210> 222
 <211> 652
 <212> DNA
 <213> Homo sapiens

 <220>
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 <222> 38..436

 <400> 222
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 Met Gly His Gly Asp Glu
 1 5
 atc gtt ctt gcg gac ttg aac ttc ccg gcc tcc tcc atc tgc cag tgt 103
 Ile Val Leu Ala Asp Leu Asn Phe Pro Ala Ser Ser Ile Cys Gln Cys
 10 15 20
 ggg ccc atg gag atc cgt gca gac ggc ctg ggc atc ccg cag ctc ctg 151
 Gly Pro Met Glu Ile Arg Ala Asp Gly Leu Gly Ile Pro Gln Leu Leu
 25 30 35
 gag gcc gtg ctg aag ctg ctg ccc ctg gac acc tat gtg gag agt ccg 199
 Glu Ala Val Leu Lys Leu Leu Pro Leu Asp Thr Tyr Val Glu Ser Pro
 40 45 50
 gct gca gtc atg gag ctg gtg ccc agc gac aag gag agg ggc ctg cag 247
 Ala Ala Val Met Glu Leu Val Pro Ser Asp Lys Glu Arg Gly Leu Gln
 55 60 65 70
 acc cca gtg tgg acg gag tac gag tcc atc cta cgc agg gcc ggc tgt 295
 Thr Pro Val Trp Thr Glu Tyr Glu Ser Ile Leu Arg Arg Ala Gly Cys
 75 80 85
 gtg aga gcc ctg gca aag ata gag agg ttt gag ttt tat gaa cgg gct 343
 Val Arg Ala Leu Ala Lys Ile Glu Arg Phe Glu Phe Tyr Glu Arg Ala
 90 95 100
 aag aag gct ttt gct gtt gtg gca acg ggg gag acg gcc ctc tac gga 391
 Lys Lys Ala Leu Val Val Ala Thr Gly Glu Thr Ala Leu Tyr Gly
 105 110 115
 aac ctc atc ctc agg aag ggg gtg ctt gcc ctc aac ccc ctg ctg 436
 Asn Leu Ile Leu Arg Lys Gly Val Leu Ala Leu Asn Pro Leu Leu
 120 125 130
 taggcctggt gaagaccacc tgggcccggaa gaggaactgg gggcaccctg agctccagta 496
 ccaccactca caacaggcct cccagtgga gctcccagac ctggggccctg gccagggctc 556
 taggggcggc cagtcttggt gtgggcctg ccaattggga cgagtatccc tgattttgta 616
 aaatgatgga aaaacgttca aaaaaaaaaa aaaaaa 652

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Ser	Ser	Tyr	Cys	Lys	Arg	Gly	Asn	Gly	Tyr	Arg	Ser	Arg	Val	Pro	Lys	
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gaa	tgc	gaa	tgc	aac	tgg	ctt	cat	ctt	gaa	agc	gac	act	ctg	aag	aaa	375
Glu	Cys	Glu	Cys	Asn	Trp	Leu	His	Leu	Glu	Ser	Asp	Thr	Leu	Lys	Lys	
			45				50				55					
tta	ccc	ata	att	tct	ccc	tct	tgg	aca	tgc	aga	att	atc	ctg	ttc	ttg	423
Leu	Pro	Ile	Ile	Ser	Pro	Ser	Trp	Thr	Cys	Arg	Ile	Ile	Leu	Phe	Leu	
			60				65				70					
tat	ttt	tct	ggc	cag	ctt	ctc	caa	ctt	tcc	ctt	tct	tgt	ttg	caa	cta	471
Tyr	Phe	Ser	Gly	Gln	Leu	Leu	Gln	Leu	Ser	Leu	Ser	Cys	Leu	Gln	Leu	
			75			80				85				90		
att	aaa	ctt	taaggataaaa	aaaaaaaaaa	aa											502
Ile	Lys	Leu														

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 171..1670

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 tgagctctga ttcaagtgcc tgccctctgcc ccttggtggg ctgaagcttc atg gag 176
 Met Glu
 1

gta	tcc	acc	aac	ccc	tcc	tcc	aac	atc	gat	cca	ggc	aac	tat	gtt	gaa	224
Val	Ser	Thr	Asn	Pro	Ser	Ser	Asn	Ile	Asp	Pro	Gly	Asn	Tyr	Val	Glu	
			5				10				15					
atg	aat	gat	tca	atc	acc	cac	cta	ccc	tct	aaa	gtg	gtg	ata	caa	gat	272
Met	Asn	Asp	Ser	Ile	Thr	His	Leu	Pro	Ser	Lys	Val	Val	Ile	Gln	Asp	
			20				25				30					
att	act	atg	gag	cta	cac	tgc	cct	ctg	tgc	aat	gat	tgg	ttc	cga	gac	320
Ile	Thr	Met	Glu	Leu	His	Cys	Pro	Leu	Cys	Asn	Asp	Trp	Phe	Arg	Asp	
			35			40				45			50			
cca	ctg	atg	cta	agc	tgt	ggc	cac	aac	ttc	tgt	gaa	gcc	tgt	atc	caa	368
Pro	Leu	Met	Leu	Ser	Cys	Gly	His	Asn	Phe	Cys	Glu	Ala	Cys	Ile	Gln	
						55				60			65			
gac	ttt	tgg	agg	ctg	caa	gca	aag	gaa	aca	ttc	tgt	cct	gag	tgt	aag	416
Asp	Phe	Trp	Arg	Leu	Gln	Ala	Lys	Glu	Thr	Phe	Cys	Pro	Glu	Cys	Lys	
			70				75					80				
atg	cta	tgt	cag	tat	aac	aac	tgt	aca	ttc	aac	cct	gta	ctg	gac	aag	464
Met	Leu	Cys	Gln	Tyr	Asn	Asn	Cys	Thr	Phe	Asn	Pro	Val	Leu	Asp	Lys	
			85				90				95					
ttg	gta	gag	aag	att	aag	aag	tta	ccc	tta	ctc	aag	ggc	cat	cca	cag	512
Leu	Val	Glu	Lys	Ile	Lys	Lys	Leu	Pro	Leu	Leu	Lys	Gly	His	Pro	Gln	
			100				105				110					
tgc	cca	gag	cat	gga	gag	aac	ctg	aaa	ctg	ttc	agt	aaa	cca	gat	ggg	560
Cys	Pro	Glu	His	Gly	Glu	Asn	Leu	Lys	Leu	Phe	Ser	Lys	Pro	Asp	Gly	
			115			120				125			130			
aaa	ctg	atc	tgc	ttt	caa	tgc	aag	gat	gct	cgg	ttg	tct	gtg	ggg	cag	608
Lys	Leu	Ile	Cys	Phe	Gln	Cys	Lys	Asp	Ala	Arg	Leu	Ser	Val	Gly	Gln	
					135				140				145			
tct	aag	gag	ttc	ctg	caa	atc	tct	gat	gct	gtc	cat	ttc	ttc	atg	gag	656
Ser	Lys	Glu	Phe	Leu	Gln	Ile	Ser	Asp	Ala	Val	His	Phe	Phe	Met	Glu	

	150		155		160		
gag	ctt gcc atc caa	cag ggt caa	ctg gag aca act	ctg aag gag ctt	704		
Glu	Leu Ala Ile Gln	Gln Gly	Gln Leu Glu Thr	Thr Leu Lys Glu Leu			
	165		170				
cag	acc ctg agg aac atg	cag aag gaa gct att	gct gct cac aag gaa	752			
Gln	Thr Leu Arg Asn Met	Gln Lys Glu Ala	Ile Ala Ala His Lys Glu				
	180		185				
aac	aag cta cat ctg	cag caa cat	gtg tcc atg gag ttt	cta aag ctg	800		
Asn	Lys Leu His Leu	Gln Gln His Val	Ser Met Glu Phe	Leu Lys Leu			
	195		200				
cat	cag ttc ctg cac agc	aaa gaa aag gac att	tta act gag ctc	cgg	848		
His	Gln Phe Leu His	Ser Lys Glu Lys	Asp Ile Leu Thr	Glu Leu Arg			
	215		220				
gaa	gag ggg aaa gcc ttg	aat gag gag atg	gag ttg aat ctg	agc cag	896		
Glu	Glu Gly Lys Ala	Leu Asn Glu Met	Glu Leu Asn Leu	Ser Gln			
	230		235				
ctt	cag gag caa tgt	ctc tta gcc aag	gat atg ttg gtg	agc att cag	944		
Leu	Gln Glu Gln Cys	Leu Leu Ala Lys	Asp Met Leu Val	Ser Ile Gln			
	245		250				
gca	aag acg gaa caa	cag aac tcc ttc	gac ttt ctc aaa	gac atc aca	992		
Ala	Lys Thr Glu Gln	Gln Asn Ser Phe	Asp Phe Leu Lys	Asp Ile Thr			
	260		265				
act	ctc tta cat agc	ttg gag caa gga	atg aag gtg ctg	gca acc aga	1040		
Thr	Leu Leu His Ser	Leu Glu Gln Gly	Met Lys Val Leu	Ala Thr Arg			
	275		280				
gag	ctt att tcc aga	aag ctg aac ctg	ggc cag tac aaa	ggt cct atc	1088		
Glu	Leu Ile Ser Arg	Lys Leu Asn Leu	Gly Gln Tyr Lys	Gly Pro Ile			
	295		300				
cag	tac atg gta tgg	agg gaa atg	cag gac act ctc	tgc cca ggc	ctg	1136	
Gln	Thr Met Val Trp	Arg Glu Met	Gln Asp Thr Leu	Cys Pro Gly Leu			
	310		315				
tct	cca cta act ctg	gac cct aaa aca	gct cac cca aat	ctg gtg ctc	1184		
Ser	Pro Leu Thr Leu	Asp Pro Lys Thr	Ala His Pro Asn	Leu Val Leu			
	325		330				
tcc	aaa agc caa acc	agc gtc tgg cat	ggt gac att aag	aag ata atg	1232		
Ser	Lys Ser Gln Thr	Ser Val Trp His	Gly Asp Ile Lys	Lys Lys Ile Met			
	340		345				
cct	gat gat cct gag	agg ttt gac tca	agt gtg gct gta	ctg ggc tca	1280		
Pro	Asp Asp Pro Glu	Arg Phe Asp Ser	Ser Val Ala Val	Leu Gly Ser			
	355		360				
aga	ggc ttc acc tct	gga aag tgg tac	tgg gaa gta gaa	gta gca aag	1328		
Arg	Gly Phe Thr Ser	Gly Lys Trp Tyr	Trp Glu Val Glu	Val Ala Lys			
	375		380				
aag	aca aaa tgg aca	gtt gga gtt gtc	aga gaa tcc atc	att cgg aag	1376		
Lys	Thr Lys Trp Thr	Val Gly Val Val	Arg Glu Ser Ile	Ile Arg Lys			
	390		395				
ggc	agc tgt cct cta	act cct gag caa	gga ttc tgg ctt	tta aga cta	1424		
Gly	Ser Cys Pro Leu	Thr Pro Glu Gln	Gly Phe Trp Leu	Leu Arg Leu			
	405		410				
agg	aac caa act gat	cta aag gct ctg	gat ttg cct tct	ttc agt ctg	1472		
Arg	Asn Gln Thr Asp	Leu Lys Ala Lys	Pro Ser Phe Ser	Leu Leu			
	420		425				
aca	ctg act aac aac	ctc gag aag gtg	ggc ata tac ctg	gat tat gaa	1520		
Thr	Leu Thr Asn Asn	Leu Asp Lys Val	Gly Ile Tyr Leu	Asp Tyr Glu			
	435		440				
gga	gga cag ttg tcc	ttc tac aat gct	aaa acc atg act	cac att tac	1568		
Gly	Gly Gln Leu Ser	Phe Tyr Asn Ala	Lys Lys Thr Met	Thr His Ile Tyr			
	455		460				
				465			

acc ttc agt aac act ttc atg gag aaa ctt tat ccc tac ttc tgc ccc 1616
Thr Phe Ser Asn Thr Phe Met Glu Lys Leu Tyr Pro Tyr Phe Cys Pro
470 475 480
tgc ctt aat gat ggt aga gag aat aaa gaa cca ttg cac atc tta cat 1664
Cys Leu Asn Asp Gly Arg Glu Asn Lys Glu Pro Leu His Ile Leu His
485 490 495
cca cag taatgagtca taatattata caaattcaga gtgttattaa agagggtttg 1720
Pro Gln
500
aaataaaaaa aaaaaaaaaa 1739

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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 199..618

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aaaataagga atgaaatggt ttcttgatgat gattttttgt ttctcatctga taataatttt 180
atatatcaca gaaacagc atg gtt ctt act aaa cct ctt caa aga aat ggc 231
Met Val Leu Thr Lys Pro Leu Gln Arg Asn Gly
1 5 10
agc atg atg agc ttt gaa aat gtg aaa gaa aag agc aga gaa gga ggg 279
Ser Met Met Ser Phe Glu Asn Val Lys Glu Lys Ser Arg Glu Gly Gly
15 20 25
ccc cat gca cac aca ccc gaa gaa gaa ttg tgt ttc gtg gta aca cac 327
Pro His Ala His Thr Pro Glu Glu Glu Leu Cys Phe Val Val Thr His
30 35 40
tac cct cag gtt cag acc aca ctc aac ctg ttt ttc cat ata ttc aag 375
Tyr Pro Gln Val Gln Thr Thr Leu Asn Leu Phe Phe His Ile Phe Lys
45 50 55
gtt ctt act caa cca ctt tcc ctt ctg tgg ggt tgt gat cag aag cct 423
Val Leu Thr Gln Pro Leu Ser Leu Leu Trp Gly Cys Asp Gln Lys Pro
60 65 70 75
cgt act gtt cct acc ctt gga aac ggc gca tgg gat acc tgc caa caa 471
Arg Thr Val Pro Thr Leu Gly Asn Gly Ala Trp Asp Thr Cys Gln Gln
80 85 90
cac ata cgc act tca tca tgg aca gca aac aca ctc gtc att caa aac 519
His Ile Arg Thr Ser Ser Trp Thr Ala Asn Thr Leu Val Ile Gln Asn
95 100 105
cag cat tca cgg gaa agc act gtt tct gtt tgc ctt ttt atg tta atc 567
Gln His Ser Arg Glu Ser Thr Val Ser Val Cys Leu Phe Met Leu Ile
110 115 120
cgc atg caa cat att ttg aaa aca gat aca ctt caa cag ttc aga ata 615
Arg Met Gln His Ile Leu Lys Thr Asp Thr Leu Gln Gln Phe Arg Ile
125 130 135
tgc tagtactaat aaaaccaaca tgttaaaaaa aaaaaaaaaa 657
Cys
140

<210> 227
<211> 888
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 182..481

<400> 227

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agggcctatt ctctgcctc acagggaccg gccaggatct ctatccttac agcacgttgg 180
a atg tat atg ctc ctc tcc cca cat cgc ctt agg gag cag gca ggt gtc 229
Met Tyr Met Leu Leu Ser Pro His Arg Leu Arg Glu Gln Ala Gly Val
1 5 10 15
agg ggc agc ata agg acg gcc aac agg aca gaa gac ggg ttg aag atc 277
Arg Gly Ser Ile Arg Thr Ala Asn Arg Thr Glu Asp Gly Leu Lys Ile
20 25 30
cga gag gct gag tca ctt cca caa agt aac aca gct gat ttt aaa tgc 325
Arg Glu Ala Glu Ser Leu Pro Gln Ser Asn Thr Ala Asp Phe Lys Cys
35 40 45
ctg cat tca gca tcc ctg cag cag gct cca ggt gga att cta atg gga 373
Leu His Ser Ala Ser Leu Gln Gln Ala Pro Gly Gly Ile Leu Met Gly
50 55 60
cca gcc tcc agt ccc tgg acc tta gcc gtg gaa gga gag aag agg aca 421
Pro Ala Ser Ser Pro Trp Thr Leu Ala Val Glu Gly Glu Lys Arg Thr
65 70 75 80
tct gca cct cct ctc aga gaa agc ctg atg cct act aaa gga ctt ggg 469
Ser Ala Pro Pro Leu Arg Glu Ser Leu Met Pro Thr Lys Gly Leu Gly
85 90 95
tgg tgg acg cag tgacctcag tetggagctt gtctactgaa cattggagac 521
Trp Trp Thr Gln
100
tatcatttgc gcagatggtc ttgggcctct atgagcagca ggctgcaccc cacagtgacc 581
tcctcattct actctgaggc atcttcatga aagcagatgt ccattgaaaa gcacccaagt 641
gcagctctcag ctgatgaact teagaggcga ttgagacaaa ggctctcggt cccctctgcc 701
cttggatggt gcctctggta tgcacttggc ctctgtgtct ttatttagac tggctacttc 761
acaacccatc atgtcacccc acccctaacc gtgcccactc tgggtcctcc cctcaactgc 821
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aaaaaaaa 888

<210> 228

<211> 716

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 161..517

<400> 228

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caggggtgtg tgaccccggt ggttactgtg ctgcgtaga gcacctaggg cctgctgaag 120
ccctccctcg ccgcgcctc tccttagtcc ttgagatgag atg gca agt tac agc 175
Met Ala Ser Tyr Ser
1 5
ggc ttc tcc ggc ctg ctg gag att cgc tac ggg cca gga cac cgc agc 223
Gly Phe Ser Gly Leu Leu Glu Ile Arg Tyr Gly Pro Gly His Arg Ser
10 15 20
tgc ctt ccc caa ttc gct ttc ttt ccg cag ccg ccg ctg ccc cga ccc 271

Cys	Leu	Pro	Gln	Phe	Ala	Phe	Phe	Pro	Gln	Pro	Pro	Leu	Pro	Arg	Pro		
			25					30					35				
cgg	atc	tgc	atg	tgg	gtg	ctg	gct	gag	ctg	gag	cta	ggg	tgt	cct		319	
Arg	Ile	Cys	Met	Trp	Val	Leu	Ala	Glu	Leu	Leu	Glu	Leu	Gly	Cys	Pro		
			40					45				50					
gag	cag	agc	ctg	agg	gac	gcc	atc	acc	ctg	gac	ctc	ttc	tgc	cac	gcg	367	
Glu	Gln	Ser	Leu	Arg	Asp	Ala	Ile	Thr	Leu	Asp	Leu	Phe	Cys	His	Ala		
			55				60				65						
ctc	att	ttc	tgc	cgc	cag	cag	ggc	ttc	tca	ctg	gag	cag	acg	tca	gcg	415	
Leu	Ile	Phe	Cys	Arg	Gln	Gln	Gly	Phe	Ser	Leu	Glu	Gln	Thr	Ser	Ala		
			70			75				80				85			
gct	tgt	gcc	ctg	ctc	cag	gat	ctt	cac	aag	gct	tgt	att	ggt	gag	agg	463	
Ala	Cys	Ala	Leu	Leu	Gln	Asp	Leu	His	Lys	Ala	Cys	Ile	Gly	Glu	Arg		
			90						95				100				
ggg	cag	cta	cca	ggt	ttg	agc	ccc	agg	gag	aag	agg	aac	cgg	gcc	tgg	511	
Gly	Gln	Leu	Pro	Gly	Leu	Ser	Pro	Arg	Glu	Lys	Arg	Asn	Arg	Ala	Trp		
			105				110					115					
cac	aag	tgaccatggg	aagcagaagc	aggggatttc	tgctctggaat	atgctcattat										567	
His	Lys																
tagtagcatc	atcacacaca	agccatcagc	tttccaatcc	actgcttccct	tatctagaaa											627	
ttaaggatac	agcacacatt	ttacaggact	gttctgagaa	ataatatatg	caaatatatg											687	
catagtgcac	aataaaaaaaaa	aaaaaaaaaa														716	

<210> 229
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 86..505

<400> 229																	
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ccgggtgaatc	ctgccgctgg	cgtgg	atg	aga	agt	gaa	tgc	gtg	ctc	gga	gct					112	
			Met	Arg	Ser	Glu	Cys	Val	Leu	Gly	Ala						
			1				5										
gcg	agt	gac	agc	ggg	cag	gag	gcg	ccc	agg	gac	act	tgg	ttt	ctc	cag	160	
Ala	Ser	Asp	Ser	Gly	Gln	Glu	Ala	Pro	Arg	Asp	Thr	Trp	Phe	Leu	Gln		
			10			15				20				25			
ggc	tgg	aag	gct	tct	aga	agg	ttc	ctc	atc	aag	gga	agt	gtg	gct	ggg	208	
Gly	Trp	Lys	Ala	Ser	Arg	Arg	Phe	Leu	Ile	Lys	Gly	Ser	Val	Ala	Gly		
			30					35						40			
ggc	gcc	gtc	tac	ctg	gtg	tac	gac	cag	gag	ctg	ctg	ggg	ccc	agc	gac	256	
Gly	Ala	Val	Tyr	Leu	Val	Tyr	Asp	Gln	Glu	Leu	Leu	Gly	Pro	Ser	Asp		
			45					50					55				
aag	agc	cag	gca	gcc	cta	cag	aag	gct	ggg	gag	gtg	gtc	ccc	ccc	gcc	304	
Lys	Ser	Gln	Ala	Ala	Leu	Gln	Lys	Ala	Gly	Glu	Val	Val	Pro	Pro	Ala		
			60				65					70					
atg	tac	cag	ttc	agc	cag	tac	gtg	tgt	cag	cag	aca	ggc	ctg	cag	ata	352	
Met	Tyr	Gln	Phe	Ser	Gln	Tyr	Val	Cys	Gln	Gln	Thr	Gly	Leu	Gln	Ile		
			75				80				85						
ccc	cag	ctc	cca	gcc	cct	cca	aag	att	tac	ttt	ccc	atc	cgt	gac	tcc	400	
Pro	Gln	Leu	Pro	Ala	Pro	Pro	Lys	Ile	Tyr	Phe	Pro	Ile	Arg	Asp	Ser		
			90			95				100				105			
tgg	aat	gca	ggc	atc	atg	acg	gtg	atg	tca	gct	ctg	tcg	gtg	gcc	ccc	448	
Trp	Asn	Ala	Gly	Ile	Met	Thr	Val	Met	Ser	Ala	Leu	Ser	Val	Ala	Pro		
			110						115					120			

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tcc aag gcc cgc gag tac tcc aag gag ggc tgg gag tat gtg aag gcg      496
Ser Lys Ala Arg Glu Tyr Ser Lys Glu Gly Trp Glu Tyr Val Lys Ala
      125      130      135
cgc acc aag tagcgagtca gcagggggccg cctgccccgg ccagaacggg      545
Arg Thr Lys
      140
cagggtgcgc actgacctga agactccgga ctgggacccc actccgaggg cagctcccg      605
ccttgccggc ccaataaagg acttcagaag tcaaaaaaaaa aaaaaaaaaa      654

<210> 230
<211> 635
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 56..382

<400> 230
aattcgggtg gagctgagcc ggagacaggc agttgtgaaa aacttcagga caaaa atg      58
Met
      1
ttt cat tta agg act tgt gct gct aag ttg agg cca ttg acg gct tcc      106
Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala Ser
      5      10      15
cag act gtt aag aca ttt tca caa aac aga cca gca gca gct agg aca      154
Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg Thr
      20      25      30
ttt caa cag att cgg tgc tat tct gca cct gtt gct gct gag ccc ttt      202
Phe Gln Gln Ile Arg Cys Tyr Ser Ala Pro Val Ala Ala Glu Pro Phe
      35      40      45
ctc agt ggg act agt tgc aac tat gtg gag gag atg tac tgt gct tgg      250
Leu Ser Gly Thr Ser Ser Asn Tyr Val Glu Glu Met Tyr Cys Ala Trp
      50      55      60      65
ctg gaa aac ccc aaa agt gta cat aag aca ggg tcc cac tgt tgt cca      298
Leu Glu Asn Pro Lys Ser Val His Lys Thr Gly Ser His Cys Cys Pro
      70      75      80
ggc tgg agt gca gtg gcg gga tct cgg ctt gct gca acc tcc gac tcc      346
Gly Trp Ser Ala Val Ala Gly Ser Arg Leu Ala Ala Thr Ser Asp Ser
      85      90      95
tgg gtt caa gtg att ctt atg cct cag cct ccc gag taactgggac      392
Trp Val Gln Val Ile Leu Met Pro Gln Pro Pro Glu
      100      105
tacagggtgca cgtcaccacg cctgactagt ttttgtat tttagtagaga tgggatttta      452
ctttgttgcc caggctgggc ttgaaccctt ggccctcaagt gatccaccca ccttgccctc      512
ccaaagtgcct gggattacag gtatgatcaa ccacgcctgg ccatgtcatg ccttgtagaca      572
gaattccttt attctgtttt gagccaataa atatttatag gtttcgaaaa aaaaaaaaaa      632
aaa      635

<210> 231
<211> 634
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 56..355

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Met
1
ttt cat tta agg act tgt gct gct aag ttg agg cca ttg acg gct tcc 106
Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala Ser
5 10 15
cag act gtt aag aca ttt tca caa aac aga cca gca gca gct agg aca 154
Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg Thr
20 25 30
ttt caa cag att cgt gct att ctg cac ctg ttg ctg ctg agc cct ttc 202
Phe Gln Gln Ile Arg Ala Ile Leu His Leu Leu Leu Leu Ser Pro Phe
35 40 45
tca gtg gga cta gtt cga act atg tgg agg aga tgt act gtg ctt ggc 250
Ser Val Gly Leu Val Arg Thr Met Trp Arg Arg Cys Thr Val Leu Gly
50 55 60 65
tgg aaa acc cca aaa gtg tac ata aga cag ggt ccc act gtt gtc cag 298
Trp Lys Thr Pro Lys Val Tyr Ile Arg Gln Gly Pro Thr Val Val Gln
70 75 80
gct gga gtg cag tgg cgg gat ctc ggc ttg ctg caa cct ccg act cct 346
Ala Gly Val Gln Trp Arg Asp Leu Gly Leu Leu Gln Pro Pro Thr Pro
85 90 95
ggg ttc aag tgattcttat gcctcagcct cccgagtaac tgggactaca 395
Gly Phe Lys
100
ggtgcacgtc accacgcctg actagttttt gtatttttag tagagatggg attttacttt 455
gttggccagg ctggctctga acccctggcc tcaagtgatc caccocctt ggccctccaa 515
agtgtcggga ttacaggtat gatcaaccac gcctggccat gtcatgcctt gtgacagaat 575
tcctttattc tgttttgagc caataaatat ttataggttt cgaaaaaaaa aaaaaaaaaa 634

<210> 232
<211> 583
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 76..498

<400> 232
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tcgagattgc gggct atg gcg ccg aag gtt ttt cgt cag tac tgg gat atc 111
Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile
1 5 10
ccc gat ggc acc gat tgc cac cgc aaa gcc tac agc acc acc agt att 159
Pro Asp Gly Thr Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile
15 20 25
gcc agc gtc gct ggc ctg acc gcc gct gcc tac aga gtc aca ctc aat 207
Ala Ser Val Ala Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn
30 35 40
cct ccg ggc acc ttc ett gaa gga gtg gct aag gtt gga caa tac acg 255
Pro Pro Gly Thr Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr
45 50 55 60
ttc act gca gct gct gtc ggg gcc gtg ttt ggc ctc acc acc tgc atc 303
Phe Thr Ala Ala Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile
65 70 75
agc gcc cat gtc cgc gag aag ccc gac gac ccc ctg aac tac ttc ctc 351
Ser Ala His Val Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu

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      80              85              90
ggg ggc tgc gcc gga ggc ctg act ctg gga gca cgc acg cac aac tac      399
Gly Gly Cys Ala Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr
      95              100              105
ggg att ggc gcc gcc gcc tgc gtg tac ttt ggc ata gcg gcc tcc ctg      447
Gly Ile Gly Ala Ala Cys Val Tyr Phe Gly Ile Ala Ala Ser Leu
      110              115              120
gtc aag atg ggc cgg ctg gag ggc tgg gag gtg ttt gca aaa ccc aag      495
Val Iys Met Gly Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys
      125              130              135              140
gtg tgagccctgt gctgccggg acctccagcc tgcagaatgc gtccagaaat      548
Val
aaattctgtg tctgtgtgaa aaaaaaaaaa aaaaa      583

<210> 233
<211> 753
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 199..600

<400> 233
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ggcctctcca ggccctgaag gcttctctgg gctgatgcga gctggggaac gggagggacg      120
gacgtgggag cgagaacgtc acactggagg cagctgggtg cagcatgggg gacagagtga      180
aagagccttc gtgtcacc atg gcc aca cac ccc gat ggc ttc cgg ctt gag      231
      Met Ala Thr His Pro Asp Gly Phe Arg Leu Glu
      1              5              10
gga ccc ctg gct gca gcc cac agc cct ggg cct tgc act gtg ctc tac      279
Gly Pro Leu Ala Ala Ala His Ser Pro Gly Pro Cys Thr Val Leu Tyr
      15              20              25
gaa ggc cct gtc cgt ggg ctc tgc ccy ttt gcc ccg cga aat tcc aac      327
Glu Gly Pro Val Arg Gly Leu Cys Pro Phe Ala Pro Arg Asn Ser Asn
      30              35              40
acc atg gcg gcg gct gcc ctg gct gcc ccc agc ctg ggc ttc gat ggg      375
Thr Met Ala Ala Ala Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly
      45              50              55
gtg att ggg gtg ctc gtg gct gat acc agc ctc acg gac atg cac gtg      423
Val Ile Gly Val Leu Val Ala Asp Thr Ser Thr Asp Met His Val
      60              65              70              75
gtg gat gta gag ctg agc gga ccc cgg ggc ccc act ggc cga agc ttt      471
Val Asp Val Glu Leu Ser Gly Pro Arg Gly Pro Thr Gly Arg Ser Phe
      80              85              90
gct gtg cac acc cgc aga gag aac cct gcc gag cca ggc gcg gtc acc      519
Ala Val His Thr Arg Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr
      95              100              105
ggc tcc gcc acc gtc acg gcc ttc tgg cgg agc ctc ctg gcc tgc tgc      567
Gly Ser Ala Thr Val Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys
      110              115              120
cag ctc ccc tcc agg ccg ggg atc cat ctc tgc tgagaagcct cctccctccc      620
Gln Leu Pro Ser Arg Pro Gly Ile His Leu Cys
      125              130
gagacaaagt catctgacct gacctcacc accaccatcc caccctgcc ctgccccact      680
tccccagggt ctcccttctg actcagtaaa gatcaccgct gcctccccc gcaataaaaa      740
aaaaaaaaa aaa      753

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<210> 234
 <211> 762
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 211..612

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cctctccagg cctcgaaggc ttctcctggg ctgatgcgag ctgggggaacg ggaggggacgg      120
acgtggggagc gagaacgtca cactggaggc agctgggtggc acgatggggg acagagtgaa      180
aggttagcaag tcaagagcct tegtgtcacc atg gcc aca cac ccc gat ggc ttc      234
                               Met Ala Thr His Pro Asp Gly Phe
                               1                               5

cgg ctt gag gga ccc ctg gct gca gcg cac agc cct ggg cct tgc act      282
Arg Leu Glu Gly Pro Leu Ala Ala Ala His Ser Pro Gly Pro Cys Thr
10                               15                               20

gtg ctc tac gaa ggc cct gtc cgt ggg ctc tgc ccc ttt gcc ccg cga      330
Val Leu Tyr Glu Gly Pro Val Arg Gly Leu Cys Pro Phe Ala Pro Arg
25                               30                               35                               40

aat tcc aac acc atg tcg gcg gct gcc ctg gct gcc ccc agc ctg ggc      378
Asn Ser Asn Thr Met Ser Ala Ala Ala Leu Ala Ala Pro Ser Leu Gly
45                               50                               55

ttc gat ggg gtg att ggg gtg ctc gtg gct gat acc agc ctc acg gac      426
Phe Asp Gly Val Ile Gly Val Leu Val Ala Asp Thr Ser Leu Thr Asp
60                               65                               70

atg cac gtg gtg gat gta gag ctg agc gga ccc cgg ggc ccc acg tgc      474
Met His Val Val Asp Val Glu Leu Ser Gly Pro Arg Gly Pro Thr Cys
75                               80                               85

cga agc ttt gct gtg cac acc cgc aga gag aac cct gcc gag cca ggc      522
Arg Ser Phe Ala Val His Thr Arg Arg Glu Asn Pro Ala Glu Pro Gly
90                               95                               100

gcg gtc acc ggc tcc gcc acc gtc acg gcc ttc tgg cgg agc ctc ctg      570
Ala Val Thr Gly Ser Ala Thr Val Thr Ala Phe Trp Arg Ser Leu Leu
105                               110                               115                               120

gcc tgc tgc cag ctc ccc tcc agg ccg ggg atc cat ctc tgc      612
Ala Cys Cys Gln Leu Pro Ser Arg Pro Gly Ile His Leu Cys
125                               130

tgagaagcct cctccctcc gagacaagat catctgcctg gcctctcacc accaccatcc      672
caccctcgcc ctgccccact tocccagggt ctcccttctg actcagtaaa gatcaccggc      732
gcctcccccc gccaaaaaaa aaaaaaaaaa      762

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<210> 235
 <211> 537
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 5..259

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<400> 235
aaaa atg cta aag gta gaa gca act ggt agt ccc gag gaa ggg tgg gcg      49
Met Leu Lys Val Glu Ala Thr Gly Ser Pro Glu Glu Gly Trp Ala
1                               5                               10                               15

ggt gga gag ccc cgg act gga gct cct gcg aac tcc cct tcc tgc cct      97

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Gly	Gly	Glu	Pro	Arg	Thr	Gly	Ala	Pro	Ala	Asn	Ser	Pro	Ser	Cys	Pro	
				20					25					30		
cag	gag	atg	cca	ctg	cag	gac	cca	agg	agc	agg	gag	gag	gag	gag	gag	145
Gln	Glu	Met	Pro	Leu	Gln	Asp	Pro	Arg	Ser	Arg	Glu	Glu	Ala	Ala	Arg	
			35				40						45			
acc	cag	cag	cta	ttg	ctg	gcc	act	ctg	cag	gag	gca	gag	acc	acc	cag	193
Thr	Gln	Gln	Leu	Leu	Leu	Ala	Thr	Leu	Gln	Glu	Ala	Ala	Thr	Thr	Gln	
			50				55					60				
gag	aac	gtg	gcc	tgg	agg	aag	aac	tgg	atg	gtt	ggc	ggc	gaa	ggc	ggc	241
Glu	Asn	Val	Ala	Trp	Arg	Lys	Asn	Trp	Met	Val	Gly	Gly	Glu	Gly	Gly	
		65				70					75					
gcc	agc	ggg	agg	tca	ccg	tgagaccgga	cttgccctccg	tgggcgccgg								289
Ala	Ser	Gly	Arg	Ser	Pro											
		80			85											
accttggett	ggcgcgagga	atccgaggca	gcctttctcc	ttcgtgggcc	cagcggagag											349
tccggaccga	gataccatgc	caggactctc	cggggtctctg	tgagctgccg	tccgggtgagc											409
acgtttcccc	caaacctcgg	actgactgct	ttaagggtccg	caaggcgggc	caggggcgag											469
acgcgagtcg	gatgtggtga	actgaaaaga	ccaataaaat	catgttctctc	caaaaaaaa											529
aaaaaaaa																537

<210> 236
 <211> 994
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 23..370

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	Met Gly Arg Pro Trp Met Val Met Ile Leu
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gag tca aaa tct ctc ttc ttt cat gtc cct gct gga tta ctg gcc ctc	100
Glu Ser Lys Ser Glu Glu Lys Met Trp Tyr Gly Val Phe Leu Trp Ala	
	15 20 25
ctg gtg tct tct ctc ttc ttt cat gtc cct gct gga tta ctg gcc ctc	148
Leu Val Ser Ser Leu Phe Phe His Val Pro Ala Gly Leu Leu Ala Leu	
	30 35 40
ttc acc ctc aga cat cac aaa tat ggt agg ttc atg tct gta agc atc	196
Phe Thr Leu Arg His His Lys Tyr Gly Arg Phe Met Ser Val Ser Ile	
	45 50 55
ctg ttg atg ggc atc gtg gga cca att act gct gga atc ttg aca agt	244
Leu Leu Met Gly Ile Val Gly Pro Ile Thr Ala Gly Ile Leu Thr Ser	
	60 65 70
gca gct att gct gga gtt tac cga gca gca ggg aag gaa atg ata cca	292
Ala Ala Ile Ala Gly Val Tyr Arg Ala Ala Gly Lys Glu Met Ile Pro	
	75 80 85 90
ttt gaa gcc ctc aca ctg ggc act gga cag aca ttt tgc gtc ttg gtg	340
Phe Glu Ala Leu Thr Leu Gly Thr Gly Gln Thr Phe Cys Val Leu Val	
	95 100 105
gtc tcc ttt tta cgg att tta gct act cta tagcatatcat ccttatgctg	390
Val Ser Phe Leu Arg Ile Leu Ala Thr Leu	
	110 115
agatgttgaa	cttaaacctt
	atggaatcct
	ccaaaagaat
	acattatgga
	gtgtagtgtt
ttcttagtgc	ttcacaaggga
	agcaacttgg
	atgaacagga
	acatgaagga
	caacacatct
cagccttttc	ttcattttga
	agctcctaga
	attgaagact
	tatgtggact
	cctattgttc
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	ggctttcttt
	ttttagata
	tttaatttaa
	gcagttttca

Leu	Gly	Asp	His	Gly	Trp	Glu	Leu	Ser	Leu	Glu	Glu	Asp	Ala	Gln	
1				5				10					15		
ctg	tgg	ggg	ggg	gtg	gtg	aag	agt	tgt	ttt	gag	gga	aaa	ggc	cca	95
Leu	Trp	Gly	Gly	Val	Val	Lys	Ser	Cys	Phe	Glu	Gly	Lys	Gly	Pro	Gln
				20				25					30		
aga	gaa	gcc	caa	cca	gcc	agc	ccc	cag	gcc	gcc	ccg	cca	gga	ccc	143
Arg	Glu	Ala	Gln	Pro	Ala	Ser	Pro	Gln	Ala	Ala	Pro	Pro	Gly	Pro	Thr
			35				40					45			
aat	gag	gca	cag	atg	gca	gcc	gct	gcc	gcc	cta	gcc	cgg	ctg	gag	191
Asn	Glu	Ala	Gln	Met	Ala	Ala	Ala	Ala	Ala	Leu	Ala	Arg	Leu	Glu	Gln
			50				55					60			
aag	cag	tcc	cgg	gcc	tgg	ggc	ccc	aca	tcg	cag	gac	acc	atc	cga	239
Lys	Gln	Ser	Arg	Ala	Trp	Gly	Pro	Thr	Ser	Gln	Asp	Thr	Ile	Arg	Asn
			65				70				75				
cag	gtg	aga	aag	gaa	ctt	caa	gcc	gaa	gcc	acc	gtc	agc	ggg	agc	ccc
Gln	Val	Arg	Lys	Glu	Leu	Gln	Ala	Glu	Ala	Thr	Val	Ser	Gly	Ser	Pro
				80			85				90			95	
gag	gcc	cca	ggg	acc	aac	gtg	gta	tct	gag	ccc	aga	gag	gaa	ggc	335
Glu	Ala	Pro	Gly	Thr	Asn	Val	Val	Ser	Glu	Pro	Arg	Glu	Glu	Gly	Ser
				100						105			110		
gcc	cac	ctg	gct	gtg	cct	ggc	gtg	tac	ttc	acc	tgt	ccg	ctc	act	383
Ala	His	Leu	Ala	Val	Pro	Gly	Val	Tyr	Phe	Thr	Cys	Pro	Leu	Thr	Gly
				115				120					125		
gcc	acc	ctg	agg	aag	gac	cag	cgg	gac	gcc	tgc	atc	aag	gag	gcc	431
Ala	Thr	Leu	Arg	Lys	Asp	Gln	Arg	Asp	Ala	Cys	Ile	Lys	Glu	Ala	Ile
				130				135					140		
ctc	ttg	cac	ttc	tcc	acc	gac	cca	gtg	gcc	gcc	tcc	atc	atg	aag	479
Leu	Leu	His	Phe	Ser	Thr	Asp	Pro	Val	Ala	Ala	Ser	Ile	Met	Lys	Ile
							145				150				
tac	acg	ttc	aac	aaa	gac	cag	gac	cgg	gtg	aag	ctg	ggg	gtg	gac	527
Tyr	Thr	Phe	Asn	Lys	Asp	Gln	Asp	Arg	Val	Lys	Leu	Gly	Val	Asp	Thr
				160				165			170			175	
att	gcc	aag	tac	ctg	gac	aac	atc	cac	ctg	cac	ccc	gag	gag	gag	575
Ile	Ala	Lys	Tyr	Leu	Asp	Asn	Ile	His	Leu	His	Pro	Glu	Glu	Glu	Lys
							180			185			190		
tac	cgg	aag	atc	aag	ctg	cag	aac	aag	gtg	ttt	cag	gag	cgc	att	aac
Tyr	Arg	Lys	Ile	Lys	Leu	Gln	Asn	Lys	Val	Phe	Gln	Glu	Arg	Ile	Asn
				195				200					205		
tgc	ctg	gaa	ggg	acc	cac	gag	ttt	ttt	gag	gcc	att	ggg	ttc	cag	671
Cys	Leu	Glu	Gly	Thr	His	Glu	Phe	Phe	Glu	Ala	Ile	Gly	Phe	Gln	Lys
				210				215				220			
gtg	ttg	ctt	ccc	gcc	cag	gat	cag	gag	gac	ccc	gag	gag	ttc	tac	719
Val	Leu	Leu	Pro	Ala	Gln	Asp	Gln	Glu	Asp	Pro	Glu	Glu	Phe	Tyr	Val
				225				230							
ctg	agc	gag	acc	acc	ttg	gcc	cag	ccc	cag	agc	ctg	gag	agg	cac	767
Leu	Ser	Glu	Thr	Thr	Leu	Ala	Gln	Pro	Gln	Ser	Leu	Glu	Arg	His	Lys
				240			245			250				255	
gaa	cag	ctg	ctg	gct	gcg	gag	ccc	gtg	cgc	gcc	aag	ctg	gac	agg	815
Glu	Ala	Leu	Leu	Ala	Ala	Glu	Pro	Val	Arg	Ala	Lys	Leu	Asp	Arg	Gln
				260				265					270		
cgc	cgc	gtc	ttc	cag	ccc	tcg	ccc	ctg	gcc	tcg	cag	ttc	gaa	ctg	863
Arg	Arg	Val	Phe	Gln	Pro	Ser	Pro	Leu	Ala	Ser	Gln	Phe	Glu	Leu	Pro
				275				280					285		
ggg	gac	ttc	ttc	aac	ctc	aca	gca	gag	gag	atc	aag	cgg	gag	cag	911
Gly	Asp	Phe	Phe	Asn	Leu	Thr	Ala	Glu	Glu	Ile	Lys	Arg	Glu	Gln	Arg
				290			295					300			
ctc	agg	tcc	gag	gcg	gtg	gag	cgg	ctg	agc	gtg	ctg	cgg	acc	aag	959
Leu	Arg	Ser	Glu	Ala	Val	Glu	Arg	Leu	Ser	Val	Leu	Arg	Thr	Lys	Ala

Arg Lys Met Glu Gly Leu Leu Ala Gly Leu Ser Ser Ser Pro Arg Lys
 35 40 45
 tca tgc tgg ccc ttt tgg gtc cat ggg cca aag gtt cat gaa ggt ggc 612
 Ser Cys Trp Pro Phe Trp Val His Gly Pro Lys Val His Glu Gly Gly
 50 55 60
 tct gcc tgt gag aca tca agc tcc tgg gtt gaa gga ctt gga tta aga 660
 Ser Ala Cys Glu Thr Ser Ser Ser Trp Val Glu Gly Leu Gly Leu Arg
 65 70 75 80
 aga gtg aca tca gtg cac agt tta tgc caa ggg ctt ggg gcc tca gtc 708
 Arg Val Thr Ser Val His Ser Leu Cys Gln Gly Leu Gly Ala Ser Val
 85 90 95
 cag ctt ctt cct gga cca cca cca aca acc agt gat aaa aat aat 756
 Gln Leu Leu Pro Gly Pro Pro Pro Thr Thr Thr Ser Asp Lys Asn Asn
 100 105 110
 tat act agt ggc tgacatttat ggattcttcc tacacactag gctataccac 808
 Tyr Thr Ser Gly
 115
 agcgagtgcc tcgaaggaa atatagtata gcactgtgcc gtccaacatg gcggccacta 868
 gccacatgca ctactgagca cttgaaatgt ggctagccca cattgagatg tgctgtaaata 928
 aaagaataga caccagattt ccaagactta gtaccaaaaa aagaatgtaa aatttctcat 988
 taacaatttt ttttcttaca tttattacat gttaacatga cgctatttgg agtttaataa 1048
 aatgcattat taaaattcaa aaaaaaaaaa aaaaa 1083

 <210> 240
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 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 78..590

 <400> 240
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 cgcgcctccc tccccgc atg cag ccc gcc gag cgc tcg cgg gtc ccc agg 110
 Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg
 1 5 10
 atc gac ccg tac gga ttc gag cgg cct gag gac ttc gac gac gcc gcc 158
 Ile Asp Pro Tyr Gly Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Ala
 15 20 25
 tac gag aag ttt ttc tcc agc tac ctg gtc acg ctc acc cgc agg gcg 206
 Tyr Glu Lys Phe Phe Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala
 30 35 40
 atc aaa tgg tcc cgg ctg ctg cag gcc ggg gcc gtc ccc agg agc cgg 254
 Ile Lys Trp Ser Arg Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg
 45 50 55
 aca gtg aag cgc tat gtc cgg aaa ggg gtc ccg ctg gag cac cgt gcc 302
 Thr Val Lys Arg Tyr Val Arg Lys Gly Val Pro Leu Glu His Arg Ala
 60 65 70 75
 cgc gtc tgg atg gtg ctg agt ggg gcc cag gcg cag atg gac cag aat 350
 Arg Val Trp Met Val Leu Ser Gly Ala Gln Ala Gln Met Asp Gln Asn
 80 85 90
 ccc gcc tac tac cac cag ctt ctc cag gga gag aga aac ccc agg ctg 398
 Pro Gly Tyr Tyr His Gln Leu Leu Gln Gly Glu Arg Asn Pro Arg Leu
 95 100 105
 gag gac gcc atc agg aca gac ctg aac cgg acc ttc ccc gac aac gtg 446
 Glu Asp Ala Ile Arg Thr Asp Leu Asn Arg Thr Phe Pro Asp Asn Val
 110 115 120

aag ttc cgg aag acc acg gac ccc tgc tta cag agg acc ctg tac aat	494
Lys Phe Arg Lys Thr Thr Asp Pro Cys Leu Gln Arg Thr Leu Tyr Asn	
125 130 135	
gtg ctg ctg gca tat ggg cac cat aac cag gga gtg ggc tac tgc cag	542
Val Leu Leu Ala Tyr Gly His His Asn Gln Gly Val Gly Tyr Cys Gln	
140 145 150 155	
gga atg aat ttt ata gca gga tat ctg att ctt ata aca aat aat gaa	590
Gly Met Asn Phe Ile Ala Gly Tyr Leu Ile Leu Ile Thr Asn Asn Glu	
160 165 170	
taagaatctt tttggctgtt agatgctctt gttggaagaa tactaccaga ttactacagc	650
ccggccatgc tgggcctgaa gaccgaccag gaggtcctcg gggagctggt gcgggcgaag	710
ctgcggcgctg tgggggcccct gatggagcgt ctcggtgtgc tgtggacgct gctggtgtcc	770
cgctgggttca tctgcctgtt tgtggacatc ttgcccgctgg agacagtgct tcggatctgg	830
gactgtttgt ttaacgaagg ctccaagatt atcttcctgg tggccctgac cttaatgaag	890
cagcaccagg agttgatttt ggaagccacc agcgttccag acattttcga taagtttaag	950
cagataacca aagggagttt cgtgatggag tgtcacacgt ttatgcaggt gtgtggggct	1010
gcacgtggct cagtcctctc ccagggggcc ccgectcacc tgcagcccg gggctgctct	1070
gaccaccggg aggatgcaca ggaatgggcac cagtgggcat agggcacagg atgagctctc	1130
agctctgttc tgcattctgcc cctcgcgcct ggccctccag ggctttcctg tctatggcgg	1190
ccctgtcttc ttggccctgg cactgeggac gctgctcctg gtccctaatgg ctgtactcat	1250
ctgtgtgtgt tggtgccaga agtgtggctt cccgaggccc ggccctccca ctgggtcctg	1310
gacctggcgc agggccgtata gactcaggtc ctgatgaggg cgttgaggga gctgtacctg	1370
acaggccttc tgagggaagcc aaagacgccag gagaggctca ggctggggag tcagtagttt	1430
ctcaagagg agtggagggt cggggccact ctgggtgcag catggcaaac gtggggcgga	1490
tttcagcagg tgggccttca tcaagagaa gacctgttg gccggggcgcg ttggctcacg	1550
ctcgcagtc cagcactttg ggaggccaag cgtgtgggat cacttgaggt caggagtcca	1610
agaccagcct ggccaacacg gtgaaacccc gtctctacta aaaaatacaa aaattagcca	1670
ggtgtgtgtg ctacagctta tgtagtccca gttactcggg aggcctgaggc acgagaatca	1730
cttgaacctg ggaggcgag gttgcagtga gccgagatcg gccactcgca ctccagcctg	1790
ggcaacagag tgagactctg tctcaaaaaa aaaaaaaaaa a	1831

<210> 241
 <211> 1830
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 78..608

<400> 241
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 cgcgcctccc tccccgc atg cag ccc gcc gag cgc tcg cgg gtc ccc agg 110
 Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg
 1 5 10
 atc gac ccg tac gga ttc gag cgg cct gag gac ttc gac gac gcc gcc 158
 Ile Asp Pro Tyr Gly Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Ala
 15 20 25
 tac gag aag ttt ttc tcc agc tac ctg gtc acg ctc acc cgc agg gcg 206
 Tyr Glu Lys Phe Phe Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala
 30 35 40
 atc aaa tgg tcc cgg ctg ctg cag ggc ggg ggc gtc ccc agg agc cgg 254
 Ile Lys Trp Ser Arg Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg
 45 50 55
 aca gtg aag cgc tat gtc cgg aaa ggg gtc cgc ctg gag cac cgt gcc 302
 Thr Val Lys Arg Tyr Val Arg Lys Gly Val Pro Leu Glu His Arg Ala
 60 65 70 75
 cgc gtc tgg atg gtg ctg agt ggg gcc cag gcg cag atg gac cag aat 350

Arg	Val	Trp	Met	Val	Leu	Ser	Gly	Ala	Gln	Ala	Gln	Met	Asp	Gln	Asn				
																80	85	90	
ccc	ggc	tac	tac	cac	cag	ctt	ctc	cag	gga	gag	aga	aac	ccc	agg	ctg	398			
Pro	Gly	Tyr	Tyr	His	Gln	Leu	Leu	Gln	Gly	Glu	Arg	Asn	Pro	Arg	Leu				
																95	100	105	
gag	gac	gcc	atc	agg	aca	gac	ctg	aac	cgg	acc	ttc	ccc	gac	aac	gtg	446			
Glu	Asp	Ala	Ile	Arg	Thr	Asp	Leu	Asn	Arg	Thr	Phe	Pro	Asp	Asn	Val				
																110	115	120	
aag	ttc	cgg	aag	acc	acg	gac	ccc	tgc	tta	cag	agg	acc	ctg	tac	aat	494			
Lys	Phe	Arg	Lys	Thr	Thr	Asp	Pro	Cys	Leu	Gln	Arg	Thr	Leu	Tyr	Asn				
																125	130	135	
gtg	ctg	ctg	gca	tat	ggg	cac	cat	aac	cag	gga	gtg	ggc	tac	tgc	cag	542			
Val	Leu	Leu	Ala	Tyr	Gly	His	His	Asn	Gln	Gly	Val	Gly	Tyr	Cys	Gln				
																140	145	150	155
gga	atg	aat	ttt	ata	gca	gga	tat	ctg	att	ctt	ata	aca	aat	aat	gat	590			
Gly	Met	Asn	Phe	Ile	Ala	Gly	Tyr	Leu	Ile	Leu	Ile	Thr	Asn	Asn	Asp				
																160	165	170	
aag	aat	ctt	ttt	ggc	tgt	tagatgctct	tgttggaaga	atactaccag								638			
Lys	Asn	Leu	Phe	Gly	Cys														
																175			
attactacag	cccgcccatg	ctggggcctga	agaccgacca	ggaggctcctc	ggggagctgg	698													
tgccggcgaa	gctgccggct	gtggggggccc	tgatggagcg	tctcggtgtg	ctgtggacgc	758													
tgctgggtgc	ccgctgggttc	atctgectgt	ttgtggacat	cttgcccggtg	gagacagtgc	818													
ttcggtatctg	ggactgtttg	tttaacgaag	gctcgaagat	tatcttccgg	ttggccctga	878													
ccttaattaa	gcagaccacg	gagttgat	ttggaagccac	cagcggtcca	gacatttgcg	938													
ataagtttaa	gcagataacc	aaaggagatt	tcgtgatgga	gtgtcacacg	tttatgcag	998													
tgtgtggggc	tgacgtggc	tcagtccct	cccagggggc	ccgcctcac	ctgcagccg	1058													
ggggctgctc	tgaccaccg	gaggatgcac	aggatgggca	ccagtgggca	tagggcacag	1118													
gatgagcctc	cagctctgtc	ctgcattctgc	cccctgcgcc	tgccctccga	gggctttctg	1178													
gtctatggcg	gccctgtctt	cttggccctg	gcactgcgga	cgtctgctct	ggtcctaatg	1238													
gctgtactca	tctgctgtgt	gtgggtccag	aagtgtggct	tcccagggcc	cggcctcccc	1298													
actgggtcct	ggaccctggc	caggccgtat	agactcaggt	cctgatgagg	gcgttgtggg	1358													
agctgtacct	gcagagcctt	ctgagggaagc	caagacgcc	ggagaggctc	aggcctggga	1418													
gtcagtagtt	tcctaagagg	gagtgaggc	tcggggccac	tctgggtgca	gcattggcaaa	1478													
cgtggggcgt	atttcagcag	ctgggccttc	atcaaaagaga	agaccatggt	ggccggggcg	1538													
gggtggctcac	gcctgcagtc	ccagcacttt	gggaggccaa	ggcgtgtgga	tcacctgagg	1598													
tcaggagttc	aagaccagcc	tggccaacac	gggtaaaccc	cgtctctact	aaaaaataca	1658													
aaaattagcc	aggtgtgggt	gctcacgcct	atgtagtccc	agttactcgg	gaggctgagg	1718													
cacgagaatc	acttgaacct	gggaggcgga	ggttcagtg	agccgagatc	gcgcactcgc	1778													
actccagcct	gggcaacaga	gtgagactct	gtctcaaaaa	aaaaaaaaaa	aa	1830													

<210> 242
 <211> 508
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 242
 Met Asp Pro Lys Leu Gly Arg Met Ala Ala Ser Leu Leu Ala Val Leu
 -25 -20 -15
 Leu Leu Leu Leu Leu Glu Arg Gly Met Phe Ser Ser Pro Ser Pro Pro
 -10 -5 1 5
 Pro Ala Leu Leu Glu Lys Val Phe Gln Tyr Ile Asp Leu His Gln Asp
 10 15 20
 Glu Phe Val Gln Thr Leu Lys Glu Trp Val Ala Ile Glu Ser Asp Ser

<210> 243
 <211> 331
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<400> 243
 Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe
 -30 -25 -20
 Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys
 -15 -10 -5 1
 Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu
 5 10 15
 Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg
 20 25 30
 Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn
 35 40 45
 Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val
 50 55 60 65
 Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His
 70 75 80
 Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp
 85 90 95
 Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg
 100 105 110
 Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Met Glu Ala
 115 120 125
 Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys
 130 135 140 145
 Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu
 150 155 160
 Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu
 165 170 175
 Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu
 180 185 190
 Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg
 195 200 205
 Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu
 210 215 220 225
 Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser
 230 235 240
 Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys
 245 250 255
 Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe
 260 265 270
 Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Tyr Ile Thr
 275 280 285
 Asp Ser Met Val Glu Asp Cys Glu Pro His Phe
 290 295 300

<210> 244
 <211> 274
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 244
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 -15 -10 -5
 Gly Val Ser Val Asp Leu Ile Leu Phe Pro Leu Asp Thr Ile Lys Thr
 1 5 10 15
 Arg Leu Gln Ser Pro Gln Gly Phe Ser Lys Ala Gly Gly Phe His Gly
 20 25 30
 Ile Tyr Ala Gly Val Pro Ser Ala Ala Ile Gly Ser Phe Pro Asn Ala
 35 40 45
 Ala Ala Phe Phe Ile Thr Tyr Glu Tyr Val Lys Trp Phe Leu His Ala
 50 55 60
 Asp Ser Ser Ser Tyr Leu Thr Pro Met Lys His Met Leu Ala Ala Ser
 65 70 75
 Ala Gly Glu Val Val Ala Cys Leu Ile Arg Val Pro Ser Glu Val Val
 80 85 90 95
 Lys Gln Arg Ala Gln Val Ser Ala Ser Thr Arg Thr Phe Gln Ile Phe
 100 105 110
 Ser Asn Ile Leu Tyr Glu Glu Gly Ile Gln Gly Leu Tyr Arg Gly Tyr
 115 120 125
 Lys Ser Thr Val Leu Arg Glu Ile Pro Phe Ser Leu Val Gln Phe Pro
 130 135 140
 Leu Trp Glu Ser Leu Lys Ala Leu Trp Ser Trp Arg Gln Asp His Val
 145 150 155
 Val Asp Ser Trp Gln Ser Ala Val Cys Gly Ala Phe Ala Gly Gly Phe
 160 165 170 175
 Ala Ala Ala Val Thr Thr Pro Leu Asp Val Ala Lys Thr Arg Ile Met
 180 185 190
 Leu Ala Lys Ala Gly Ser Ser Thr Ala Asp Gly Asn Val Leu Ser Val
 195 200 205
 Leu His Gly Val Trp Arg Ser Gln Gly Leu Ala Gly Leu Phe Ala Gly
 210 215 220
 Val Phe Pro Arg Met Ala Ala Ile Ser Leu Gly Gly Phe Ile Phe Leu
 225 230 235
 Gly Ala Tyr Asp Arg Thr His Ser Leu Leu Leu Glu Val Gly Arg Lys
 240 245 250 255
 Ser Pro

<210> 245
 <211> 406
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35...-1

<400> 245
 Met Arg Gly Ser Val Glu Cys Thr Trp Gly Trp Gly His Cys Ala Pro
 -35 -30 -25 -20
 Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly
 -15 -10 -5
 Leu Leu Gly Glu Lys Thr Arg Gln Val Ser Leu Glu Val Ile Pro Asn
 1 5 10
 Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Ala Val Gly Thr

Pro Ser Ala Ser Val Ile Arg Thr
1 5

<210> 247
<211> 348
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29...-1

<400> 247
Met Ala Pro Gln Ser Leu Pro Ser Ser Arg Met Ala Pro Leu Gly Met
-25 -20 -15
Leu Leu Gly Pro Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser His
-10 -5 1
Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser Thr
5 10 15
Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu Leu Asp Ala
20 25 30 35
Glu Val Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu Gln
40 45 50
Pro Gly Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu Gln
55 60 65
Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn
70 75 80
Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr Ser
85 90 95
Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu Met
100 105 110 115
Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val Lys Arg Leu
120 125 130
Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp Phe Asp Glu Leu Asn Val
135 140 145
Val Ile Glu Thr Asp Met Gln Ile Met Val Arg Leu Ile Asn Lys Phe
150 155 160
Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala Leu Phe Asp
165 170 175
Leu Glu Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp Leu Leu Ser
180 185 190 195
Phe Gly Gly Leu Gln Val Val Ile Asn Gly Leu Asn Ser Thr Glu Pro
200 205 210
Leu Val Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala Ala Phe Ser Ser
215 220 225
Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Gly Ala Leu Gln Lys
230 235 240
Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr Ala Lys Lys Lys
245 250 255
Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe Pro Tyr Ala Gln
260 265 270 275
Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val Leu Arg Thr Leu Val
280 285 290
Gln Glu Lys Gly Thr Glu Val Leu Ala Val Arg Val Val Thr Leu Leu
295 300 305
Tyr Asp Leu Val Thr Glu Lys Met Phe Ala Glu Glu
310 315

<210> 248
 <211> 397
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36..-1

<400> 248
 Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Gln Leu Arg Leu Cys Phe
 -35 -30 -25
 Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Arg Leu Asn Asp Ala
 -20 -15 -10 -5
 Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro Val
 1 5 10
 Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro Gly
 15 20 25
 Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu Gly
 30 35 40
 Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser Gly
 45 50 55 60
 Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile Ile
 65 70 75
 Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly His
 80 85 90
 Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr Gly
 95 100 105
 Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu Glu
 110 115 120
 Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser Leu
 125 130 135 140
 Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser Gln
 145 150 155
 Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser Ala
 160 165 170
 Ser Arg Lys Arg Leu Asp Lys Lys Arg Ser Val Pro Val Ala Thr Val
 175 180 185
 Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Ser Pro
 190 195 200
 Leu Gln Gly Leu Thr Asn Gln Asp Leu Gln Glu Gly Glu Asp Trp Glu
 205 210 215 220
 Gln Glu Asp Glu Asp Met Asp Pro Arg Leu Glu His Ser Ser Ser Val
 225 230 235
 Gln Glu Asp Ser Glu Ser Pro Ser Pro Glu Asp Ile Pro Asp Tyr Leu
 240 245 250
 Leu Gln Tyr Arg Ala Ile His Ser Ala Glu Gln Gln His Ala Tyr Glu
 255 260 265
 Gln Asp Phe Glu Thr Asp Tyr Ala Glu Tyr Arg Ile Leu His Ala Arg
 270 275 280
 Val Gly Thr Ala Ser Gln Arg Phe Ile Glu Leu Gly Ala Glu Ile Lys
 285 290 295 300
 Arg Val Arg Arg Gly Thr Pro Glu Tyr Lys Val Leu Glu Asp Lys Ile
 305 310 315
 Ile Gln Glu Tyr Lys Lys Phe Arg Lys Gln Tyr Pro Ser Tyr Arg Glu
 320 325 330
 Glu Lys Arg Arg Cys Glu Tyr Leu His Gln Lys Leu Ser His Ile Lys
 335 340 345

Gly Leu Ile Leu Glu Phe Glu Glu Lys Asn Arg Gly Ser
 350 355 360

<210> 249
 <211> 403
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 249
 Met Val Asn Asp Pro Pro Val Pro Ala Leu Leu Trp Ala Gln Glu Val
 -20 -15 -10
 Gly Gln Val Leu Ala Gly Arg Ala Arg Arg Leu Leu Gln Phe Gly
 -5 1 5 10
 Val Leu Phe Cys Thr Ile Leu Leu Leu Leu Trp Val Ser Val Phe Leu
 15 20 25
 Tyr Gly Ser Phe Tyr Tyr Ser Tyr Met Pro Thr Val Ser His Leu Ser
 30 35 40
 Pro Val His Phe Tyr Tyr Arg Thr Asp Cys Asp Ser Ser Thr Thr Ser
 45 50 55
 Leu Cys Ser Phe Pro Val Ala Asn Val Ser Leu Thr Lys Gly Gly Arg
 60 65 70 75
 Asp Arg Val Leu Met Tyr Gly Gln Pro Tyr Arg Val Thr Leu Glu Leu
 80 85 90
 Glu Leu Pro Glu Ser Pro Val Asn Gln Asp Leu Gly Met Phe Leu Val
 95 100 105
 Thr Ile Ser Cys Tyr Thr Arg Gly Gly Arg Ile Ile Ser Thr Ser Ser
 110 115 120
 Arg Ser Val Met Leu His Tyr Arg Ser Asp Leu Leu Gln Met Leu Asp
 125 130 135
 Thr Leu Val Phe Ser Ser Leu Leu Leu Phe Gly Phe Ala Glu Gln Lys
 140 145 150 155
 Gln Leu Leu Glu Val Glu Leu Tyr Ala Asp Tyr Arg Glu Asn Ser Val
 160 165 170
 Ser Glu Tyr Val Pro Thr Thr Gly Ala Ile Ile Glu Ile His Ser Lys
 175 180 185
 Arg Ile Gln Leu Tyr Gly Ala Tyr Leu Arg Ile His Ala His Phe Thr
 190 195 200
 Gly Leu Arg Tyr Leu Leu Tyr Asn Phe Pro Met Thr Cys Ala Phe Ile
 205 210 215
 Gly Val Ala Ser Asn Phe Thr Phe Leu Ser Val Ile Val Leu Phe Ser
 220 225 230 235
 Tyr Met Gln Trp Val Trp Gly Gly Ile Trp Pro Arg His Arg Phe Ser
 240 245 250
 Leu Gln Val Asn Ile Arg Lys Arg Asp Asn Ser Arg Lys Glu Val Gln
 255 260 265
 Arg Arg Ile Ser Ala His Gln Pro Gly Ala Gly Pro Glu Gly Gln Glu
 270 275 280
 Glu Ser Thr Pro Gln Ser Asp Val Thr Glu Asp Gly Glu Ser Pro Glu
 285 290 295
 Asp Pro Ser Gly Thr Glu Gly Gln Leu Ser Glu Glu Glu Lys Pro Asp
 300 305 310 315
 Gln Gln Pro Leu Ser Gly Glu Glu Glu Leu Glu Pro Glu Ala Ser Asp
 320 325 330
 Gly Ser Gly Ser Trp Glu Asp Ala Ala Leu Thr Glu Ala Asn Leu

335 340 345
 Pro Ala Pro Ala Pro Ala Ser Ala Ser Ala Pro Val Leu Glu Thr Leu
 350 355 360
 Gly Ser Ser Glu Pro Ala Gly Gly Ala Leu Arg Gln Arg Pro Thr Cys
 365 370 375
 Ser Ser Ser
 380

<210> 250
 <211> 111
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 250
 Met Pro His Leu Met Glu Arg Met Val Gly Ser Gly Leu Leu Trp Leu
 -25 -20 -15
 Ala Leu Val Ser Cys Ile Leu Thr Gln Ala Ser Ala Val Gln Arg Gly
 -10 -5 1 5
 Tyr Gly Asn Pro Ile Glu Ala Ser Ser Tyr Gly Leu Asp Leu Asp Cys
 10 15 20
 Gly Ala Pro Gly Thr Pro Glu Ala His Val Cys Phe Asp Pro Cys Gln
 25 30 35
 Asn Tyr Thr Leu Leu Asp Leu Gly Pro Ile Thr Arg Arg Gly Ala Gln
 40 45 50
 Ser Pro Gly Val Met Asn Gly Thr Pro Ser Thr Ala Gly Phe Leu Val
 55 60 65 70
 Ala Trp Pro Met Val Leu Leu Thr Val Leu Leu Ala Trp Leu Phe
 75 80 85

<210> 251
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 251
 Met Asp Arg Pro Gly Phe Val Ala Ala Leu Val Ala Gly Gly Val Ala
 -15 -10 -5
 Gly Val Ser Val Asp Leu Ile Leu Phe Pro Leu Asp Thr Ile Lys Thr
 1 5 10 15
 Arg Leu Gln Ser Pro Gln Gly Phe Asn Lys Ala Gly Gly Phe His Gly
 20 25 30
 Ile Tyr Ala Gly Val Pro Ser Ala Ala Ile Gly Ser Phe Pro Asn Gly
 35 40 45
 Cys Leu Pro Asp Ser Ser Ser Ile
 50 55

<210> 252
 <211> 138
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 252
 Met Lys Phe Thr Thr Leu Leu Phe Leu Ala Ala Val Ala Gly Ala Leu
 -15 -10 -5 1
 Val Tyr Ala Glu Asp Ala Ser Ser Asp Ser Thr Gly Ala Asp Pro Ala
 5 10 15
 Gln Glu Ala Gly Thr Ser Lys Pro Asn Glu Glu Ile Ser Gly Pro Ala
 20 25 30
 Glu Pro Ala Ser Pro Pro Glu Thr Thr Thr Ala Gln Glu Thr Ser
 35 40 45
 Ala Ala Ala Val Gln Gly Thr Ala Lys Val Thr Ser Ser Arg Gln Glu
 50 55 60 65
 Leu Asn Pro Leu Lys Ser Ile Val Glu Lys Ser Ile Leu Leu Thr Glu
 70 75 80
 Gln Ala Leu Ala Lys Ala Gly Lys Gly Met His Gly Gly Val Pro Gly
 85 90 95
 Gly Lys Gln Phe Ile Glu Asn Gly Ser Glu Phe Ala Gln Lys Leu Leu
 100 105 110
 Lys Lys Phe Ser Leu Leu Lys Pro Trp Ala
 115 120

<210> 253
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<220>
 <221> UNSURE
 <222> 45
 <223> Xaa = Glu,Gln

<220>
 <221> UNSURE
 <222> 44
 <223> Xaa = Lys,Asn

<400> 253
 Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe
 -30 -25 -20
 Leu Leu Leu Val Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys
 -15 -10 -5 1
 Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu
 5 10 15
 Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg
 20 25 30
 Ile Ser Ala Ile Ala His Arg Gly Gly Ser Xaa Xaa Ala Pro Glu Asn
 35 40 45
 Thr Leu Ala Ala Ile Arg Gln Leu Arg Met Glu Gln Gln Ala Trp Ser
 50 55 60 65
 Trp Thr Leu Ser Leu Leu Leu Thr Gly Phe Leu Ser

70

75

<210> 254
 <211> 147
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 254
 Met Val Met Gly Leu Gly Val Leu Leu Leu Val Phe Val Leu Gly Leu
 -20 -15 -10
 Gly Leu Thr Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His
 -5 1 5
 Phe Leu Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg
 10 15 20 40
 Tyr Cys Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys
 25 30 35 40
 Asp Ile Asn Thr Phe Ile His Gly Asn Lys Arg Thr Ile Lys Ala Ile
 45 50 55
 Cys Glu Asn Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile Ser
 60 65 70
 Lys Ser Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro
 75 80 85
 Trp Pro Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn Val Val
 90 95 100
 Val Ala Cys Glu Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile Phe
 105 110 115 120
 Arg Arg Pro

<210> 255
 <211> 381
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<400> 255
 Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser
 -30 -25 -20
 Val Gly Ala Asn Phe Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln
 -15 -10 -5
 Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser
 1 5 10 15
 Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu
 20 25 30
 Lys Pro Val His His Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val
 35 40 45
 Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu
 50 55 60
 Leu Ala Leu Val Asp Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met
 65 70 75
 Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro Asn Ile Val Cys
 80 85 90 95

Ser Lys Asp Tyr Phe Val Thr Ala Asn Ser Asn Leu Val Ile Ile Thr
 100 105 110
 Ala Gly Ala Arg Gln Glu Lys Gly Glu Thr Arg Leu Asn Leu Val Gln
 115 120 125
 Arg Asn Val Ala Ile Phe Lys Leu Met Ile Ser Ser Ile Val Gln Tyr
 130 135 140
 Ser Pro His Cys Lys Leu Ile Ile Val Ser Asn Pro Val Asp Ile Leu
 145 150 155
 Thr Tyr Val Ala Trp Lys Leu Ser Ala Phe Pro Lys Asn Arg Ile Ile
 160 165 170 175
 Gly Ser Gly Cys Asn Leu Asp Thr Ala Arg Phe Arg Phe Leu Ile Gly
 180 185 190
 Gln Lys Leu Gly Ile His Ser Glu Ser Cys His Gly Trp Ile Leu Gly
 195 200 205
 Glu His Gly Asp Ser Ser Val Pro Val Trp Ser Gly Val Asn Ile Ala
 210 215 220
 Gly Val Pro Leu Lys Asp Leu Asn Ser Asp Ile Gly Thr Asp Lys Asp
 225 230 235
 Pro Glu Gln Trp Lys Asn Val His Lys Glu Val Thr Ala Thr Ala Tyr
 240 245 250 255
 Glu Ile Ile Lys Met Lys Gly Tyr Thr Ser Trp Ala Ile Gly Leu Ser
 260 265 270
 Val Ala Asp Leu Thr Glu Ser Ile Leu Lys Asn Leu Arg Arg Ile His
 275 280 285
 Pro Val Ser Thr Ile Ile Lys Gly Leu Tyr Gly Ile Asp Glu Glu Val
 290 295 300
 Phe Leu Ser Ile Pro Cys Ile Leu Gly Glu Asn Gly Ile Thr Asn Leu
 305 310 315
 Ile Lys Ile Lys Leu Thr Pro Glu Glu Glu Ala His Leu Lys Lys Ser
 320 325 330 335
 Ala Lys Thr Leu Trp Glu Ile Gln Asn Lys Leu Lys Leu
 340 345

<210> 256
 <211> 139
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<400> 256
 Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln Arg Met Ser Ser
 -30 -25 -20
 Val Gly Ala Asn Phe Leu Cys Leu Gly Met Ala Leu Cys Leu Arg Gln
 -15 -10 -5
 Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser
 1 5 10 15
 Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu
 20 25 30
 Lys Pro Val His His Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val
 35 40 45
 Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu
 50 55 60
 Leu Ala Leu Val Asp Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met
 65 70 75
 Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro Ile Leu Phe Val


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<400> 258
Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro
-20 -15 -10 -5
Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr
1 5 10
Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
15 20 25
Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe
30 35 40
Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro
45 50 55 60
Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile
65 70 75
Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr Thr Glu Thr
80 85 90
Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala Leu Gly Ala
95 100 105
Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn
110 115 120
Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys Ala Val Thr
125 130 135 140
Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe Ser Ile Ile
145 150 155
Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys His Ser Glu
160 165 170
Asp Cys Asp Cys Glu Gln Cys Cys
175 180

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<210> 259
<211> 394
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> -39...-1

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<400> 259
Met Ala Thr Ala Gln Leu Gln Arg Thr Pro Met Ser Ala Leu Val Phe
-35 -30 -25
Pro Asn Lys Ile Ser Thr Glu His Gln Ser Leu Val Leu Val Lys Arg
-20 -15 -10
Leu Leu Ala Val Ser Val Ser Cys Ile Thr Tyr Leu Arg Gly Ile Phe
-5 1 5
Pro Glu Cys Ala Tyr Gly Thr Arg Tyr Leu Asp Asp Leu Cys Val Lys
10 15 20 25
Ile Leu Arg Glu Asp Lys Asn Cys Pro Gly Ser Thr Gln Leu Val Lys
30 35 40
Trp Ile Leu Gly Cys Tyr Asp Ala Leu Gln Lys Lys Tyr Leu Arg Met
45 50 55
Val Val Leu Ala Val Tyr Thr Asn Pro Glu Asp Pro Gln Thr Ile Ser
60 65 70
Glu Cys Tyr Gln Phe Lys Phe Lys Tyr Thr Asn Asn Gly Pro Leu Met
75 80 85
Asp Phe Ile Ser Lys Asn Gln Ser Asn Glu Ser Ser Met Leu Ser Thr
90 95 100 105
Asp Thr Lys Lys Ala Ser Ile Leu Leu Ile Arg Lys Ile Tyr Ile Leu
110 115 120

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Met Gln Asn Leu Gly Pro Leu Pro Asn Asp Val Cys Leu Thr Met Lys
      125      130      135
Leu Phe Tyr Tyr Asp Glu Val Thr Pro Pro Asp Tyr Gln Pro Pro Gly
      140      145      150
Phe Lys Asp Gly Asp Cys Glu Gly Val Ile Phe Glu Gly Glu Pro Met
      155      160      165
Tyr Leu Asn Val Gly Glu Val Ser Thr Pro Phe His Ile Phe Lys Val
      170      175      180      185
Lys Val Thr Thr Glu Arg Glu Arg Met Glu Asn Ile Asp Ser Thr Ile
      190      195
Leu Ser Pro Lys Gln Ile Lys Thr Pro Phe Gln Lys Ile Leu Arg Asp
      205      210      215
Lys Asp Val Glu Asp Glu Gln Glu His Tyr Thr Ser Asp Asp Leu Asp
      220      225      230
Ile Glu Thr Lys Met Glu Glu Gln Glu Lys Asn Pro Ala Ser Ser Glu
      235      240      245
Leu Glu Glu Pro Ser Leu Val Cys Glu Glu Asp Glu Ile Met Arg Ser
      250      255      260      265
Lys Glu Ser Pro Asp Leu Ser Ile Ser His Ser Gln Val Glu Gln Leu
      270      275      280
Val Asn Lys Thr Ser Glu Leu Asp Met Ser Glu Ser Lys Thr Arg Ser
      285      290      295
Gly Lys Val Phe Gln Asn Lys Met Ala Asn Gly Asn Gln Pro Val Lys
      300      305      310
Ser Ser Lys Glu Asn Arg Lys Arg Ser Gln His Glu Ser Gly Arg Ile
      315      320      325
Val Leu His His Phe Asp Ser Ser Ser Gln Glu Ser Val Pro Lys Arg
      330      335      340      345
Arg Lys Phe Ser Glu Pro Lys Glu His Ile
      350      355

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<210> 260
 <211> 158
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

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<400> 260
Met Ala Leu Glu Val Leu Met Leu Leu Ala Val Leu Ile Trp Thr Gly
      -15      -10      -5
Ala Glu Asn Leu His Val Lys Ile Ser Cys Ser Leu Asp Trp Leu Met
      1      5      10      15
Val Ser Val Ile Pro Val Ala Glu Ser Arg Asn Leu Tyr Ile Phe Ala
      20      25      30
Asp Glu Leu His Leu Gly Met Gly Cys Pro Ala Asn Arg Ile His Thr
      35      40      45
Tyr Val Tyr Glu Phe Ile Tyr Leu Val Arg Asp Cys Gly Ile Arg Thr
      50      55      60
Arg Val Val Ser Glu Glu Thr Leu Leu Phe Gln Thr Glu Leu Tyr Phe
      65      70      75
Thr Pro Arg Asn Ile Asp His Asp Pro Gln Glu Ile His Leu Glu Cys
      80      85      90      95
Ser Thr Ser Arg Lys Ser Val Trp Leu Thr Pro Val Ser Thr Glu Asn
      100      105      110
Glu Ile Lys Leu Asp Pro Ser Pro Phe Ile Ala Asp Phe Gln Thr Thr

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115 120 125
 Ala Glu Glu Leu Gly Leu Leu Ser Ser Ser Pro Asn Leu Leu
 130 135 140

<210> 261
 <211> 233
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32..-1

<400> 261
 Met Ala Thr Pro Pro Phe Arg Leu Ile Arg Lys Met Phe Ser Phe Lys
 -30 -25 -20
 Val Ser Arg Trp Met Gly Leu Ala Cys Phe Arg Ser Leu Ala Ala Ser
 -15 -10 -5
 Ser Pro Ser Ile Arg Gln Lys Lys Leu Met His Lys Leu Gln Glu Glu
 1 5 10 15
 Lys Ala Phe Arg Glu Glu Met Lys Ile Phe Arg Glu Lys Ile Glu Asp
 20 25 30
 Phe Arg Glu Glu Met Trp Thr Phe Arg Gly Lys Ile His Ala Phe Arg
 35 40 45
 Gly Gln Ile Leu Gly Phe Trp Glu Glu Glu Arg Pro Phe Trp Glu Glu
 50 55 60
 Glu Lys Thr Phe Trp Lys Glu Glu Lys Ser Phe Trp Glu Met Glu Lys
 65 70 75 80
 Ser Phe Arg Glu Glu Glu Lys Thr Phe Trp Lys Lys Tyr Arg Thr Phe
 85 90 95
 Trp Lys Glu Asp Lys Ala Phe Trp Lys Glu Asp Asn Ala Leu Trp Glu
 100 105 110
 Arg Asp Arg Asn Leu Leu Gln Glu Asp Lys Ala Leu Trp Glu Glu Glu
 115 120 125
 Lys Ala Leu Trp Val Glu Glu Arg Ala Leu Leu Glu Gly Glu Lys Ala
 130 135 140
 Leu Trp Glu Asp Lys Thr Ser Leu Trp Glu Glu Glu Asn Ala Leu Trp
 145 150 155 160
 Glu Glu Glu Arg Ala Phe Trp Met Glu Asn Asn Gly His Ile Ala Gly
 165 170 175
 Glu Gln Met Leu Glu Asp Gly Pro His Asn Ala Asn Arg Gly Gln Arg
 180 185 190
 Leu Leu Ala Phe Ser Arg Gly Arg Ala
 195 200

<210> 262
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 262
 Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro
 -20 -15 -10 -5
 Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr

1 5 10
 Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
 15 20 25
 Ile Leu Gly Asp Ile His Ser Gly Ala Leu Phe Cys Ser Leu Ile Leu
 30 35 40
 Glu Pro Ser
 45

<210> 263
 <211> 94
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25..-1

<400> 263
 Met Cys Phe Leu Val Ser Phe Asn Leu Pro Ile His Ile Ser Leu Ser
 -25 -20 -15 -10
 His Leu Phe Leu Asp Leu Ser Arg Ser Leu Trp Phe Leu Ala Cys Pro
 -5 1 5
 Gly Leu Asn Leu Val Tyr Leu Ala Leu Asp Ser Phe Ser Asp Leu Arg
 10 15 20
 Pro Ser Leu Asn Leu Leu Phe Tyr Phe Val Pro Gly Phe Gly Val Ser
 25 30 35
 Lys Tyr Leu Thr Ser Ala Gln Pro Val Leu Gly Phe Leu Leu Leu Pro
 40 45 50 55
 Asp Ile Asp Asn Pro Ala Leu Leu Gly Thr Glu Arg Trp Ser
 60 65

<210> 264
 <211> 174
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 264
 Met Phe Leu Thr Val Lys Leu Leu Leu Gly Gln Arg Cys Ser Leu Lys
 -15 -10 -5
 Val Ser Gly Gln Glu Ser Val Ala Thr Leu Lys Arg Leu Val Ser Arg
 1 5 10
 Arg Leu Lys Val Pro Glu Glu Gln His Leu Leu Phe Arg Gly Gln
 15 20 25
 Leu Leu Glu Asp Asp Lys His Leu Ser Asp Tyr Cys Ile Gly Pro Asn
 30 35 40 45
 Ala Ser Ile Asn Val Ile Met Gln Pro Leu Glu Lys Met Ala Leu Lys
 50 55 60
 Glu Ala His Gln Pro Gln Thr Gln Pro Leu Trp His Gln Leu Gly Leu
 65 70 75
 Val Leu Ala Lys His Phe Glu Pro Gln Asp Ala Lys Ala Val Leu Gln
 80 85 90
 Leu Leu Arg Gln Glu His Glu Glu Arg Leu Gln Lys Ile Ser Leu Glu
 95 100 105
 His Leu Glu Gln Leu Ala Gln Tyr Leu Leu Ala Glu Glu Pro His Val

110 115 120 125
 Glu Pro Ala Gly Glu Arg Glu Leu Glu Ala Lys Ala Arg Pro Gln Ser
 130 135 140
 Ser Cys Asp Met Glu Glu Lys Glu Glu Ala Ala Asp Gln
 145 150 155

<210> 265
 <211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 265
 Met Ala Leu Glu Val Leu Met Leu Leu Ala Val Leu Ile Trp Thr Gly
 -15 -10 -5
 Ala Glu Asn Leu His Val Lys Ile Ser Cys Ser Leu Asp Trp Leu Met
 1 5 10 15
 Val Ser Val Ile Pro Val Ala Glu Ser Arg Asn Leu Tyr Ile Phe Ala
 20 25 30
 Asp Glu Leu His Leu Gly Met Gly Cys Pro Ala Asn Arg Ile His Thr
 35 40 45
 Tyr Val Tyr Glu Phe Ile Tyr Leu Val Arg Asp Cys Gly Ile Arg Thr
 50 55 60
 Arg Val Arg Thr Val Ile Val Cys Lys Lys Tyr Cys Met Phe Cys Gln
 65 70 75
 Thr Phe Met Pro Ser Ile Lys Ile Val Phe
 80 85

<210> 266
 <211> 124
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 266
 Met Val Leu Cys Trp Leu Leu Leu Leu Val Met Ala Leu Pro Pro Gly
 -15 -10 -5
 Thr Thr Gly Val Lys Asp Cys Val Phe Cys Glu Leu Thr Asp Ser Met
 1 5 10
 Gln Cys Pro Gly Thr Tyr Met His Cys Gly Asp Asp Glu Asp Cys Phe
 15 20 25 30
 Thr Gly His Gly Val Ala Pro Gly Thr Gly Pro Val Ile Asn Lys Gly
 35 40 45
 Cys Leu Arg Ala Thr Ser Cys Gly Leu Glu Glu Pro Val Ser Tyr Arg
 50 55 60
 Gly Val Thr Tyr Ser Leu Thr Asn Cys Cys Thr Gly Arg Leu Cys
 65 70 75
 Asn Arg Ala Pro Ser Ser Gln Thr Val Gly Ala Thr Thr Ser Leu Ala
 80 85 90
 Leu Gly Leu Gly Met Leu Leu Pro Pro Arg Leu Leu
 95 100 105

<210> 267
 <211> 261
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 267
 Met Glu Asn Phe Ser Leu Leu Ser Ile Ser Gly Pro Pro Ile Ser Ser
 -15 -10 -5
 Ser Ala Leu Ser Ala Phe Pro Asp Ile Met Phe Ser Arg Ala Thr Ser
 5 10 15
 1 Leu Pro Asp Ile Ala Lys Thr Ala Val Pro Thr Glu Ala Ser Ser Pro
 20 25 30
 Ala Gln Ala Leu Pro Pro Gln Tyr Gln Ser Ile Ile Val Arg Gln Gly
 35 40 45
 Ile Gln Asn Thr Val Leu Ser Pro Asp Cys Ser Leu Gly Asp Thr Gln
 50 55 60
 His Gly Glu Lys Leu Arg Arg Asn Cys Thr Ile Tyr Arg Pro Trp Phe
 65 70 75 80
 Ser Pro Tyr Ser Tyr Phe Val Cys Ala Asp Lys Glu Ser Gln Leu Glu
 85 90 95
 Ala Tyr Asp Phe Pro Glu Val Gln Gln Asp Glu Gly Lys Trp Asp Asn
 100 105 110
 Cys Leu Ser Glu Asp Met Ala Glu Asn Ile Cys Ser Ser Ser Ser Ser
 115 120 125
 Pro Glu Asn Thr Cys Pro Arg Glu Ala Thr Lys Lys Ser Arg His Gly
 130 135 140
 Leu Asp Ser Ile Thr Ser Gln Asp Ile Leu Met Ala Ser Arg Trp His
 145 150 155 160
 Pro Ala Gln Gln Asn Gly Tyr Lys Cys Val Ala Cys Cys Arg Met Tyr
 165 170 175
 Pro Thr Leu Asp Phe Leu Lys Ser His Ile Lys Arg Gly Phe Arg Glu
 180 185 190
 Gly Phe Ser Cys Lys Val Tyr Tyr Arg Lys Leu Lys Ala Leu Trp Ser
 195 200 205
 Lys Glu Gln Lys Ala Arg Leu Gly Asp Arg Leu Ser Ser Gly Ser Cys
 210 215 220
 Gln Ala Phe Asn Ser Pro Ala Glu His Leu Arg Gln Ile Gly Gly Glu
 225 230 235 240
 Ala Tyr Leu Cys Leu
 245

<210> 268
 <211> 76
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 268
 Met Cys Met Ser Leu Ser Met Lys Val Pro Cys Cys Leu Cys Ala Leu
 -25 -20 -15 -10
 Leu Ser Asn Phe Cys Pro Ser Thr Thr Val Lys Gly Asp Val Val Thr

Asp	Asp	Met	Ile	Pro	Pro	Asp	Ser	Asn	Ile	Arg	Leu	Thr	Thr	Lys	Ser
280					285					290				295	
Phe	Arg	Pro	Phe	Val	Pro	Arg	Leu	Ala	Arg	Leu	Tyr	Pro	Asn	Met	Asn
				300					305					310	
Leu	Glu	Leu	Gln	Gly	Ser	Val	Pro	Ser	Ala	Pro	Leu	Leu	Asn	Phe	Ser
			315					320					325		
Pro	Gly	Asn	Leu	Ser	Val	Asp	Pro	Tyr	Met	Glu	Ile	Asp	Ala	Phe	Val
	330						335					340			
Leu	Leu	Pro	Ser	Ser	Ser	Lys	Glu	Pro	Val	Phe	Arg	Leu	Ser	Val	Ala
	345					350				355					
Thr	Asn	Val	Ser	Ala	Thr	Leu	Thr	Phe	Asn	Thr	Ser	Lys	Ile	Thr	Gly
360					365					370				375	
Phe	Leu	Lys	Pro	Gly	Lys	Val	Lys	Val	Glu	Leu	Lys	Glu	Ser	Lys	Val
				380					385					390	
Gly	Leu	Phe	Asn	Ala	Glu	Leu	Leu	Glu	Ala	Leu	Leu	Asn	Tyr	Tyr	Ile
			395					400					405		
Leu	Asn	Thr	Phe	Tyr	Pro	Lys	Phe	Asn	Asp	Lys	Leu	Ala	Glu	Gly	Phe
	410						415					420			
Pro	Leu	Pro	Leu	Leu	Lys	Arg	Val	Gln	Leu	Tyr	Asp	Leu	Gly	Leu	Gln
	425					430					435				
Ile	His	Lys	Asp	Phe	Leu	Phe	Leu	Gly	Ala	Asn	Val	Gln	Tyr	Met	Arg
440					445					450					455
Val															

<210> 272
 <211> 143
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -43...-1

Met	Ala	Lys	Tyr	Gln	Gly	Glu	Val	Gln	Ser	Leu	Lys	Leu	Asp	Asp	Asp
			-40					-35					-30		
Ser	Val	Ile	Glu	Gly	Val	Ser	Asp	Gln	Val	Leu	Val	Ala	Val	Val	Val
		-25					-20					-15			
Ser	Phe	Ala	Leu	Ile	Ala	Thr	Leu	Val	Tyr	Ala	Leu	Phe	Arg	Asn	Val
-10					-5					1				5	
His	Gln	Asn	Ile	His	Pro	Glu	Asn	Gln	Glu	Leu	Val	Arg	Val	Leu	Arg
		10						15						20	
Glu	Gln	Leu	Gln	Thr	Glu	Gln	Asp	Ala	Pro	Ala	Ala	Thr	Arg	Gln	Gln
		25					30					35			
Phe	Tyr	Thr	Asp	Met	Tyr	Cys	Pro	Ile	Cys	Leu	His	Gln	Ala	Ser	Phe
	40					45					50				
Pro	Val	Glu	Thr	Asn	Cys	Gly	His	Leu	Phe	Cys	Gly	Ala	Cys	Ile	Ile
	55				60					65					
Ala	Tyr	Trp	Arg	Tyr	Gly	Ser	Trp	Leu	Gly	Ala	Ile	Ser	Cys	Pro	Ile
70					75				80					85	
Cys	Arg	Gln	Thr	Arg	His	Gly	His	Ile	Ala	Leu	Ser	Arg	Thr	Ala	
			90						95					100	

<210> 273
 <211> 82
 <212> PRT
 <213> Homo sapiens

<400> 273
 Met Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp
 1 5 10 15
 Ser Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val
 20 25 30
 Ser Phe Ala Leu Ile Ala Thr Leu Val Tyr Ala Leu Phe Arg Asn Val
 35 40 45
 His Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg
 50 55 60
 Glu Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Asp Ser Thr Ala Val
 65 70 75 80
 Leu His

<210> 274
 <211> 373
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27..-1

<400> 274
 Met Ala Thr Gln Ala His Ser Leu Ser Tyr Ala Gly Cys Asn Phe Leu
 -25 -20 -15
 Cys Gln Arg Leu Val Leu Ser Thr Leu Ser Gly Arg Pro Val Lys Ile
 -10 -5 1 5
 Arg Lys Ile Arg Ala Arg Asp Asp Asn Pro Gly Leu Arg Asp Phe Glu
 10 15 20
 Ala Ser Phe Ile Arg Leu Leu Asp Lys Ile Thr Asn Gly Ser Arg Ile
 25 30 35
 Glu Ile Asn Gln Thr Gly Thr Thr Leu Tyr Tyr Gln Pro Gly Leu Leu
 40 45 50
 Tyr Gly Gly Ser Val Glu His Asp Cys Ser Val Leu Arg Gly Ile Gly
 55 60 65
 Tyr Tyr Leu Glu Ser Leu Leu Cys Leu Ala Pro Phe Met Lys His Pro
 70 75 80 85
 Leu Lys Ile Val Leu Arg Gly Val Thr Asn Asp Gln Ile Asp Pro Ser
 90 95 100
 Val Asp Val Leu Lys Ala Thr Ala Leu Pro Leu Leu Lys Gln Phe Gly
 105 110 115
 Ile Asp Gly Glu Ser Phe Glu Leu Lys Ile Val Arg Arg Gly Met Pro
 120 125 130
 Pro Gly Gly Gly Glu Val Val Phe Ser Cys Pro Val Arg Lys Val
 135 140 145
 Leu Lys Pro Ile Gln Leu Thr Asp Pro Gly Lys Ile Lys Arg Ile Arg
 150 155 160 165
 Gly Met Ala Tyr Ser Val Arg Val Ser Pro Gln Met Ala Asn Arg Ile
 170 175 180
 Val Asp Ser Ala Arg Ser Ile Leu Asn Lys Phe Ile Pro Asp Ile Tyr
 185 190 195
 Ile Tyr Thr Asp His Ile Lys Gly Val Asn Ser Gly Lys Ser Pro Gly
 200 205 210
 Phe Gly Leu Ser Leu Val Ala Glu Thr Thr Ser Gly Thr Phe Leu Ser
 215 220 225
 Ala Glu Leu Ala Ser Asn Pro Gln Gly Gln Gly Ala Ala Val Leu Pro
 230 235 240 245
 Glu Asp Leu Gly Arg Asn Cys Ala Arg Leu Leu Leu Glu Glu Ile Tyr

250 255 260
 Arg Gly Gly Cys Val Asp Ser Thr Asn Gln Ser Leu Ala Leu Leu Leu
 265 270 275
 Met Thr Leu Gly Gln Gln Asp Val Ser Lys Val Leu Leu Gly Pro Leu
 280 285 290
 Ser Pro Tyr Thr Ile Glu Phe Leu Arg His Leu Lys Ser Phe Phe Gln
 295 300 305
 Ile Met Phe Lys Ile Glu Thr Lys Pro Cys Gly Glu Glu Leu Lys Gly
 310 315 320 325
 Gly Asp Lys Val Leu Met Thr Cys Val Gly Ile Gly Phe Ser Asn Leu
 330 335 340
 Ser Arg Thr Leu Lys
 345

<210> 275
 <211> 94
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 275
 Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser
 -25 -20 -15 -10
 Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser
 -5 1 5
 Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly
 10 15 20
 Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly
 25 30 35
 Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His
 40 45 50 55
 Val Ser Cys Ser Val Ala Ala Pro Leu Phe Pro Phe Leu Gly
 60 65

<210> 276
 <211> 197
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 276
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly
 -20 -15 -10 -5
 Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln
 1 5 10
 Ser Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
 15 20 25
 Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln
 30 35 40
 Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala
 45 50 55 60
 Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile

Val Phe Met Leu Gly Phe Val Val Val Leu Ser Phe Leu Leu Gly Gly
 230 235 240
 Tyr Leu Leu Phe Val Leu Tyr Leu Ala Ala Thr Asn Gln Thr Thr Asn
 245 250 255
 Glu Trp Tyr Arg Gly Asp Trp Ala Trp Cys Gln Arg Cys Pro Leu Val
 260 265 270 275
 Ala Trp Pro Pro Ser Ala Glu Pro Gln Val His Arg Asn Ile His Ser
 280 285 290
 His Gly Leu Arg Ser Asn Leu Gln Glu Ile Phe Leu Pro Ala Phe Pro
 295 300 305
 Cys His Glu Arg Lys Lys Gln Glu
 310 315

<210> 278
 <211> 541
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28..-1

<400> 278
 Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ser Ser Ser
 -25 -20 -15
 Gly Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn
 -10 -5 1
 Ala Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn
 5 10 15 20
 Val Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu
 25 30 35
 Ala Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser
 40 45 50
 Gln Thr Leu Asn Leu Leu Trp Leu Thr Val Pro Leu Gly Val Phe Trp
 55 60 65
 Ser Leu Phe Leu Gly Trp Ile Trp Leu Gln Leu Leu Glu Val Pro Asp
 70 75 80
 Pro Asn Val Val Pro His Tyr Ala Thr Gly Val Val Leu Phe Gly Leu
 85 90 95 100
 Ser Ala Val Val Glu Leu Leu Gly Glu Pro Phe Trp Val Leu Ala Gln
 105 110 115
 Ala His Met Phe Val Lys Leu Lys Val Ile Ala Glu Ser Leu Ser Val
 120 125 130
 Ile Leu Lys Thr Val Leu Thr Ala Phe Leu Val Leu Trp Leu Pro His
 135 140 145
 Trp Gly Leu Tyr Ile Phe Ser Leu Ala Gln Leu Phe Tyr Thr Thr Val
 150 155 160
 Leu Val Leu Cys Tyr Val Ile Tyr Phe Thr Lys Leu Leu Gly Ser Pro
 165 170 175 180
 Glu Ser Thr Lys Leu Gln Thr Leu Pro Val Ser Arg Ile Thr Asp Leu
 185 190 195
 Leu Pro Asn Ile Thr Arg Asn Gly Ala Phe Ile Asn Trp Lys Glu Ala
 200 205 210
 Lys Leu Thr Trp Ser Phe Phe Lys Gln Ser Phe Leu Lys Gln Ile Leu
 215 220 225
 Thr Glu Gly Glu Arg Tyr Val Met Thr Phe Leu Asn Val Leu Asn Phe
 230 235 240
 Gly Asp Gln Gly Val Tyr Asp Ile Val Asn Asn Leu Gly Ser Leu Val

245 250 255 260
 Ala Arg Leu Ile Phe Gln Pro Ile Glu Glu Ser Phe Tyr Ile Phe Phe
 265 270 275
 Ala Lys Val Leu Glu Arg Gly Lys Asp Ala Thr Leu Gln Lys Gln Glu
 280 285 290
 Asp Val Ala Val Ala Ala Ala Val Leu Glu Ser Leu Leu Lys Leu Ala
 295 300 305
 Leu Leu Ala Gly Leu Thr Ile Thr Val Phe Gly Phe Ala Tyr Ser Gln
 310 315 320
 Leu Ala Leu Asp Ile Tyr Gly Gly Thr Met Leu Ser Ser Gly Ser Gly
 325 330 335 340
 Pro Val Leu Leu Arg Ser Tyr Cys Leu Tyr Val Leu Leu Leu Ala Ile
 345 350 355
 Asn Gly Val Thr Glu Cys Phe Thr Phe Ala Ala Met Ser Lys Glu Glu
 360 365 370
 Val Asp Arg Tyr Asn Phe Val Met Leu Ala Leu Ser Ser Ser Phe Leu
 375 380 385
 Val Leu Ser Tyr Leu Leu Thr Arg Trp Cys Gly Ser Val Gly Phe Ile
 390 395 400
 Leu Ala Asn Cys Phe Asn Met Gly Ile Arg Ile Thr Gln Ser Leu Cys
 405 410 415 420
 Phe Ile His Arg Tyr Tyr Arg Arg Ser Pro His Arg Pro Leu Ala Gly
 425 430 435
 Leu His Leu Ser Pro Val Leu Leu Gly Thr Phe Ala Leu Ser Gly Gly
 440 445 450
 Val Thr Ala Val Ser Glu Val Phe Leu Cys Cys Glu Gln Gly Trp Pro
 455 460 465
 Ala Arg Leu Ala His Ile Ala Val Gly Ala Phe Cys Leu Gly Ala Thr
 470 475 480
 Leu Gly Thr Ala Phe Leu Thr Glu Thr Lys Leu Ile His Phe Leu Arg
 485 490 495 500
 Thr Gln Leu Gly Val Pro Arg Arg Thr Asp Lys Met Thr
 505 510

<210> 279
 <211> 267
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 279
 Met Ala Arg Phe Leu Thr Leu Cys Thr Trp Leu Leu Leu Leu Gly Pro
 -20 -15 -10
 Gly Leu Leu Ala Thr Val Arg Ala Glu Cys Ser Gln Asp Cys Ala Thr
 -5 1 5
 Cys Ser Tyr Arg Leu Val Arg Pro Ala Asp Ile Asn Phe Leu Ala Cys
 10 15 20
 Val Met Glu Cys Glu Gly Lys Leu Pro Ser Leu Lys Ile Trp Glu Thr
 25 30 35 40
 Cys Lys Glu Leu Leu Gln Leu Ser Lys Pro Asp Leu Pro Gln Asp Gly
 45 50 55
 Thr Ser Thr Leu Arg Glu Asn Ser Lys Pro Glu Glu Ser His Leu Leu
 60 65 70
 Ala Lys Arg Tyr Gly Gly Phe Met Lys Arg Tyr Gly Gly Phe Met Lys
 75 80 85

Lys Met Asp Glu Leu Tyr Pro Met Glu Pro Glu Glu Glu Ala Asn Gly
 90 95 100
 Ser Glu Ile Leu Ala Lys Arg Tyr Gly Gly Phe Met Lys Lys Asp Ala
 105 110 115 120
 Glu Glu Asp Asp Ser Leu Ala Asn Ser Ser Asp Leu Leu Lys Glu Leu
 125 130 135
 Leu Glu Thr Gly Asp Asn Arg Glu Arg Ser His His Gln Asp Gly Ser
 140 145 150
 Asp Asn Glu Glu Glu Val Ser Lys Arg Tyr Gly Gly Phe Met Arg Gly
 155 160 165
 Leu Lys Arg Ser Pro Gln Leu Glu Asp Glu Ala Lys Glu Leu Gln Lys
 170 175 180
 Arg Tyr Gly Gly Phe Met Arg Arg Val Gly Arg Pro Glu Trp Trp Met
 185 190 195 200
 Asp Tyr Gln Lys Arg Tyr Gly Gly Phe Leu Lys Arg Phe Ala Glu Ala
 205 210 215
 Leu Pro Ser Asp Glu Glu Gly Glu Ser Tyr Ser Lys Glu Val Pro Glu
 220 225 230
 Met Glu Lys Arg Tyr Gly Gly Phe Met Arg Phe
 235 240

<210> 280
 <211> 362
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -40...-1

<400> 280
 Met Pro Phe Ala Tyr Phe Phe Thr Glu Ser Glu Gly Phe Ala Gly Ser
 -40 -35 -30 -25
 Arg Lys Gly Val Leu Gly Arg Val Tyr Glu Thr Val Val Met Leu Met
 -20 -15 -10
 Leu Leu Thr Leu Leu Val Leu Gly Met Val Trp Val Ala Ser Ala Ile
 -5 1 5
 Val Asp Lys Asn Lys Ala Asn Arg Glu Ser Leu Tyr Asp Phe Trp Glu
 10 15 20
 Tyr Tyr Leu Pro Tyr Leu Tyr Ser Cys Ile Ser Phe Leu Gly Val Leu
 25 30 35 40
 Leu Leu Leu Val Cys Thr Pro Leu Gly Leu Ala Arg Met Phe Ser Val
 45 50 55
 Thr Gly Lys Leu Leu Val Lys Pro Arg Leu Leu Glu Asp Leu Glu Glu
 60 65 70
 Gln Leu Tyr Cys Ser Ala Phe Glu Glu Ala Ala Leu Thr Arg Arg Ile
 75 80 85
 Cys Asn Pro Thr Ser Cys Trp Leu Pro Leu Asp Met Glu Leu Leu His
 90 95 100
 Arg Gln Val Leu Ala Leu Gln Thr Gln Arg Val Leu Leu Glu Lys Arg
 105 110 115 120
 Arg Lys Ala Ser Ala Trp Gln Arg Asn Leu Gly Tyr Pro Leu Ala Met
 125 130 135
 Leu Cys Leu Leu Val Leu Thr Gly Leu Ser Val Leu Ile Val Ala Ile
 140 145 150
 His Ile Leu Glu Leu Leu Ile Asp Glu Ala Ala Met Pro Arg Gly Met
 155 160 165
 Gln Gly Thr Ser Leu Gly Gln Val Ser Phe Ser Lys Leu Gly Ser Phe

170 175 180
 Gly Ala Val Ile Gln Val Val Leu Ile Phe Tyr Leu Met Val Ser Ser
 185 190 195 200
 Val Val Gly Phe Tyr Ser Ser Pro Leu Phe Arg Ser Leu Arg Pro Arg
 205 210 215
 Trp His Asp Thr Ala Met Thr Gln Ile Ile Gly Asn Cys Val Cys Leu
 220 225 230
 Leu Val Leu Ser Ser Ala Leu Pro Val Phe Ser Arg Thr Leu Gly Leu
 235 240 245
 Thr Arg Phe Asp Leu Leu Gly Asp Phe Gly Arg Phe Asn Trp Leu Gly
 250 255 260
 Asn Phe Tyr Ile Val Phe Leu Tyr Asn Ala Ala Phe Ala Gly Leu Thr
 265 270 275 280
 Thr Leu Tyr Leu Val Lys Thr Phe Thr Ala Ala Val Arg Ala Glu Leu
 285 290 295
 Ile Arg Ala Phe Gly Leu Asp Arg Leu Pro Leu Pro Val Ser Gly Phe
 300 305 310
 Pro Gln Ala Ser Arg Lys Thr Gln His Gln
 315 320

<210> 281
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 281
 Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu Thr
 -20 -15 -10
 Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp Gln Gln
 -5 1 5 10
 Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln Ile Arg Lys
 15 20 25
 Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile Leu Thr Glu Gln
 30 35 40
 Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala Lys Gly Ser Gln Lys
 45 50 55
 Ser
 60

<210> 282
 <211> 541
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 282
 Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser
 -25 -20 -15
 Gly Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn
 -10 -5 1
 Ala Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn

470 475 480
 Leu Gly Thr Ala Phe Leu Thr Glu Thr Lys Leu Ile His Phe Leu Arg
 485 490 495 500
 Thr Gln Leu Gly Val Pro Arg Arg Thr Asp Lys Met Thr
 505 510

<210> 283
 <211> 468
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 283
 Met Gly Thr Gln Glu Gly Trp Cys Leu Leu Cys Leu Ala Leu Ser
 -20 -15 -10
 Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Trp Arg Ala
 -5 1 5 10
 Val Asp Val Val Leu Asp Cys Phe Leu Val Lys Asp Gly Ala His Arg
 15 20 25
 Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala Arg Ala Ser Leu Val Leu
 30 35 40
 Lys Gln Val Pro Val Leu Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp
 45 50 55
 Phe Gln Gly Gly Thr Leu Ala Gln Asp Asp Pro Ile Ile Phe Glu
 60 65 70 75
 Ala Ser Val Asp Leu Val Gln Ile Pro Gln Ala Glu Ala Leu Leu His
 80 85 90
 Ala Asp Cys Ser Gly Lys Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe
 95 100 105
 Leu Gln Met Thr Glu Thr Thr Val Lys Thr Ala Ala Trp Phe Met Ala
 110 115 120
 Asn Val Gln Val Ser Gly Gly Gly Pro Ser Ile Ser Leu Val Met Lys
 125 130 135
 Thr Pro Arg Val Ala Lys Asn Glu Val Leu Trp His Pro Thr Leu Asn
 140 145 150 155
 Leu Pro Leu Ser Pro Gln Gly Thr Val Arg Thr Ala Val Glu Phe Gln
 160 165 170
 Val Met Thr Gln Thr Gln Ser Leu Ser Phe Leu Leu Gly Ser Ser Ala
 175 180 185
 Ser Leu Asp Cys Gly Phe Ser Met Ala Pro Gly Leu Asp Leu Ile Ser
 190 195 200
 Val Glu Trp Arg Leu Gln His Lys Gly Arg Gly Gln Leu Val Tyr Ser
 205 210 215
 Trp Thr Ala Gly Gln Gly Gln Ala Val Arg Lys Gly Ala Thr Leu Glu
 220 225 230 235
 Pro Ala Gln Leu Gly Met Ala Arg Asp Ala Ser Leu Thr Leu Pro Gly
 240 245 250
 Leu Thr Ile Gln Asp Glu Gly Thr Tyr Ile Cys Gln Ile Thr Thr Ser
 255 260 265
 Leu Tyr Arg Ala Gln Gln Ile Ile Gln Leu Asn Ile Gln Ala Ser Pro
 270 275 280
 Lys Val Arg Leu Ser Leu Ala Asn Glu Ala Leu Leu Pro Thr Leu Ile
 285 290 295
 Cys Asp Ile Ala Gly Tyr Tyr Pro Leu Asp Val Val Val Thr Trp Thr
 300 305 310 315

195 200 205
 Val Pro Leu Gln Ser Lys Asn Lys Leu Arg Lys Arg Leu Ala Pro Leu
 210 215 220 225
 Val Tyr Val Gln Ser Tyr Cys Asp Pro Pro Ser Asp Arg Asp Ser Tyr
 230 235 240
 Val Arg Glu Leu Met Thr Tyr Ile Glu Val Asp Ser Tyr Gly Glu Cys
 245 250 255
 Leu Arg Asn Lys Asp Leu Pro Gln Gln Leu Lys Asn Pro Ala Ser Met
 260 265 270
 Asp Ala Asp Gly Phe Tyr Arg Ile Ile Ala Gln Tyr Lys Phe Ile Leu
 275 280 285
 Ala Phe Glu Asn Ala Val Cys Asp Asp Tyr Ile Thr Glu Lys Phe Trp
 290 295 300 305
 Arg Pro Leu Lys Leu Gly Val Val Pro Val Tyr Tyr Gly Ser Pro Ser
 310 315 320
 Ile Thr Asp Trp Leu Pro Ser Asn Lys Ser Ala Ile Leu Val Ser Glu
 325 330 335
 Phe Ser His Pro Arg Glu Leu Ala Ser Tyr Ile Arg Arg Leu Asp Ser
 340 345 350
 Asp Asp Arg Leu Tyr Glu Ala Tyr Val Glu Trp Lys Leu Lys Gly Arg
 355 360 365
 Ser Leu Thr Ser Asp Phe
 370 375

<210> 285
 <211> 305
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 285
 Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
 -25 -20 -15
 Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
 -10 -5 1 5
 Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu
 10 15 20
 Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe
 25 30 35
 Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly
 40 45 50
 Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg
 55 60 65 70
 Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu
 75 80 85
 Val Ile Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly
 90 95 100
 Gly Lys Met Ser Gln Tyr Leu Asp Ser Leu Lys Val Gly Asp Val Val
 105 110 115
 Glu Phe Arg Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His
 120 125 130
 Phe Asn Ile Gln Pro Asn Lys Lys Ser Pro Pro Glu Pro Arg Val Ala
 135 140 145 150
 Lys Lys Leu Gly Met Ile Ala Gly Gly Thr Gly Ile Thr Pro Met Leu
 155 160 165

Gln Leu Ile Arg Ala Ile Leu Lys Val Pro Glu Asp Pro Thr Gln Cys
 170 175 180
 Phe Leu Leu Phe Ala Asn Gln Thr Glu Lys Asp Ile Ile Leu Arg Glu
 185 190 195
 Asp Leu Glu Glu Leu Gln Ala Arg Tyr Pro Asn Arg Phe Lys Leu Trp
 200 205 210
 Phe Thr Leu Asp His Pro Pro Lys Asp Trp Ala Tyr Ser Lys Gly Phe
 215 220 225 230
 Val Thr Ala Asp Met Ile Arg Glu His Leu Pro Ala Pro Gly Asp Asp
 235 240 245
 Val Leu Val Leu Leu Cys Gly Pro Pro Pro Met Val Gln Leu Ala Cys
 250 255 260
 His Pro Asn Leu Asp Lys Leu Gly Tyr Ser Gln Lys Met Arg Phe Thr
 265 270 275
 Tyr

<210> 286
 <211> 442
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1
 <220>
 <221> UNSURE
 <222> 132
 <223> Xaa = Pro,Arg

<400> 286
 Met Gly Thr Gln Glu Gly Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser
 -20 -15 -10
 Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Leu Arg Ala
 -5 1 5 10
 Val Asp Val Val Leu Asp Cys Phe Leu Ala Lys Asp Gly Ala His Arg
 15 20 25
 Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala Arg Ala Ser Leu Val Leu
 30 35 40
 Lys Gln Val Pro Val Leu Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp
 45 50 55
 Phe Gln Gly Gly Thr Leu Ala Gln Asp Asp Pro Pro Ile Ile Phe Glu
 60 65 70 75
 Ala Ser Val Asp Leu Val Gln Ile Pro Gln Ala Glu Ala Leu Leu His
 80 85 90
 Ala Asp Cys Ser Gly Lys Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe
 95 100 105
 Leu Gln Met Thr Glu Thr Thr Val Lys Thr Ala Ala Trp Phe Met Ala
 110 115 120
 Asn Met Gln Val Ser Gly Gly Gly Xaa Ser Ile Ser Leu Val Met Lys
 125 130 135
 Thr Pro Arg Val Thr Lys Asn Glu Ala Leu Trp His Pro Thr Leu Asn
 140 145 150 155
 Leu Pro Leu Ser Pro Gln Gly Thr Val Arg Thr Ala Val Glu Phe Gln
 160 165 170
 Val Met Thr Gln Thr Gln Ser Leu Ser Phe Leu Leu Gly Ser Ser Ala
 175 180 185
 Ser Leu Asp Cys Gly Phe Ser Met Ala Pro Gly Leu Asp Leu Ile Ser

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      190              195              200
Val  Glu  Trp  Arg  Leu  Gln  His  Lys  Gly  Arg  Gly  Gln  Leu  Val  Tyr  Ser
      205              210              215
Trp  Thr  Ala  Gly  Gln  Gly  Gln  Ala  Val  Arg  Lys  Gly  Ala  Thr  Leu  Glu
220              225              230
Pro  Ala  Gln  Leu  Gly  Met  Ala  Arg  Asp  Ala  Ser  Leu  Thr  Leu  Pro  Gly
      240              245              250
Leu  Thr  Ile  Gln  Asp  Glu  Gly  Thr  Tyr  Ile  Cys  Gln  Ile  Thr  Thr  Ser
      255              260              265
Leu  Tyr  Arg  Ala  Gln  Gln  Ile  Ile  Gln  Leu  Asn  Ile  Gln  Ala  Ser  Pro
      270              275              280
Lys  Val  Arg  Leu  Ser  Leu  Ala  Asn  Glu  Ala  Leu  Leu  Pro  Thr  Leu  Ile
      285              290              295
Cys  Asp  Ile  Ala  Gly  Tyr  Tyr  Pro  Leu  Asp  Val  Val  Val  Thr  Trp  Thr
300              305              310
Arg  Glu  Glu  Leu  Gly  Gly  Ser  Pro  Ala  Gln  Val  Ser  Gly  Ala  Ser  Phe
      320              325              330
Ser  Ser  Leu  Arg  Gln  Ser  Val  Ala  Gly  Thr  Tyr  Ser  Ile  Ser  Ser  Ser
      335              340              345
Leu  Thr  Ala  Glu  Pro  Gly  Ser  Ala  Gly  Ala  Thr  Tyr  Thr  Cys  Gln  Val
      350              355              360
Thr  His  Ile  Ser  Leu  Glu  Glu  Pro  Leu  Gly  Ala  Ser  Thr  Gln  Val  Val
      365              370              375
Pro  Pro  Glu  Arg  Arg  Thr  Ala  Leu  Gly  Val  Ile  Phe  Ala  Ser  Ser  Leu
380              385              390
Phe  Leu  Leu  Ala  Leu  Met  Phe  Leu  Gly  Leu  Gln  Arg  Arg  Gln  Ala  Pro
      400              405              410
Thr  Gly  Leu  Gly  Leu  Leu  Gln  Ala  Glu  Arg
      415              420

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<210> 287
<211> 286
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> -48...-1

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<400> 287
Met  Asn  Pro  Ala  Ser  Asp  Gly  Gly  Thr  Ser  Glu  Ser  Ile  Phe  Asp  Leu
      -45              -40              -35
Asp  Tyr  Ala  Ser  Trp  Gly  Ile  Arg  Ser  Thr  Leu  Met  Val  Ala  Gly  Phe
      -30              -25              -20
Val  Phe  Tyr  Leu  Gly  Val  Phe  Val  Val  Cys  His  Gln  Leu  Ser  Ser  Ser
      -15              -10              -5
Leu  Asn  Ala  Thr  Tyr  Arg  Ser  Leu  Val  Ala  Arg  Glu  Lys  Val  Phe  Trp
1              5              10              15
Asp  Leu  Ala  Ala  Thr  Arg  Ala  Val  Phe  Gly  Val  Gln  Ser  Thr  Ala  Ala
      20              25              30
Gly  Leu  Trp  Ala  Leu  Leu  Gly  Asp  Pro  Val  Leu  His  Ala  Asp  Lys  Ala
      35              40              45
Arg  Gly  Gln  Gln  Asn  Trp  Cys  Trp  Phe  His  Ile  Thr  Thr  Ala  Thr  Gly
50              55              60
Phe  Phe  Cys  Phe  Glu  Asn  Val  Ala  Val  His  Leu  Ser  Asn  Leu  Ile  Phe
65              70              75              80
Arg  Thr  Phe  Asp  Leu  Phe  Leu  Val  Ile  His  His  Leu  Phe  Ala  Phe  Leu
      85              90              95

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Gly Phe Leu Gly Cys Leu Val Asn Leu Gln Ala Gly His Tyr Leu Ala
 100 105 110
 Met Thr Thr Leu Leu Leu Glu Met Ser Thr Pro Phe Thr Cys Val Ser
 115 120 125
 Trp Met Leu Leu Lys Ala Gly Trp Ser Glu Ser Leu Phe Trp Lys Leu
 130 135 140
 Asn Gln Trp Leu Met Ile His Met Phe His Cys Arg Met Val Leu Thr
 145 150 155 160
 Tyr His Met Trp Trp Val Cys Phe Trp His Trp Asp Gly Leu Val Ser
 165 170 175
 Ser Leu Tyr Leu Pro His Leu Thr Leu Phe Leu Val Gly Leu Ala Leu
 180 185 190
 Leu Thr Leu Ile Ile Asn Pro Tyr Trp Thr His Lys Lys Thr Gln Gln
 195 200 205
 Leu Leu Asn Pro Val Asp Trp Asn Phe Ala Gln Pro Glu Ala Lys Ser
 210 215 220
 Arg Pro Glu Gly Asn Gly Gln Leu Leu Arg Lys Lys Arg Pro
 225 230 235

<210> 288
 <211> 398
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 288
 Met Val Asn Asp Pro Pro Val Pro Ala Leu Leu Trp Ala Gln Glu Val
 -20 -15 -10
 Gly Gln Val Leu Ala Gly Arg Ala Arg Arg Leu Leu Gln Phe Gly
 -5 1 5 10
 Val Leu Phe Cys Thr Ile Leu Leu Leu Trp Val Ser Val Phe Leu
 15 20 25
 Tyr Gly Ser Phe Tyr Tyr Ser Tyr Met Pro Thr Val Ser His Leu Ser
 30 35 40
 Pro Val His Phe Tyr Tyr Arg Thr Asp Cys Asp Ser Ser Thr Thr Ser
 45 50 55
 Leu Cys Ser Phe Pro Val Ala Asn Val Ser Leu Thr Lys Gly Gly Arg
 60 65 70 75
 Asp Arg Val Leu Met Tyr Gly Gln Pro Tyr Arg Val Thr Leu Glu Leu
 80 85 90
 Glu Leu Pro Glu Ser Pro Val Asn Gln Asp Leu Gly Met Phe Leu Val
 95 100 105
 Thr Ile Ser Cys Tyr Thr Arg Gly Gly Arg Ile Ile Ser Thr Ser Ser
 110 115 120
 Arg Ser Val Met Leu His Tyr Arg Ser Asp Leu Leu Gln Met Leu Asp
 125 130 135
 Thr Leu Val Phe Ser Ser Leu Leu Leu Phe Gly Phe Ala Glu Gln Lys
 140 145 150 155
 Gln Leu Leu Glu Glu Leu Tyr Ala Asp Tyr Arg Glu Asn Ser Tyr
 160 165 170
 Val Pro Thr Thr Gly Ala Ile Ile Glu Ile His Ser Lys Arg Ile Gln
 175 180 185
 Leu Tyr Gly Ala Tyr Leu Arg Ile His Ala His Phe Thr Gly Leu Arg
 190 195 200
 Tyr Leu Leu Tyr Asn Phe Pro Met Thr Cys Ala Phe Ile Gly Val Ala

205 210 215
 Ser Asn Phe Thr Phe Leu Ser Val Ile Val Leu Phe Ser Tyr Met Gln
 220 225 230 235
 Trp Val Trp Gly Gly Ile Trp Pro Arg His Arg Phe Ser Leu Gln Val
 240 245 250
 Asn Ile Arg Lys Arg Asp Asn Ser Arg Lys Glu Val Gln Arg Arg Ile
 255 260 265
 Ser Ala His Gln Pro Gly Pro Glu Gly Gln Glu Glu Thr Pro Gln
 270 275 280
 Ser Asp Val Thr Glu Asp Gly Glu Ser Pro Glu Asp Pro Ser Gly Thr
 285 290 295
 Glu Gly Gln Leu Ser Glu Glu Glu Lys Pro Asp Gln Gln Pro Leu Ser
 300 305 310 315
 Gly Glu Glu Glu Leu Glu Pro Glu Ala Ser Asp Gly Ser Gly Ser Trp
 320 325 330
 Glu Asp Ala Ala Leu Leu Thr Glu Ala Asn Leu Pro Ala Pro Ala Pro
 335 340 345
 Ala Ser Ala Ser Ala Pro Val Leu Glu Thr Leu Gly Ser Ser Glu Pro
 350 355 360
 Ala Gly Gly Ala Leu Arg Gln Arg Pro Thr Cys Ser Ser Ser
 365 370 375

<210> 289
 <211> 130
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 289
 Met Arg Gln Lys Ala Val Ser Leu Phe Phe Cys Tyr Leu Leu Leu Phe
 -20 -15 -10 -5
 Thr Cys Ser Gly Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser
 1 5 10
 Asp Ser Gly Ser Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly
 15 20 25
 Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala
 30 35 40
 Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala
 45 50 55 60
 Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu Val Ala Thr Leu
 65 70 75
 Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile Gly Asn Ile Gly
 80 85 90
 Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp Ser Glu Glu Asp
 95 100 105
 Glu Glu
 110

<210> 290
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

<222> -20...-1

<400> 290

Met Ala Val Gly Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly
-20 -15 -10 -5
Phe Thr Gly Ala Gly Ile Ala Ala Asn Ser Val Ala Ser Leu Met
1 5 10
Ser Trp Ser Ala Ile Leu Asn Gly Gly Val Pro Ala Gly Gly Leu
15 20 25
Val Ala Thr Leu Gln Ser Leu Gly Ala Gly Gly Ser Val Val Ile
30 35 40
Gly Asn Ile Gly Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp
45 50 55 60
Ser Glu Glu Asp Glu Glu
65

<210> 291

<211> 207

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23...-1

<400> 291

Met Ala Pro Phe Glu Pro Leu Ala Ser Gly Ile Leu Leu Leu Trp
-20 -15 -10
Leu Ile Ala Pro Ser Arg Ala Cys Thr Cys Val Pro His Pro Gln
-5 1 5
Thr Ala Phe Cys Asn Ser Asp Leu Val Ile Arg Ala Lys Phe Val Gly
10 15 20 25
Thr Pro Glu Val Asn Gln Thr Thr Leu Tyr Gln Arg Tyr Glu Ile Lys
30 35 40
Met Thr Lys Met Tyr Lys Gly Phe Gln Ala Leu Gly Asp Ala Ala Asp
45 50 55
Ile Arg Phe Val Tyr Thr Pro Ala Met Glu Ser Val Cys Gly Tyr Phe
60 65 70
His Arg Ser His Asn Arg Ser Glu Glu Phe Leu Ile Ala Gly Lys Leu
75 80 85
Gln Asp Gly Leu Leu His Ile Thr Thr Cys Ser Phe Val Ala Pro Trp
90 95 100 105
Asn Ser Leu Ser Leu Ala Gln Arg Arg Gly Phe Thr Lys Thr Tyr Thr
110 115 120
Val Gly Cys Glu Glu Cys Thr Val Phe Pro Cys Leu Ser Phe Pro Cys
125 130 135
Lys Leu Gln Ser Gly Thr His Cys Leu Trp Thr Asp Gln Leu Leu Gln
140 145 150
Gly Ser Glu Lys Gly Phe Gln Ser Arg His Leu Ala Cys Leu Pro Arg
155 160 165
Glu Pro Gly Leu Cys Thr Trp Gln Ser Leu Arg Ser Gln Ile Ala
170 175 180

<210> 292

<211> 111

<212> PRT

<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 292
 Met Lys Tyr Asp Cys Pro Phe Ser Gly Thr Ser Phe Val Val Phe Ser
 -20 -15 -10
 Leu Phe Leu Ile Cys Ala Met Ala Gly Asp Val Val Tyr Ala Asp Ile
 -5 1 5
 Lys Thr Val Arg Thr Ser Pro Leu Glu Leu Ala Phe Pro Leu Gln Arg
 10 15 20
 Ser Val Ser Phe Asn Phe Ser Thr Val His Lys Ser Cys Pro Ala Lys
 25 30 35 40
 Asp Trp Lys Val His Lys Gly Lys Cys Tyr Trp Ile Ala Glu Thr Lys
 45 50 55
 Lys Ser Trp Asn Lys Ser Gln Asn Asp Cys Ala Ile Asn Asn Ser Tyr
 60 65 70
 Leu Met Val Ile Gln Asp Ile Thr Ala Met Val Arg Phe Asn Ile
 75 80 85

<210> 293
 <211> 139
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 293
 Met Glu Ala Val Val Phe Val Phe Ser Leu Leu Asp Cys Cys Ala Leu
 -15 -10 -5 1
 Ile Phe Leu Ser Val Tyr Phe Ile Ile Thr Leu Ser Asp Leu Glu Cys
 5 10 15
 Asp Tyr Ile Asn Ala Arg Ser Cys Cys Ser Lys Leu Asn Lys Trp Val
 20 25 30
 Ile Pro Glu Leu Ile Gly His Thr Ile Val Thr Val Leu Leu Leu Met
 35 40 45
 Ser Leu His Trp Phe Ile Phe Leu Leu Asn Leu Pro Val Ala Thr Trp
 50 55 60 65
 Asn Ile Tyr Arg Tyr Ile Met Val Pro Ser Gly Asn Met Gly Val Phe
 70 75 80
 Asp Pro Thr Glu Ile His Asn Arg Gly Gln Leu Lys Ser His Met Lys
 85 90 95
 Glu Ala Met Ile Lys Leu Gly Phe His Leu Leu Cys Phe Phe Met Tyr
 100 105 110
 Leu Tyr Ser Met Ile Leu Ala Leu Ile Asn Asp
 115 120

<210> 294
 <211> 160
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<211> 247
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 296
 Met Gly Leu Pro Gly Leu Phe Cys Leu Ala Val Leu Ala Ala Ser Ser
 -15 -10 -5
 Phe Ser Lys Ala Arg Glu Glu Glu Ile Thr Pro Val Val Ser Ile Ala
 1 5 10
 Tyr Lys Val Leu Glu Val Phe Pro Lys Gly Arg Trp Val Leu Ile Thr
 15 20 25 30
 Cys Cys Ala Pro Gln Pro Pro Pro Ile Thr Tyr Ser Leu Cys Gly
 35 40 45
 Thr Lys Asn Ile Lys Val Ala Lys Lys Val Val Lys Thr His Glu Pro
 50 55 60
 Ala Ser Phe Asn Leu Asn Val Thr Leu Lys Ser Ser Pro Asp Leu Leu
 65 70 75
 Thr Tyr Phe Cys Arg Ala Ser Ser Thr Ser Gly Ala His Val Asp Ser
 80 85 90
 Ala Arg Leu Gln Met His Trp Glu Leu Trp Ser Lys Pro Val Ser Glu
 95 100 105 110
 Leu Arg Ala Asn Phe Thr Leu Gln Asp Arg Gly Ala Gly Pro Arg Val
 115 120 125
 Glu Met Ile Cys Gln Ala Ser Ser Gly Ser Pro Pro Ile Thr Asn Ser
 130 135 140
 Leu Ile Gly Lys Asp Gly Gln Val His Leu Gln Gln Arg Pro Cys His
 145 150 155
 Arg Gln Pro Ala Asn Phe Ser Phe Leu Pro Ser Gln Thr Ser Asp Trp
 160 165 170
 Phe Trp Cys Gln Ala Ala Asn Asn Ala Asn Val Gln His Ser Ala Leu
 175 180 185 190
 Thr Val Val Pro Pro Gly Gly Leu Pro Arg Ala Pro Thr Ile Val Leu
 195 200 205
 Val Gly Ser Leu Ala Ser Thr Ala Ala Ile Thr Ser Arg Met Leu Gly
 210 215 220
 Trp Thr Thr Trp Ala Arg Trp
 225

<210> 297
 <211> 132
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41...-1

<400> 297
 Met Glu Gly Gly Ala Tyr Gly Ala Gly Lys Ala Gly Gly Ala Phe Asp
 -40 -35 -30
 Pro Tyr Thr Leu Val Arg Gln Pro His Thr Ile Leu Arg Val Val Ser
 -25 -20 -15 -10
 Trp Leu Phe Ser Ile Val Val Phe Gly Ser Ile Val Asn Glu Gly Tyr
 -5 1 5

Leu Asn Ser Ala Ser Glu Gly Glu Gln Phe Cys Ile Tyr Asn Arg Asn
 10 15 20
 Pro Asn Ala Cys Ser Tyr Gly Val Ala Val Gly Val Leu Ala Phe Leu
 25 30 35
 Thr Cys Leu Leu Tyr Leu Ala Leu Asp Val Tyr Phe Pro Gln Ile Ser
 40 45 50 55
 Ser Val Lys Asp Arg Lys Lys Ala Val Leu Ser Asp Ile Gly Val Ser
 60 65 70
 Gly Glu Pro His Pro Ala Gly Thr Pro Cys Thr Glu Ser Thr Glu Gly
 75 80 85
 Cys Pro Gly Pro
 90

<210> 298
 <211> 251
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 298
 Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys Ser Val
 -20 -15 -10
 Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro Leu Leu
 -5 1 5
 Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr Ala Arg
 10 15 20
 Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp Gly Ala
 25 30 35 40
 Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu Asp Ala
 45 50 55
 Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu Cys Met
 60 65 70
 Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro Glu Asn
 75 80 85
 Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val Tyr His
 90 95 100
 Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys Arg Ala
 105 110 115 120
 Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg
 125 130 135
 Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg
 140 145 150
 His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val
 155 160 165
 Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln
 170 175 180
 Gly Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu
 185 190 195 200
 Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
 205 210 215
 Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
 220 225

<210> 299
 <211> 137

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 299
 Met Leu Ser Gly Arg Leu Val Leu Gly Leu Val Ser Met Ala Gly Arg
 -20 -15 -10
 Val Cys Leu Cys Gln Gly Ser Ala Gly Ser Gly Ala Ile Gly Pro Val
 -5 1 5 10
 Glu Ala Ala Ile Arg Thr Lys Leu Glu Glu Ala Leu Ser Pro Glu Val
 15 20 25
 Leu Glu Leu Arg Asn Glu Ser Gly Gly His Ala Val Pro Gly Ser
 30 35 40
 Glu Thr His Phe Arg Val Ala Val Val Ser Ser Arg Phe Glu Gly Leu
 45 50 55
 Ser Pro Leu Gln Arg His Arg Leu Val His Ala Ala Leu Ala Glu Glu
 60 65 70
 Leu Gly Gly Pro Val His Ala Leu Ala Ile Gln Ala Arg Thr Pro Ala
 75 80 85 90
 Gln Trp Arg Glu Asn Ser Gln Leu Asp Thr Ser Pro Pro Cys Leu Gly
 95 100 105
 Gly Asn Lys Lys Thr Leu Gly Thr Pro
 110 115

<210> 300
 <211> 541
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 300
 Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser
 -25 -20 -15
 Gly Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn
 -10 -5 1
 Ala Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn
 5 10 15 20
 Val Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu
 25 30 35
 Ala Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser
 40 45 50
 Gln Thr Leu Asn Leu Leu Trp Leu Thr Val Pro Leu Gly Val Phe Trp
 55 60 65
 Ser Leu Phe Leu Gly Trp Ile Trp Leu Gln Leu Leu Glu Val Pro Asp
 70 75 80
 Pro Asn Val Val Pro His Tyr Ala Thr Gly Val Val Leu Phe Gly Leu
 85 90 95 100
 Ser Ala Val Val Glu Leu Leu Gly Glu Pro Phe Trp Val Leu Ala Gln
 105 110 115
 Ala His Met Phe Val Lys Leu Lys Val Ile Ala Glu Ser Leu Ser Val
 120 125 130
 Ile Leu Lys Ser Val Leu Thr Ala Phe Leu Val Leu Trp Leu Pro His

Met Glu Leu Glu Arg Ile Val Ser Ala Ala Leu Leu Ala Phe Val Gln
 -15 -10 -5
 Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu Asp Glu Val Ile Phe
 1 5 10 15
 Ser Tyr Val Leu Gly Val Leu Glu Asp Leu Gly Pro Ser Gly Pro Ser
 20 25 30
 Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu Met Met Glu Ala Tyr
 35 40 45
 Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr Ile Gly Asp Met Met
 50 55 60
 Gln Lys Leu Ser Gly Gln Leu Ser Asp Ala Arg Asn Lys Glu Asn Leu
 65 70 75
 Gln Pro Gln Ser Ser Gly Val Gln Gly Gln Val Pro Ile Ser Pro Glu
 80 85 90 95
 Pro Leu Gln Arg Pro Glu Met Leu Lys Glu Glu Thr Arg Ser Ser Ala
 100 105 110
 Ala Ala Ala Ala Asp Thr Gln Asp Glu Ala Thr Gly Ala Glu Glu Glu
 115 120 125
 Leu Leu Pro Gly Val Asp Val Leu Leu Glu Val Phe Pro Thr Cys Ser
 130 135 140
 Val Glu Gln Ala Gln Trp Val Leu Ala Lys Ala Arg Gly Asp Leu Glu
 145 150 155
 Glu Ala Val Gln Met Leu Val Glu Gly Lys Glu Glu Gly Pro Ala Ala
 160 165 170 175
 Trp Glu Gly Pro Asn Gln Asp Leu Pro Arg Arg Leu Arg Gly Pro Gln
 180 185 190
 Lys Asp Glu Leu Lys Ser Phe Ile Leu Gln Lys Tyr Met Met Val Asp
 195 200 205
 Ser Ala Glu Asp Gln Lys Ile His Arg Pro Met Ala Pro Lys Glu Ala
 210 215 220
 Pro Lys Lys Leu Ile Arg Tyr Ile Asp Asn Gln Val Val Ser Thr Lys
 225 230 235
 Gly Glu Arg Phe Lys Asp Val Arg Asn Pro Glu Ala Glu Glu Met Lys
 240 245 250 255
 Ala Thr Tyr Ile Asn Leu Lys Pro Ala Arg Lys Tyr Arg Phe His
 260 265 270

<210> 302
 <211> 165
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35...-1

<400> 302
 Met Met Arg Cys Cys Arg Arg Arg Cys Cys Cys Arg Gln Pro Pro His
 -35 -30 -25 -20
 Ala Leu Arg Pro Leu Leu Leu Pro Leu Val Leu Leu Pro Pro Leu
 -15 -10 -5
 Ala Ala Ala Ala Ala Gly Pro Asn Arg Cys Asp Thr Ile Tyr Gln Gly
 1 5 10
 Phe Ala Glu Cys Leu Ile Arg Leu Gly Asp Ser Met Gly Arg Gly Gly
 15 20 25
 Glu Leu Glu Thr Ile Cys Arg Ser Trp Asn Tyr Phe His Ala Cys Ala
 30 35 40 45
 Ser Gln Val Leu Ser Gly Cys Pro Glu Glu Ala Ala Ala Val Trp Glu

50 55 60
 Ser Leu Gln Gln Glu Ala Arg Gln Ala Pro Arg Pro Asn Asn Leu His
 65 70 75
 Thr Leu Cys Gly Ala Pro Val His Val Arg Glu Arg Gly Thr Gly Ser
 80 85 90
 Glu Thr Asn Gln Glu Thr Leu Arg Ala Thr Ala Pro Ala Leu Pro Met
 95 100 105
 Ala Pro Ala Pro Pro Leu Leu Ala Ala Ala Leu Ala Leu Ala Tyr Leu
 110 115 120 125
 Leu Arg Pro Leu Ala
 130

<210> 303
 <211> 148
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25..-1

<400> 303
 Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser
 -25 -20 -15 -10
 Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser
 -5 1 5
 Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly
 10 15 20
 Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly
 25 30 35
 Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His
 40 45 50 55
 Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala Leu Glu Glu Gly Ile
 60 65 70
 Val Arg Tyr Thr Lys Glu Val Tyr Val Pro His Pro Arg Asn Thr Glu
 75 80 85
 Ala Val Asp Leu Ile Thr Arg Leu Pro Lys Gly Ala Val Leu Tyr Lys
 90 95 100
 Thr Phe Val His Val Val Pro Ala Lys Pro Glu Gly Thr Phe Lys Leu
 105 110 115
 Val Ala Met Leu
 120

<210> 304
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34..-1

<400> 304
 Met Glu Ser Glu Arg Ser Lys Arg Met Gly Asn Ala Cys Ile Pro Leu
 -30 -25 -20
 Lys Arg Ile Ala Tyr Phe Leu Cys Leu Leu Ser Ala Leu Leu Leu Thr
 -15 -10 -5
 Glu Gly Lys Lys Pro Ala Lys Pro Lys Cys Pro Ala Val Cys Thr Cys

1 5 10
 Thr Lys Asp Asn Ala Leu Cys Glu Asn Ala Arg Ser Ile Pro Arg Thr
 15 20 25 30
 Val Pro Pro Asp Val Ile Ser Leu Ser Phe Val Arg Ser Gly Phe Thr
 35 40 45
 Glu Ile Ser Glu Gly Ser Phe Leu Phe Thr Pro Ser Leu Gln Leu Leu
 50 55 60
 Leu Phe Thr Ser Asn Ser Phe Asp Val Ile Ser Asp Asp Ala Phe Ile
 65 70 75
 Gly Leu Pro His Leu Glu Tyr Leu Phe Ile Glu Asn Asn Asn Ile Lys
 80 85 90
 Ser Ile Ser Arg His Thr Phe Arg Gly Leu Lys Ser Leu Ile His Leu
 95 100 105 110
 Ser Leu Ala Asn Asn Asn Leu Gln Thr Leu Pro Lys Asp Ile Phe Lys
 115 120 125
 Gly Leu Asp Ser Leu Thr Asn Val Asp Leu Arg Gly Asn Ser Phe Asn
 130 135 140
 Cys Asp Cys Lys Leu Lys Trp Leu Val Glu Trp Leu Gly His Thr Asn
 145 150 155
 Ala Thr Val Glu Asp Ile Tyr Cys Glu Gly Pro Pro Glu Tyr Lys Lys
 160 165 170
 Arg Lys Ile Asn Ser Leu Ser Ser Lys Asp Phe Asp Cys Ile Ile Thr
 175 180 185 190
 Glu Phe Ala Lys Ser Gln Asp Leu Pro Tyr Gln Ser Leu Ser Ile Asp
 195 200 205
 Thr Phe Ser Tyr Leu Asn Asp Glu Tyr Val Val Ile Ala Gln Pro Phe
 210 215 220
 Thr Gly Lys Cys Ile Phe Leu Glu Trp Asp His Val Glu Lys Thr Phe
 225 230 235
 Arg Asn Tyr Asp Asn Ile Thr Val Leu Arg Glu Ile His Arg Phe Thr
 240 245 250
 Asn Met Ser
 255

<210> 305
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -49...-1

<400> 305
 Met Glu Gly Ala Gly Ala Gly Ser Gly Phe Arg Lys Glu Leu Val Ser
 -45 -40 -35
 Arg Leu Leu His Leu His Phe Lys Asp Asp Lys Thr Lys Val Ser Gly
 -30 -25 -20
 Asp Ala Leu Gln Leu Met Val Glu Leu Lys Val Phe Val Val Glu
 -15 -10 -5
 Ala Ala Val Arg Gly Val Arg Gln Ala Gln Ala Glu Asp Ala Leu Arg
 1 5 10 15
 Val Asp Val Asp Gln Leu Glu Lys Val Leu Pro Gln Leu Leu Asp
 20 25 30
 Phe

<210> 306
 <211> 233

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

<400> 306
 Met Ala Ala Thr Ser Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val
 -30 -25 -20 -15
 Ser Val Ala His Ala Leu Ser Leu Pro Ala Glu Ser Tyr Gly Asn Asp
 -10 -5 1
 Pro Asp Ile Glu Met Ala Trp Ala Met Arg Ala Met Gln His Ala Glu
 5 10 15
 Val Tyr Tyr Lys Leu Ile Ser Ser Val Asp Pro Gln Phe Leu Lys Leu
 20 25 30
 Thr Lys Val Asp Asp Gln Ile Tyr Ser Glu Phe Arg Lys Asn Phe Glu
 35 40 45 50
 Thr Leu Arg Ile Asp Val Leu Asp Pro Glu Glu Leu Lys Ser Glu Ser
 55 60 65
 Ala Lys Glu Lys Trp Arg Pro Phe Cys Leu Lys Phe Asn Gly Ile Val
 70 75 80
 Glu Asp Phe Asn Tyr Gly Thr Leu Leu Arg Leu Asp Cys Ser Gln Gly
 85 90 95
 Tyr Thr Glu Glu Asn Thr Ile Phe Ala Pro Arg Ile Gln Phe Phe Ala
 100 105 110
 Ile Glu Ile Ala Arg Asn Arg Glu Gly Tyr Asn Lys Ala Val Tyr Ile
 115 120 125 130
 Ser Val Gln Asp Lys Glu Gly Glu Lys Gly Val Asn Asn Gly Gly Glu
 135 140 145
 Lys Arg Ala Asp Ser Gly Glu Glu Glu Asn Thr Lys Asn Gly Gly Glu
 150 155 160
 Lys Gly Ala Asp Ser Gly Glu Glu Lys Glu Glu Gly Ile Asn Arg Glu
 165 170 175
 Asp Lys Thr Asp Lys Gly Gly Glu Lys Gly Lys Glu Ala Asp Lys Glu
 180 185 190
 Ile Asn Lys Ser Gly Glu Lys Ala Met
 195 200

<210> 307
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 307
 Met Arg Gln Lys Ala Val Ser Leu Phe Leu Cys Tyr Leu Leu Leu Phe
 -20 -15 -10 -5
 Thr Cys Ser Gly Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser
 1 5 10
 Asp Ser Gly Ser Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly
 15 20 25
 Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala
 30 35 40
 Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala


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115      120      125
Gly Leu Asp Ser Leu Thr Asn Val Asp Leu Arg Gly Asn Ser Phe Asn
130
Cys Asp Cys Lys Leu Lys Trp Leu Val Glu Trp Leu Gly His Thr Asn
145      150      155
Ala Thr Val Glu Asp Ile Tyr Cys Glu Gly Pro Pro Glu Tyr Lys Lys
160      165      170
Arg Lys Ile Asn Ser Leu Ser Ser Lys Asp Phe Asp Cys Ile Ile Thr
175      180      185
Glu Phe Ala Lys Ser Gln Asp Leu Pro Tyr Gln Ser Leu Ser Ile Asp
195      200      205
Thr Phe Ser Tyr Leu Asn Asp Glu Tyr Val Val Ile Ala Gln Pro Phe
210      215      220
Thr Gly Lys Cys Ile Phe Leu Glu Trp Asp His Val Glu Lys Thr Phe
225      230      235
Arg Asn Tyr Asp Asn Ile Thr Val Leu Arg Glu Ile His Arg Phe Thr
240      245      250
Asn Met Ser
255

<210> 310
<211> 426
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28...-1

<400> 310
Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly
-25      -20      -15
Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val
-10      -5      1
Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu
5      10      15      20
His Gln Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro
25      30      35
Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg
40      45      50
Asn Leu Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val
55      60      65
Asp Ile Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg
70      75      80
Trp Thr Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro
85      90      95      100
Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His
105      110      115
Lys Leu Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr
120      125      130
Tyr Thr Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr
135      140      145
Asn Pro Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys
150      155      160
Glu Asn Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn
165      170      175      180
Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu Lys Met Gly
185      190      195

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Thr Arg Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala Ala Asn Gln
 200 205 210
 Ile Arg Lys Cys Gln Gln Ser Thr Ser Ala Val Ile Gly Val Arg Val
 215 220 225
 Cys Gly Met Gln Val Tyr Gln Ala Gly Ser Gly Gln Leu Met Phe Met
 230 235 240
 Asn Lys Tyr His Gly Arg Lys Leu Ser Met Gln Gly Phe Lys Glu Ala
 245 250 255 260
 Leu Phe Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg Glu Leu Leu
 265 270 275
 Gly Pro Val Leu Lys Lys Leu Thr Glu Leu Lys Ala Val Leu Glu Arg
 280 285 290
 Gln Glu Ser Tyr Arg Phe Tyr Ser Ser Ser Leu Leu Val Ile Tyr Asp
 295 300 305
 Gly Lys Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala Glu Asp Leu
 310 315 320
 Glu Asp Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly Ala Tyr Ala
 325 330 335 340
 Tyr Lys Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met Ile Asp Phe
 345 350 355
 Ala His Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val Val His Glu
 360 365 370
 Gly Gln Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu Ile Asp Ile
 375 380 385
 Val Thr Glu Ile Ser Glu Glu Ser Gly Glu
 390 395

<210> 311
 <211> 466
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 311
 Met Gly Leu Tyr Ala Ala Ala Ala Gly Val Leu Ala Gly Val Glu Ser
 -15 -10 -5
 Arg Gln Gly Ser Ile Lys Gly Leu Val Tyr Ser Ser Asn Phe Gln Asn
 1 5 10 15
 Val Lys Gln Leu Tyr Ala Leu Val Cys Glu Thr Gln Arg Tyr Ser Ala
 20 25 30
 Val Leu Asp Ala Val Ile Ala Ser Ala Gly Leu Leu Arg Ala Glu Lys
 35 40 45
 Lys Leu Arg Pro His Leu Ala Lys Val Leu Val Tyr Glu Leu Leu Leu
 50 55 60
 Gly Lys Gly Phe Arg Gly Gly Gly Gly Arg Trp Lys Ala Leu Leu Gly
 65 70 75 80
 Arg His Gln Ala Arg Leu Lys Ala Glu Leu Ala Arg Leu Lys Val His
 85 90 95
 Arg Gly Val Ser Arg Asn Glu Asp Leu Leu Glu Val Gly Ser Arg Pro
 100 105 110
 Gly Pro Ala Ser Gln Leu Pro Arg Phe Val Arg Val Asn Thr Leu Lys
 115 120 125
 Thr Cys Ser Asp Asp Val Val Asp Tyr Phe Lys Arg Gln Gly Phe Ser
 130 135 140
 Tyr Gln Gly Arg Ala Ser Ser Leu Asp Asp Leu Arg Ala Leu Lys Gly

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145          150          155          160
Lys His Phe Leu Leu Asp Pro Leu Met Pro Glu Leu Leu Val Phe Pro
165          170          175
Ala Gln Thr Asp Leu His Glu His Pro Leu Tyr Arg Ala Gly His Leu
180          185          190
Ile Leu Gln Asp Arg Ala Ser Cys Leu Pro Ala Met Leu Leu Asp Pro
195          200          205
Pro Pro Gly Ser His Val Ile Asp Ala Cys Ala Ala Pro Gly Asn Lys
210          215          220
Thr Ser His Leu Ala Ala Leu Leu Lys Asn Gln Gly Lys Ile Phe Ala
225          230          235
Phe Asp Leu Asp Ala Lys Arg Leu Ala Ser Met Ala Thr Leu Leu Ala
245          250          255
Arg Ala Gly Val Ser Cys Cys Glu Leu Ala Glu Glu Asp Phe Leu Ala
260          265          270
Val Ser Pro Ser Asp Pro Arg Tyr His Glu Val His Tyr Ile Leu Leu
275          280          285
Asp Pro Ser Cys Ser Gly Ser Gly Met Pro Ser Arg Gln Leu Glu Glu
290          295          300
Pro Gly Ala Gly Thr Pro Ser Pro Val Arg Leu His Ala Leu Ala Gly
305          310          315
Phe Gln Gln Arg Ala Leu Cys His Ala Leu Thr Phe Pro Ser Leu Gln
320          325          330
Arg Leu Val Tyr Ser Thr Cys Ser Leu Cys Gln Glu Glu Asn Glu Asp
335          340          345
Val Val Arg Asp Ala Leu Gln Gln Asn Pro Gly Ala Phe Arg Leu Ala
350          355          360
Pro Ala Leu Pro Ala Trp Pro His Arg Gly Leu Ser Thr Phe Pro Gly
365          370          375
Ala Glu His Cys Leu Arg Ala Ser Pro Glu Thr Thr Leu Ser Ser Gly
380          385          390
Phe Phe Val Ala Val Ile Glu Arg Val Glu Val Pro Ser Ser Ala Ser
395          400          405
Gln Ala Lys Ala Ser Ala Pro Glu Arg Thr Pro Ser Pro Ala Pro Lys
410          415          420
Arg Lys Lys Arg Gln Gln Arg Ala Ala Ala Gly Ala Cys Thr Pro Pro
425          430          435
Cys Thr
440          445          450

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<210> 312
<211> 382
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> -16...-1

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<400> 312
Met Gly Leu Tyr Ala Ala Ala Ala Gly Val Leu Ala Gly Val Glu Ser
-15          -10          -5
Arg Gln Gly Ser Ile Lys Gly Leu Val Tyr Ser Ser Asn Phe Gln Asn
1          5          10          15
Val Lys Gln Leu Tyr Ala Leu Val Cys Glu Thr Gln Arg Tyr Ser Ala
20          25          30
Val Leu Asp Ala Val Ile Ala Ser Ala Gly Leu Leu Arg Ala Glu Lys
35          40          45

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Lys Leu Arg Pro His Leu Ala Lys Val Leu Val Tyr Glu Leu Leu Leu
 50 55 60
 Gly Lys Gly Phe Arg Gly Gly Gly Arg Trp Lys Ala Leu Leu Gly
 65 70 75 80
 Arg His Gln Ala Arg Leu Lys Ala Glu Leu Ala Arg Leu Lys Val His
 85 90 95
 Arg Gly Val Ser Arg Asn Glu Asp Leu Leu Glu Val Gly Ser Arg Pro
 100 105 110
 Gly Pro Ala Ser Gln Leu Pro Arg Phe Val Arg Val Asn Thr Leu Lys
 115 120 125
 Thr Cys Ser Asp Asp Val Val Asp Tyr Phe Lys Arg Gln Gly Phe Ser
 130 135 140
 Tyr Gln Gly Arg Ala Ser Ser Leu Asp Asp Leu Arg Ala Leu Lys Gly
 145 150 155 160
 Lys His Phe Leu Leu Asp Pro Leu Met Pro Glu Leu Leu Val Phe Pro
 165 170 175
 Ala Gln Thr Asp Leu His Glu His Pro Leu Tyr Arg Ala Gly His Leu
 180 185 190
 Ile Leu Gln Asp Arg Ala Ser Cys Leu Pro Ala Met Leu Leu Asp Pro
 195 200 205
 Pro Pro Gly Ser His Val Ile Asp Ala Cys Ala Ala Pro Gly Asn Lys
 210 215 220
 Thr Ser His Leu Ala Ala Leu Leu Lys Asn Gln Gly Lys Ile Phe Ala
 225 230 235 240
 Phe Asp Leu Asp Ala Lys Arg Leu Ala Ser Met Ala Thr Leu Leu Ala
 245 250 255
 Arg Ala Gly Val Ser Cys Cys Glu Leu Ala Glu Glu Asp Phe Leu Ala
 260 265 270
 Val Ser Pro Ser Asp Pro Arg Tyr His Glu Val His Tyr Ile Leu Leu
 275 280 285
 Asp Pro Ser Cys Ser Gly Ser Gly Met Pro Ser Arg Gln Leu Glu Glu
 290 295 300
 Pro Gly Ala Gly Thr Pro Ser Pro Val Arg Leu His Ala Leu Ala Ala
 305 310 315 320
 Ser Ser Ser Glu Pro Cys Ala Thr Arg Ser Leu Ser Leu Pro Cys Ser
 325 330 335
 Gly Ser Ser Thr Pro Arg Ala Pro Ser Ala Arg Arg Met Lys Thr
 340 345 350
 Trp Cys Glu Met Arg Cys Ser Arg Thr Arg Ala Pro Ser Gly
 355 360 365

<210> 313

<211> 258

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -36...-1

<400> 313

Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Glu Leu Arg Leu Cys Phe
 -35 -30 -25
 Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp Ala
 -20 -15 -10 -5
 Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro Val
 1 5 10
 Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro Gly

15 20 25
 Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu Gly
 30 35 40
 Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser Gly
 45 50 55 60
 Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile Ile
 65 70 75
 Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly His
 80 85 90
 Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr Gly
 95 100 105
 Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu Glu
 110 115 120
 Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser Leu
 125 130 135
 Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser Gln
 145 150 155
 Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser Ala
 160 165 170
 Ser Arg Lys Arg Leu Asp Lys Lys Arg Ser Val Pro Val Ala Thr Val
 175 180 185
 Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Pro Pro
 190 195 200
 Thr Arg Pro Asp Gln Ser Gly Phe Thr Arg Gly Arg Arg Leu Gly Ala
 205 210 215 220
 Arg Arg

<210> 314
 <211> 280
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<400> 314
 Met Lys Ser Cys Gly Ser Met Leu Gly Leu Trp Gly Gln Arg Leu Pro
 -30 -25 -20
 Ala Ala Trp Val Leu Leu Leu Leu Pro Phe Leu Pro Leu Leu Leu
 -15 -10 -5
 Ala Ala Pro Ala Pro His Arg Ala Ser Tyr Lys Pro Val Ile Val Val
 1 5 10 15
 His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu Tyr
 20 25 30
 Ile Asn Glu Thr His Pro Gly Thr Val Val Thr Val Leu Asp Leu Phe
 35 40 45
 Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly Phe
 50 55 60
 Arg Glu Ala Val Val Pro Ile Met Ala Lys Ala Pro Gln Gly Val His
 65 70 75
 Leu Ile Cys Tyr Ser Gln Gly Gly Leu Val Cys Arg Ala Leu Leu Ser
 80 85 90 95
 Val Met Asp Asp His Asn Val Asp Ser Phe Ile Ser Leu Ser Ser Pro
 100 105 110
 Gln Met Gly Gln Tyr Gly Asp Thr Asp Tyr Leu Lys Trp Leu Phe Pro
 115 120 125
 Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro Leu Ile

130 135 140
 Asn Gly Glu Arg Asp His Pro Asn Ala Thr Val Trp Arg Lys Asn Phe
 145 150 155
 Leu Arg Val Gly His Leu Val Leu Ile Gly Gly Pro Asp Asp Gly Val
 160 165 170 175
 Ile Thr Pro Trp Gln Ser Ser Phe Phe Gly Phe Tyr Asp Ala Asn Glu
 180 185 190
 Thr Val Leu Glu Met Glu Glu Gln Leu Val Tyr Leu Arg Asp Ser Phe
 195 200 205
 Gly Leu Lys Thr Leu Leu Ala Arg Gly Ala Ile Val Arg Cys Pro Met
 210 215 220
 Ala Gly Ile Ser His Thr Ala Trp His Ser Asn Arg Thr Leu Tyr Glu
 225 230 235
 Thr Cys Ile Glu Pro Trp Leu Ser
 240 245

<210> 315
 <211> 174
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<400> 315
 Met Lys Ser Cys Gly Ser Met Leu Gly Leu Trp Gly Gln Arg Leu Pro
 -30 -25 -20
 Ala Ala Trp Val Leu Leu Leu Pro Phe Leu Pro Leu Leu Leu Leu
 -15 -10 -5
 Ala Ala Pro Ala Pro His Arg Ala Ser Tyr Lys Pro Val Ile Val Val
 1 5 10 15
 His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu Tyr
 20 25 30
 Ile Asn Glu Thr His Pro Gly Thr Val Val Thr Val Leu Asp Leu Phe
 35 40 45
 Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly Phe
 50 55 60
 Arg Glu Ala Val Val Pro Ile Met Ala Lys Ala Pro Gln Gly Val His
 65 70 75
 Leu Ile Cys Tyr Ser Gln Gly Gly Leu Val Cys Arg Ala Leu Leu Ser
 80 85 90 95
 Val Met Asp Asp His Asn Val Asp Ser Phe Ile Ser Leu Ser Ser Pro
 100 105 110
 Gln Met Gly Gln Tyr Gly Asp Thr Asp Tyr Leu Lys Trp Leu Phe Pro
 115 120 125
 Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro
 130 135 140

<210> 316
 <211> 160
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 316
Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ser Leu Val Leu
-15 -10 -5
Cys Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala Phe Asp
1 5 10 15
Glu Leu Arg Thr Asp Phe Lys Ser Pro Ile Asp Gln Cys Asn Pro Val
20 25 30
His Ala Arg Glu Arg Leu Arg Asn Ile Glu Arg Ile Cys Phe Leu Leu
35 40 45
Arg Lys Leu Val Leu Pro Glu Tyr Ser Ile His Ser Leu Phe Cys Ile
50 55 60
Met Phe Leu Cys Ala Gln Glu Trp Leu Thr Leu Gly Leu Asn Val Pro
65 70 75
Leu Leu Phe Tyr His Phe Trp Arg Tyr Phe His Cys Pro Ala Asp Ser
80 85 90 95
Ser Glu Leu Ala Tyr Asp Pro Pro Val Val Met Asn Pro Asp Thr Leu
100 105 110
Ser Tyr Cys Gln Lys Glu Ala Trp Cys Lys Leu Ala Phe Tyr Leu Leu
115 120 125
Ser Phe Phe Tyr Tyr Leu Tyr Cys Met Ile Tyr Thr Leu Val Ser Ser
130 135 140

<210> 317
<211> 426
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28...-1

<400> 317
Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly
-25 -20 -15
Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val
-10 -5 1
Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu
5 10 15 20
His Gln Phe Tyr Glu Thr Leu Pro Ser Glu Met Arg Lys Phe Thr Pro
25 30 35
Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg
40 45 50
Asn Leu Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val
55 60 65
Asp Ile Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg
70 75 80
Trp Thr Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro
85 90 95 100
Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His
105 110 115
Lys Leu Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr
120 125 130
Tyr Thr Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr
135 140 145
Asn Pro Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys
150 155 160
Glu Asn Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn
165 170 175 180

Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu Lys Met Gly
 185 190 195
 Thr Arg Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala Ala Asn Gln
 200 205 210
 Ile Arg Lys Cys Gln Gln Ser Thr Ser Ala Val Ile Gly Val Arg Val
 215 220 225
 Cys Gly Met Gln Val Tyr Gln Ala Gly Ser Gly Glu Leu Met Phe Met
 230 235 240
 Asn Lys Tyr His Gly Arg Lys Leu Ser Val Gln Gly Phe Lys Glu Ala
 245 250 255 260
 Leu Phe Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg Glu Leu Leu
 265 270 275
 Gly Pro Val Leu Lys Lys Leu Thr Glu Leu Lys Ala Val Leu Glu Arg
 280 285 290
 Gln Glu Ser Tyr Arg Phe Tyr Ser Ser Ser Leu Leu Val Ile Tyr Asp
 295 300 305
 Gly Lys Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala Glu Asp Leu
 310 315 320
 Glu Asp Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly Ala Tyr Ala
 325 330 335 340
 Tyr Lys Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met Ile Asp Phe
 345 350 355
 Ala His Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val Val His Glu
 360 365 370
 Gly Gln Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu Ile Asp Ile
 375 380 385
 Val Thr Glu Ile Ser Glu Glu Ser Gly Glu
 390 395

<210> 318
 <211> 301
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 318
 Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu Val
 -20 -15 -10 -5
 Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val Gln
 1 5 10
 Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser Arg
 15 20 25
 Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala Ile
 30 35 40
 Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu
 45 50 55 60
 Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Leu Ser Phe Val Phe
 65 70 75
 Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met
 80 85 90
 Lys Ser Val Leu Trp Trp Leu Pro Val Glu Lys Ala Phe Trp Arg Gln
 95 100 105
 Pro Ala Gly Pro Gly Ser Gly Ile Arg Glu Arg Leu Glu His Pro Val
 110 115 120
 Leu His Val Ser Trp Asn Asp Ala Arg Ala Tyr Cys Ala Trp Arg Gly

125 130 135 140
 Lys Arg Leu Pro Thr Glu Glu Glu Trp Glu Phe Ala Ala Arg Gly Gly
 145 150 155
 Leu Lys Gly Gln Val Tyr Pro Trp Gly Asn Trp Phe Gln Pro Asn Arg
 160 165 170
 Thr Asn Leu Trp Gln Gly Lys Phe Pro Lys Gly Asp Lys Ala Glu Asp
 175 180 185
 Gly Phe His Gly Val Ser Pro Val Asn Ala Phe Pro Ala Gln Asn Asn
 190 195 200
 Tyr Gly Leu Tyr Asp Leu Leu Gly Asn Val Trp Glu Trp Thr Ala Ser
 205 210 215 220
 Pro Tyr Gln Ala Ala Glu Gln Asp Met Arg Val Leu Arg Gly Ala Ser
 225 230 235
 Trp Ile Asp Thr Ala Asp Gly Ser Ala Asn His Arg Ala Arg Val Thr
 240 245 250
 Thr Arg Met Gly Asn Thr Pro Asp Ser Ala Ser Asp Asn Leu Gly Phe
 255 260 265
 Arg Cys Ala Ala Asp Ala Gly Arg Pro Pro Gly Glu Leu
 270 275 280

<210> 319
 <211> 119
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 319
 Met Gly Ser Gly Trp Leu Thr Ala Val Ala Ser Leu Leu Pro Ser Pro
 -15 -10 -5
 Gly Asn Ser Glu Leu Pro Val Gln Ala Leu Gly Arg Arg Gly Gly Arg
 1 5 10 15
 Asp Trp Ala Arg Asn Glu Ala Gly Arg Asp Leu Glu Lys Pro Pro Arg
 20 25 30
 Leu His Cys Ser Gly Arg Gly Arg Leu Glu Glu Pro Val Pro Pro Asn
 35 40 45
 His Leu Pro Val Gly Leu Ser Val Arg Gly Ser Gln Val Leu Ser Ser
 50 55 60
 Ala Gly Pro Arg Arg Cys Arg Leu Thr Gly Thr Arg Asn Pro Val Arg
 65 70 75
 Gly Pro Arg Arg Val Glu Gln Ile Ala Arg Gly Gly Pro Glu Ala Arg
 80 85 90 95
 Arg Gln Ala Gly Asp Ser Cys
 100

<210> 320
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39...-1

<400> 320
 Met Asp Tyr Ser Arg Val Phe Gln Gly Val Phe Phe Thr Phe Lys His

-40 -35 -30
 Asp Ser Tyr Leu Gly Glu Leu Arg Ala Ser Lys Val Leu Trp Phe Leu
 -25 -20 -15 -10
 Ala Gln Ile Pro Ser Arg Val Ala Gly Ser Leu Leu Ser Val Cys Val
 -5 1 5
 Met Ser Arg Asp Gly Asn Ile Lys Asp Ser Gly Glu Asp Thr Gln Ser
 10 15 20
 Gly Thr Arg Glu Val Cys Phe Leu Pro Ala Ser Leu Ser Pro Tyr Ser
 25 30 35
 Ser Arg Leu Thr Phe Gln Arg Arg Phe
 40 45

<210> 323
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -38...-1

<400> 323
 Met Ser Ser Pro Gln Leu Pro Ala Phe Leu Trp Asp Lys Gly Thr Leu
 -35 -30 -25
 Thr Thr Ala Ile Ser Asn Pro Ala Cys Leu Val Asn Val Leu Phe Phe
 -20 -15 -10
 Phe Thr Pro Leu Met Thr Leu Val Thr Leu Leu Ile Leu Val Trp Lys
 -5 1 5 10
 Val Thr Lys Asp Lys Ser Asn Lys Asn Arg Glu Thr His Pro Arg Lys
 15 20 25
 Glu Ala Thr Trp Leu Pro
 30

<210> 324
 <211> 168
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 324
 Met Arg Gly Pro Thr Ala Gly Pro Ser Val Leu Ser Ala Ala His Leu
 -25 -20 -15 -10
 Leu Val Val Ile Leu Pro Ala Asn Ala Ala Leu Lys Leu Leu Ser Trp
 -5 1 5
 Glu Arg Leu Ala Ala Pro Ala Ile Glu Val Glu Val Pro Ser Lys Glu
 10 15 20
 Val Leu Ala Ala Pro Thr Lys Ala Lys Leu Ile Pro Ser Glu Asp Met
 25 30 35
 Leu Ala Ala Pro Ala Met Asp Leu Leu Asp Ser Phe Ser Pro Gly Phe
 40 45 50 55
 Leu Ile Ala Ala Pro Ala Ser Ala Val Ile Thr Trp Pro Gly Pro Ala
 60 65 70
 Asp Leu Val Val Ala Met Leu Ile Ala Pro Val Ala Gly Leu Ile Ala
 75 80 85
 Ala Pro Ala Ile Ala Thr Ser Val Leu Gly Pro Val Ala Val Pro Ala


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          90                      95                      100
Thr Ala Met Pro Pro Ala Val Leu Ala Ala Pro Pro Ser Ala Ala Pro
  105                      110                      115
Gly Val Leu Val Asp Gly Glu Ala Ala Leu Ala Val Pro Trp Glu Ala
  120                      125                      130                      135
Cys Trp Ile Pro Ser Pro Pro Ala
                      140

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<210> 325
<211> 166
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> -15...-1

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<400> 325
Met Leu Pro Leu Leu Ile Ile Cys Leu Leu Pro Ala Ile Glu Gly Lys
-15                      -10                      -5                      1
Asn Cys Leu Arg Cys Trp Pro Glu Leu Ser Ala Leu Ile Asp Tyr Asp
                      5                      10                      15
Leu Gln Ile Leu Trp Val Thr Pro Gly Pro Pro Thr Glu Leu Ser Gln
                      20                      25                      30
Asn Arg Asp His Leu Glu Glu Glu Thr Ala Lys Phe Phe Thr Gln Val
                      35                      40                      45
His Gln Ala Ile Lys Thr Leu Arg Asp Asp Lys Thr Val Leu Leu Glu
  50                      55                      60                      65
Glu Ile Tyr Thr His Lys Asn Leu Phe Thr Glu Arg Leu Asn Lys Ile
                      70                      75                      80
Ser Asp Gly Leu Lys Glu Lys Asp Ile Gln Ser Thr Leu Lys Val Thr
                      85                      90                      95
Ser Cys Ala Asp Cys Arg Thr His Phe Leu Ser Cys Asn Asp Pro Thr
                      100                      105                      110
Phe Cys Pro Ala Arg Asn Arg Arg Thr Ser Leu Trp Ala Val Ser Leu
                      115                      120                      125
Ser Ser Ala Leu Leu Leu Ala Ile Ala Gly Asp Val Ser Phe Thr Gly
  130                      135                      140                      145
Lys Gly Arg Arg Arg Gln
                      150

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<210> 326
<211> 156
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> -15...-1

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<400> 326
Met Asn Ile Leu Met Leu Thr Phe Ile Ile Cys Gly Leu Leu Thr Arg
-15                      -10                      -5                      1
Val Thr Lys Gly Ser Phe Glu Pro Gln Lys Cys Trp Lys Asn Asn Val
                      5                      10                      15
Gly His Cys Arg Arg Arg Cys Leu Asp Thr Glu Arg Tyr Ile Leu Leu
                      20                      25                      30
Cys Arg Asn Lys Leu Ser Cys Cys Ile Ser Ile Ile Ser His Glu Tyr

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35 40 45
 Thr Arg Arg Pro Ala Phe Pro Val Ile His Leu Glu Asp Ile Thr Leu
 50 55 60 65
 Asp Tyr Ser Asp Val Asp Ser Phe Thr Gly Ser Pro Val Ser Met Leu
 70 75 80
 Asn Asp Leu Ile Thr Phe Asp Thr Thr Lys Phe Gly Glu Thr Met Thr
 85 90 95
 Pro Glu Thr Asn Thr Pro Glu Thr Thr Met Pro Pro Ser Glu Ala Thr
 100 105 110
 Thr Pro Glu Thr Thr Met Pro Pro Ser Glu Thr Ala Thr Ser Glu Thr
 115 120 125
 Met Pro Pro Pro Ser Gln Thr Ala Leu Thr His Asn
 130 135 140

<210> 327
 <211> 105
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 327
 Met Ala Lys Met Phe Asp Leu Arg Thr Lys Ile Met Ile Gly Ile Glu
 -30 -25 -20
 Ser Ser Leu Leu Val Ala Ala Met Val Leu Leu Ser Val Val Phe Cys
 -15 -10 -5
 Leu Tyr Phe Lys Val Ala Lys Ala Leu Lys Ala Ala Lys Asp Pro Asp
 1 5 10 15
 Ala Val Ala Val Lys Asn His Asn Pro Asp Lys Val Cys Trp Ala Thr
 20 25 30
 Asn Ser Gln Ala Lys Ala Thr Thr Met Glu Ser Cys Pro Ser Leu Gln
 35 40 45
 Cys Cys Glu Gly Cys Arg Met His Ala Ser Ser Asp Ser Leu Pro Pro
 50 55 60
 Cys Cys Cys Asp Ile Asn Glu Gly Leu
 65 70

<210> 328
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 328
 Met Ser Asp Glu Asp Glu Ser Ser Asp Tyr Leu Cys Leu Ser Ile Leu
 -25 -20 -15
 Gly Leu Phe Cys Cys Leu Pro Leu Ala Ile Pro Ala Val Ile Phe Ser
 -10 -5 1 5
 Cys Leu Thr Lys Asn Tyr Asn Lys Ser Ser Asp Tyr Glu Leu Ala Ala
 10 15 20
 Lys Thr Ser Lys Gln Ala Tyr Tyr Trp Ala Ile Ala Ser Ile Thr Val
 25 30 35
 Gly Ile Leu Gly Thr Ile Leu Tyr Thr Tyr Leu Ile Tyr Leu Leu Arg

Met Val Val Val Glu Pro Gly Ala Ser Leu Phe Pro Asn Gly Val Pro
 -30 -25 -20
 Trp Leu Tyr Ala Val Phe Ala Val Leu Phe Val Phe Phe Leu Phe Ala
 -15 -10 -5
 Met Leu Ser Pro Phe Leu Leu Glu Ile Asp Gln His Ile Lys Lys Phe
 1 5 10 15
 Leu Ile Arg Cys Arg Tyr Ser Leu His Asn Thr Val His Lys Asp Lys
 20 25 30
 Lys Asn Ser Glu Ile Lys Met Asp His Leu Glu Arg Pro Gly Cys Pro
 35 40 45
 Leu Glu Ser Pro Arg Arg Gly Val Leu Gly Gly Lys Asn Gly Met
 50 55 60
 Gly Asn Asp Pro Leu Leu Phe Val Lys Val Thr Lys Glu Pro Arg Asp
 65 70 75 80
 Ser Glu Ala Glu Ile Tyr Thr Pro Gly Pro Ser Val
 85 90

<210> 332
 <211> 62
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -46...-1

<400> 332
 Met Asp Gln Leu Val Phe Lys Glu Thr Ile Trp Asn Asp Ala Phe Trp
 -45 -40 -35
 Gln Asn Pro Trp Asp Gln Gly Gly Leu Ala Val Ile Ile Leu Phe Ile
 -30 -25 -20 -15
 Thr Ala Val Leu Leu Leu Ile Leu Phe Ala Ile Val Phe Gly Leu Leu
 -10 -5 1
 Thr Ser Thr Glu Asn Thr Gln Cys Glu Ala Gly Glu Glu
 5 10 15

<210> 333
 <211> 150
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 333
 Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile Cys
 -20 -15 -10
 Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr Lys
 -5 1 5
 Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Gly Cys
 10 15 20 25
 Leu Tyr Leu Ile Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe
 30 35 40
 Val Leu Ser Val His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys
 45 50 55
 Lys Leu Lys Lys Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu Glu
 60 65 70

Ser Pro Leu Ile Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala Thr
75 80 85
Thr Ala Ser Val Ile Tyr Lys Ile Trp Glu His Arg Ser His His Pro
90 95 100 105
Ser Ser Lys Lys Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys Glu
110 115 120
Glu Gly Ala Arg Arg Tyr
125

<210> 334
<211> 198
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13...-1

<400> 334
Met Leu Leu Gly Arg Leu Thr Ser Gln Leu Leu Arg Ala Val Pro Trp
-10 -5 1
Ala Gly Gly Arg Pro Pro Trp Pro Val Ser Gly Val Leu Gly Ser Arg
5 10 15
Val Cys Gly Pro Leu Tyr Ser Thr Ser Pro Ala Gly Pro Gly Arg Ala
20 25 30 35
Ala Ser Leu Pro Arg Lys Gly Ala Gln Leu Glu Leu Glu Met Val
40 45 50
Pro Arg Lys Met Ser Val Ser Pro Leu Glu Ser Trp Leu Thr Ala Arg
55 60 65
Cys Phe Leu Pro Arg Leu Asp Thr Gly Thr Ala Gly Thr Val Ala Pro
70 75 80
Pro Gln Ser Tyr Gln Cys Pro Pro Ser Gln Ile Gly Glu Gly Ala Glu
85 90 95
Gln Gly Asp Glu Gly Val Ala Asp Ala Pro Gln Ile Gln Cys Lys Asn
100 105 110 115
Val Leu Lys Ile Arg Arg Arg Lys Met Asn His His Lys Tyr Arg Lys
120 125 130
Leu Val Lys Lys Thr Arg Phe Leu Arg Arg Lys Val Gln Glu Gly Arg
135 140 145
Leu Arg Arg Lys Gln Ile Lys Phe Glu Lys Asp Leu Arg Arg Ile Trp
150 155 160
Leu Lys Ala Gly Leu Lys Glu Ala Pro Glu Gly Trp Gln Thr Pro Lys
165 170 175
Ile Tyr Leu Arg Gly Lys
180 185

<210> 335
<211> 88
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24...-1

<400> 335
Met Val Pro Leu Pro Lys Gln Ser Leu Lys Phe Phe Cys Ala Leu Glu
-20 -15 -10

Val Val Leu Pro Ser Cys Asp Cys Arg Ser Pro Gly Ile Gly Leu Val
 -5 1 5
 Glu Glu Pro Met Asp Lys Val Glu Glu Gly Pro Leu Ser Phe Leu Met
 10 15 20
 Lys Arg Lys Thr Ala Gln Lys Leu Ala Ile Gln Lys Ala Leu Ser Asp
 25 30 35 40
 Ala Phe Gln Lys Leu Leu Ile Val Val Leu Gly Lys Thr Val Leu Ile
 45 50 55
 Ile Leu Glu Val Leu Gln Phe Gln
 60

<210> 336
 <211> 150
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -45..-1

<400> 336
 Met Val Leu Met Trp Thr Ser Gly Asp Ala Phe Lys Thr Ala Tyr Phe
 -45 -40 -35 -30
 Leu Leu Lys Gly Ala Pro Leu Gln Phe Ser Val Cys Gly Leu Leu Gln
 -25 -20 -15
 Val Leu Val Asp Leu Ala Ile Leu Gly Gln Ala Tyr Ala Phe Ala Pro
 -10 -5 1
 Pro Pro Glu Ala Gly Ala Pro Arg Arg Ala Pro His Trp His Gln Gly
 5 10 15
 Pro Leu Thr Val Gly Arg Thr Arg Met Trp Asp Arg Gln Pro Arg Ala
 20 25 30 35
 Leu Val Gly Pro Asp Leu Pro Ala Gly Arg Val Gly Ala Val Ala Pro
 40 45 50
 Ala Gly Val Ala Glu Met Gly His Gly His Trp Gly Leu His Gln Pro
 55 60 65
 Leu Trp Gly Val Ser Gly Trp Ala Val Gly Val Gly Leu Gly Arg Cys
 70 75 80
 Leu Cys Ser Ala Gly Thr Ala Arg Val Asp Leu Ala Pro Arg Val Leu
 85 90 95
 Asp Val Phe Arg Met Thr
 100 105

<210> 337
 <211> 142
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 337
 Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn Gly Gln
 -15 -10 -5
 Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Phe Tyr Cys Lys Tyr
 1 5 10
 Cys Phe Val Tyr Gly Gln Asp Trp Ala Pro Thr Ala Gly Leu Glu Glu
 15 20 25

Gly Ile Ser Gln Ile Thr Ser Lys Ser Gln Asp Val Arg Gln Ala Leu
 30 35 40 45
 Val Trp Asn Phe Pro Ile Asp Val Thr Phe Lys Ser Thr Asn Pro Tyr
 50 55 60
 Gly Trp Pro Gln Ile Val Leu Ser Val Tyr Gly Pro Asp Val Phe Gly
 65 70 75
 Asn Asp Val Val Arg Gly Tyr Gly Ala Val His Val Pro Phe Ser Pro
 80 85 90
 Gly Arg His Lys Arg Thr Ile Pro Met Phe Val Pro Glu Ser Thr Ser
 95 100 105
 Lys Leu Gln Lys Phe Thr Arg Ser Ala Ser Cys Ser Thr His
 110 115 120

<210> 338
 <211> 112
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1
 <220>
 <221> UNSURE
 <222> 21
 <223> Xaa = Ala,Pro

<400> 338
 Thr Ser Glu Glu Arg Thr Ala Met Lys Arg Glu Gly Gly Ala Ala His
 -25 -20 -15
 Leu Cys Ser Asp Ser Leu Pro Glu Ser Gln Gln Asp Gly Asn His
 -10 -5 1 5
 Ala Pro Asn Phe Ser Ser His Gly Ser Cys Arg Arg Arg Gln Arg Xaa
 10 15 20
 Asp Met Thr Arg Arg Cys Met Pro Ala Arg Pro Gly Phe Pro Ser Ser
 25 30 35
 Pro Ala Pro Gly Ser Ser Pro Pro Arg Cys His Leu Arg Pro Gly Ser
 40 45 50
 Thr Ala His Ala Ala Gly Lys Arg Thr Glu Ser Pro Gly Asp Arg
 55 60 65
 Tyr Arg Ala Glu Gly Leu Arg Arg Gly Arg Val Ala Gly Ala Arg Val
 70 75 80 85

<210> 339
 <211> 90
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 339
 Met Pro Cys Leu Asp Gln Gln Leu Thr Val His Ala Leu Pro Cys Pro
 -30 -25 -20
 Ala Gln Pro Ser Ser Leu Ala Phe Cys Gln Val Gly Phe Leu Thr Ala
 -15 -10 -5
 Gln Pro Ser Pro Pro Arg Arg Arg Asn Gly Lys Asp Arg Tyr Thr Leu

1 5 10 15
Val Leu Gln His Gln Glu Cys Gln Asp Asp Leu Ala Thr Ser Ser Leu
20 25 30
Val Tyr Leu Ser Leu Pro Cys Phe Lys Asp Leu Gly Arg Ser Lys His
35 40 45
Gln Ser Ile Thr Val Ala Asp Thr Asn Lys
50 55

<210> 340
<211> 80
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -35...-1

<400> 340
Met Pro Phe Gln Phe Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly
-35 -30 -25 -20
Gly Asp Ser Ser Ile Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala
-15 -10 -5
Cys Asn Gly Lys Glu Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro
1 5 10
Gly Ser His Cys Leu Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala
15 20 25
Thr Thr Arg Lys Pro Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys
30 35 40 45

<210> 341
<211> 131
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15...-1

<400> 341
Met Ser Leu Leu Met Phe Thr Gln Leu Leu Leu Cys Gly Phe Leu Tyr
-15 -10 -5 1
Val Arg Val Asp Gly Ser Arg Leu Arg Gln Glu Asp Phe Pro Pro Arg
5 10 15
Ile Val Glu His Pro Ser Asp Val Ile Val Ser Lys Gly Glu Pro Thr
20 25 30
Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr Pro Thr Ile Glu Trp
35 40 45
Tyr Lys Asp Gly Glu Arg Val Glu Thr Asp Lys Asp Asp Pro Arg Ser
50 55 60 65
His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe Phe Leu Arg Ile Val
70 75 80
His Gly Arg Arg Ser Lys Pro Asp Glu Gly Ser Tyr Val Cys Val Ala
85 90 95
Arg Asn Tyr Leu Gly Glu Ala Val Ser Arg Asn Ala Ser Leu Glu Val
100 105 110
Ala Cys Lys
115

<210> 342
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39..-1

<400> 342
 Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser
 -35 -30 -25
 Ile Phe Gly Tyr Lys Arg Arg Gly Gly Val Pro Ser Leu Ile Ala Gly
 -20 -15 -10
 Leu Phe Val Gly Cys Leu Ala Gly Tyr Gly Ala Tyr Arg Val Ser Asn
 -5 1 5
 Asp Lys Arg Asp Val Lys Val Ser Leu Phe Thr Ala Phe Phe Leu Ala
 10 15 20 25
 Thr Ile Met Gly Val Arg Phe Lys Arg Ser Lys Lys Ile Met Pro Ala
 30 35 40
 Gly Leu Val Ala Gly Leu Ser Leu Met Met Ile Leu Arg Leu Val Leu
 45 50 55
 Leu Leu Leu
 60

<210> 343
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -43..-1

<400> 343
 Met Cys Glu Thr Leu Leu Thr Ser Lys Trp Ala Ser Val Ser Pro Ile
 -40 -35 -30
 Pro Ala Leu Leu Gln Glu Gly Glu Asn Arg Asp Ser Arg Arg Leu Gly
 -25 -20 -15
 Asp Ala Leu Leu Phe Leu Arg Pro Ala Gly Ser Cys Ala Leu Gln Val
 -10 -5 1 5
 Ser Trp Pro Ala Ala Leu Ala Gly Pro Arg Ser His Thr Gly Gln Leu
 10 15 20
 Thr Gln His Phe Cys His Leu Lys Asn Asp Thr Cys Ile Pro Pro Ser
 25 30 35
 Leu Gly Pro Pro Arg Asn Ser Gly Ser Leu Glu Ser Leu Arg Ser Lys
 40 45 50
 Arg Tyr
 55

<210> 344
 <211> 217
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<220>
 <221> UNSURE
 <222> 185
 <223> Xaa = Phe,Val

<400> 344
 Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys Val Pro Ser Leu
 -15 -10 -5
 Cys Cys Ser Ser Tyr Val Pro Ser Val Ala Pro Thr Ala Ala His Ser
 1 5 10
 Val Arg Val Pro His Ser Ala Gly His Cys Gly Gln Arg Val Leu Ala
 15 20 25
 Cys Ser Leu Pro Gln Val Phe Leu Lys Pro Trp Ile Phe Val Glu His
 30 35 40 45
 Phe Ser Ser Trp Leu Ser Leu Glu Leu Phe Ser Phe Leu Arg Tyr Leu
 50 55 60
 Gly Thr Leu Leu Cys Ala Cys Gly His Arg Leu Arg Glu Gly Arg Leu
 65 70 75
 Leu Pro Cys Leu Leu Gly Val Gly Ser Trp Leu Leu Phe Asn Asn Trp
 80 85 90
 Thr Gly Gly Ser Trp Phe Ser Leu His Leu Gln Gln Val Ser Leu Ser
 95 100 105
 Gln Gly Ser His Val Ala Ala Phe Leu Pro Glu Ala Ile Gly Pro Gly
 110 115 120 125
 Val Pro Val Pro Val Ser Gly Glu Ser Thr Ser Ala Gln Gln Ser His
 130 135 140
 Ala Gly Trp Gln Leu Ser Ala Glu Ala Asp Ala Cys Pro Ser Val Leu
 145 150 155
 Tyr Ser Glu Val Leu Glu Trp Asn Lys Asn Ile Asn Thr Tyr Thr Ser
 160 165 170
 Phe His Asp Phe Cys Leu Ile Leu Gly Ile Phe Xaa Val Leu Phe Cys
 175 180 185
 Phe Gly Gly Asp Arg Leu Thr Leu His
 190 195

<210> 345
 <211> 183
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 345
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
 -20 -15 -10 -5
 Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
 1 5 10
 Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
 15 20 25
 Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
 30 35 40
 Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
 45 50 55 60
 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
 65 70 75

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
80 85 90
Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
95 100 105
Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser
110 115 120
Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
125 130 135 140
Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
145 150 155
Asp Arg His Lys Met Leu Ser
160

<210> 346
<211> 247
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13...1

<400> 346
Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala Leu Ala Ser Arg Thr
-10 -5 1
Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr
5 10 15
Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr Leu Lys Pro Ser Lys
20 25 30 35
Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn Ala His Leu Arg Thr
40 45 50
Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val Glu Phe Gly Gly Arg
55 60 65
Met Asn Thr Val Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg
70 75 80
Thr Glu Val Gln Lys Ala Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln
85 90 95
Phe Leu Ile Pro Asn Leu Ala Leu Ile Asp Lys Gln Glu Ser Glu Ile
100 105 110 115
Thr Tyr Leu Val Pro Trp Cys Lys Leu Glu Lys Pro Pro Lys Glu Gly
120 125 130
Val Tyr Glu Leu Ala Thr Phe Gln Met Lys Pro Gly Gly Pro Ala Leu
135 140 145
Trp Gly Asp Ala Phe Lys Arg Ala Val His Ala His Val Asn Leu Gly
150 155 160
Tyr Thr Lys Leu Val Gly Val Phe His Thr Glu Tyr Gly Ala Leu Asn
165 170 175
Arg Val His Val Leu Trp Trp Asn Glu Ser Ala Asp Ser Arg Ala Ala
180 185 190 195
Gly Arg His Lys Ser His Glu Asp Pro Arg Val Val Ala Ala Val Arg
200 205 210
Glu Ser Val Asn Tyr Leu Val Ser Gln Gln Asn Met Leu Leu Ile Pro
215 220 225
Thr Ser Phe Ser Pro Leu Lys
230

<210> 347
<211> 104

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47...-1

<400> 347
 Met Phe Ser Pro Arg Gln Ala Leu Thr Pro Asp Pro Leu His Ser Pro
 -45 -40 -35
 Ala Tyr Ser Pro Val Leu Gly Gly Trp Ser Arg Phe Arg Ser Val Asp
 -30 -25 -20
 Phe Arg Phe Leu Tyr Leu Thr Leu Asn Gln Ser Cys Ile Phe Ala Asn
 -15 -10 -5 1
 Tyr Lys Glu Ala His Ala Asn Arg Tyr Cys Thr Glu Gly Arg Tyr Thr
 5 10 15
 Arg Glu Ile Gln Arg Leu Thr Ser Pro Ala Ala Trp Pro Thr Arg Asp
 20 25 30
 Lys Asn Arg Met Ile Ser Asn Gly Met Ala Leu Asn Ser Pro Ala Glu
 35 40 45
 Gly Leu Ala Phe Gln Cys Arg Phe
 50 55

<210> 348
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 348
 Met Ala Lys Tyr Leu Ala Gln Ile Ile Val Met Gly Val Gln Val Val
 -20 -15 -10
 Gly Arg Ala Phe Ala Arg Ala Leu Arg Gln Glu Phe Ala Ala Ser Arg
 -5 1 5 10
 Ala Ala Ala Asp Ala Arg Gly Arg Ala Gly His Arg Ser Ala Ala Ala
 15 20 25
 Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala Gln Gln Ile Leu Asn
 30 35 40
 Val Ser Lys Leu Ser Pro Glu Glu Val Gln Lys Asn Tyr Glu His Leu
 45 50 55
 Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser Phe Tyr Leu Gln Ser
 60 65 70 75
 Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu Glu Leu Lys Ile Gln
 80 85 90
 Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro His Thr
 95 100

<210> 349
 <211> 302
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 349

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Met Ala Pro Asn Ser Ile Thr Leu Leu Gly Leu Ala Val Asn Val Val
      -15      -10      -5
Thr Thr Leu Val Leu Ile Ser Tyr Cys Pro Thr Ala Thr Glu Glu Ala
      1      5      10
Pro Tyr Trp Thr Tyr Leu Leu Cys Ala Leu Gly Leu Phe Ile Tyr Gln
15      20      25      30
Ser Leu Asp Ala Ile Asp Gly Lys Gln Ala Arg Arg Thr Asn Ser Cys
      35      40      45
Ser Pro Leu Gly Glu Leu Phe Asp His Gly Cys Asp Ser Leu Ser Thr
      50      55      60
Val Phe Met Ala Val Gly Ala Ser Ile Ala Ala Arg Leu Gly Thr Tyr
      65      70      75
Pro Asp Trp Phe Phe Phe Cys Ser Phe Ile Gly Met Phe Val Phe Tyr
      80      85      90
Cys Ala His Trp Gln Thr Tyr Val Ser Gly Met Leu Arg Phe Gly Lys
95      100      105      110
Val Asp Val Thr Glu Ile Gln Ile Ala Leu Val Ile Val Phe Val Leu
      115      120      125
Ser Ala Phe Gly Gly Ala Thr Met Trp Asp Tyr Thr Gly Thr Ser Val
      130      135      140
Leu Ser Pro Gly Leu His Ile Gly Leu Ile Ile Ile Leu Ala Ile Met
145      150      155
Ile Tyr Lys Lys Ser Ala Thr Asp Val Phe Glu Lys His Pro Cys Leu
160      165      170
Tyr Ile Leu Met Phe Gly Cys Val Phe Ala Lys Val Ser Gln Lys Leu
175      180      185
Val Val Ala His Met Thr Lys Ser Glu Leu Tyr Leu Gln Asp Thr Val
      195      200      205
Phe Leu Gly Pro Gly Leu Leu Phe Leu Asp Gln Tyr Phe Asn Asn Phe
210      215      220
Ile Asp Glu Tyr Val Val Leu Trp Met Ala Met Val Ile Ser Ser Phe
225      230      235
Asp Met Val Ile Tyr Phe Ser Ala Leu Cys Leu Gln Ile Ser Arg His
240      245      250
Leu His Leu Asn Ile Phe Lys Thr Ala Cys His Gln Ala Pro Glu Gln
255      260      265      270
Val Gln Val Leu Ser Ser Lys Ser His Gln Asn Asn Met Asp
      275      280

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<210> 350

<211> 107

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14...-1

<400> 350

```

Met Ile Leu Val Thr Val Pro Gly Val Cys Pro Ala Gln Cys Cys Trp
      -10      -5      1
Ala Glu Gln Arg Gly Arg Gly Ser Gly Met Tyr Phe Ile Asp Lys Trp
      5      10      15
Ala Arg Pro Ser Trp Val Pro His Trp Leu Asn Asp Leu Phe Ile Val
20      25      30
Lys Ser Gly Tyr Leu Val Cys Ile Arg Thr Val Ile Arg Gln Gly

```

35 40 45 50
 Ile Val Arg Ile Gly Arg Asn Lys Ile Ser Glu Ser Gly Arg Ser Ala
 55 60 65
 Leu Tyr Thr Ile Ala Lys Asn Lys Met Val Ile Phe Lys Val Pro Asp
 70 75 80
 Cys Met His Leu Asn Ala Asp Tyr Phe Gly Val
 85 90

<210> 351
 <211> 229
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

<400> 351
 Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
 -30 -25 -20
 Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu Leu Ala
 -15 -10 -5
 Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
 1 5 10
 Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
 15 20 25 30
 Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
 35 40 45
 Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
 50 55 60
 Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
 65 70 75
 Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
 80 85 90
 Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
 95 100 105 110
 Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
 115 120 125
 Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
 130 135 140
 Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln
 145 150 155
 Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe Gly Asp Lys Val Asn
 160 165 170
 Leu Leu Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln Thr Leu
 175 180 185 190
 Ala Ser Glu Lys Lys
 195

<210> 352
 <211> 206
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

<400> 352
Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
-30 -25 -20
Ile Gly Ala Gly Ala Leu Gly Ala Ala Leu Ala Leu Leu Ala
-15 -10 -5
Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
1 5 10
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
15 20 25 30
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
35 40 45
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
50 55 60
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
65 70 75
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
80 85 90
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
95 100 105 110
Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
115 120 125
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
130 135 140
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Ser Arg
145 150 155
Ala Phe Phe Leu Ser Thr Glu Lys Lys Asn Leu Glu Thr Lys
160 165 170

<210> 353
<211> 88
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -44...-1

<400> 353
Met Ala Ala Glu Gly Trp Ile Trp Arg Trp Gly Trp Gly Arg Arg Cys
-40 -35 -30
Leu Gly Arg Pro Gly Leu Leu Gly Pro Gly Pro Gly Pro Thr Pro
-25 -20 -15
Leu Phe Leu Leu Leu Leu Leu Gly Ser Val Thr Ala Asp Ile Thr Asp
-10 -5 1
Gly Asn Ile Glu His Leu Lys Arg Glu His Ser Leu Ile Lys Pro Tyr
5 10 15 20
Gln Gly Val Gly Ser Ser Ser Pro Ser Gly Thr Ser Arg Ala Ala Leu
25 30 35
Cys Ser Arg Ala Ser Thr Tyr Val
40

<210> 354
<211> 151
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> -32..-1

<400> 354

```
Met Asp Ser Ala Ser Asn Pro Thr Asn Leu Val Ser Thr Ser Gln Arg
      -30                      -25                      -20
His Arg Pro Leu Leu Ser Ser Cys Gly Leu Pro Pro Ser Thr Ala Ser
      -15                      -10                      -5
Ala Val Arg Arg Leu Cys Ser Arg Gly Val Leu Lys Gly Ser Asn Glu
1      5                      10                      15
Arg Arg Asp Met Glu Ser Phe Trp Lys Leu Asn Arg Ser Pro Gly Ser
      20                      25                      30
Asp Arg Tyr Leu Glu Ser Arg Asp Ala Ser Arg Leu Ser Gly Arg Asp
      35                      40                      45
Pro Ser Ser Trp Thr Val Glu Asp Val Met Gln Phe Val Arg Glu Ala
50      55                      60
Asp Pro Gln Leu Gly Pro His Ala Asp Leu Phe Arg Lys His Glu Ile
65      70                      75                      80
Asp Gly Lys Ala Leu Leu Leu Leu Arg Ser Asp Met Met Met Lys Tyr
      85                      90                      95
Met Gly Leu Lys Leu Gly Pro Ala Leu Lys Leu Ser Tyr His Ile Asp
100      105                      110
Arg Leu Lys Gln Gly Lys Phe
115
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<210> 355

<211> 65

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16..-1

<400> 355

```
Met Ala Glu Leu Ala Cys Val Arg Glu Ser Thr Ser Val Ala Trp Ala
      -15                      -10                      -5
Cys Lys Val Arg Gly Gly Thr Ala Pro Ser Pro Ser Gly Ala Glu Gly
1      5                      10                      15
His Val Met Leu Asn Lys Ser Arg Glu Glu Ser Pro Val Ser Ser
      20                      25                      30
Arg Pro Arg Cys Gly Met Pro Thr Val Pro Pro Gly Ser Leu Lys Thr
35      40                      45
Leu
```

<210> 356

<211> 189

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24..-1

<220>

<221> UNSURE

<222> 41

<223> Xaa = Ala,Gly

<400> 356

```

Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu
      -20      -15      -10
Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val
      -5      1      5
Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu
      10      15      20
Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys
      25      30      35      40
Xaa Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln
      45      50      55
Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu
      60      65      70
Thr Leu Ala Thr Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala
      75      80      85
Ala Met Trp Ala Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly
      90      95      100
Glu Val Pro Gly Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg
      105      110      115      120
Glu Lys Asp Pro Lys Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr
      125      130      135
His Gly Leu Ser Ser Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly
      140      145      150
Leu Cys Leu Ala Gly Leu Ala Leu Glu Ile Arg Ser Leu
      155      160      165

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<210> 357

<211> 183

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -47...-1

<400> 357

```

Met Thr Glu Cys Thr Ser Leu Gln Phe Val Ser Pro Phe Ala Phe Glu
      -45      -40      -35
Ala Met Gln Lys Val Asp Val Val Cys Leu Ala Ser Leu Ser Asp Pro
      -30      -25      -20
Glu Leu Arg Leu Leu Leu Pro Cys Leu Val Arg Met Ala Leu Cys Ala
      -15      -10      -5      1
Pro Ala Asp Gln Ser Gln Ser Trp Ala Gln Asp Lys Lys Leu Ile Leu
      5      10      15
Arg Leu Leu Ser Gly Val Glu Ala Val Asn Ser Ile Val Ala Leu Leu
      20      25      30
Ser Val Asp Phe His Ala Leu Glu Gln Asp Ala Ser Lys Glu Gln Gln
      35      40      45
Leu Arg Pro Ser Leu Ala Leu Leu Pro Arg Leu Glu Cys Gly Gly Val
      50      55      60      65
Ile Ser Ala His Cys Asn Leu His Leu Leu Gly Ser Ser Asp Ser Ser
      70      75      80
Ala Ser Val Ser Arg Val Asp Gly Thr Thr Gly Thr Arg His His Ala
      85      90      95
Arg Leu Phe Cys Ile Ile Ser Arg Asp Glu Val Ser Pro Tyr Trp Pro
      100      105      110
Gly Trp Ser Arg Thr Pro Asn Leu Val Ile His Leu Pro Gln Pro Pro
      115      120      125

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Lys Val Leu Gly Leu Pro Ala
130 135

<210> 358
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14...-1

<400> 358
Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln
-10 -5 1
Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys
5 10 15
Gln Asn Met Ile Arg Arg Leu Glu Ile Glu Ala Glu Asn His Tyr Trp
20 25 30
Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Ala
35 40 45 50
Val Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser
55 60 65
Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn
70 75 80
Val Thr Lys Lys Trp Ser
85

<210> 359
<211> 244
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29...-1

<400> 359
Met Glu Leu Thr Ile Phe Ile Leu Arg Leu Ala Ile Tyr Ile Leu Thr
-25 -20 -15
Phe Pro Leu Tyr Leu Leu Asn Phe Leu Gly Leu Trp Ser Trp Ile Cys
-10 -5 1
Lys Lys Trp Phe Pro Tyr Phe Leu Val Arg Phe Thr Val Ile Tyr Asn
5 10 15
Glu Gln Met Ala Ser Lys Lys Arg Glu Leu Phe Ser Asn Leu Gln Glu
20 25 30 35
Phe Ala Gly Pro Ser Gly Lys Leu Ser Leu Leu Glu Val Gly Cys Gly
40 45 50
Thr Gly Ala Asn Phe Lys Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys
55 60 65
Ile Asp Pro Asn Pro Asn Phe Glu Lys Phe Leu Ile Lys Ser Ile Ala
70 75 80
Glu Asn Arg His Leu Gln Phe Glu Arg Phe Val Val Ala Ala Gly Glu
85 90 95
Asn Met His Gln Val Ala Asp Gly Ser Val Asp Val Val Cys Thr
100 105 110 115
Leu Val Leu Cys Ser Val Lys Asn Gln Glu Arg Ile Leu Arg Glu Val
120 125 130

Cys Arg Val Leu Arg Pro Gly Gly Ala Phe Tyr Phe Met Glu His Val
 135 140 145
 Ala Ala Glu Cys Ser Thr Trp Asn Tyr Phe Trp Gln Gln Val Leu Asp
 150 155 160
 Pro Ala Trp His Leu Leu Phe Asp Gly Cys Asn Leu Thr Arg Glu Ser
 165 170 175
 Trp Lys Ala Leu Glu Arg Ala Ser Phe Ser Lys Leu Lys Leu Gln His
 180 185 190 195
 Ile Gln Ala Pro Leu Ser Trp Glu Leu Val Arg Pro His Ile Tyr Gly
 200 205 210
 Tyr Ala Val Lys
 215

<210> 360
 <211> 177
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 360
 Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile Cys
 -20 -15 -10
 Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr Lys
 -5 1 5
 Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Val Lys
 10 15 20 25
 Gly Ser Pro Ser His Cys Leu Pro Tyr Leu Leu Asp Lys Leu Cys Cys
 30 35 40
 Asp Phe Ala Asn Met Asp Ile Phe Gln Gly Cys Leu Tyr Leu Ile Tyr
 45 50 55
 Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe Val Leu Ser Val His
 60 65 70
 Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys Lys Leu Lys Lys Gln
 75 80 85
 Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu Glu Ser Pro Leu Ile Asn
 90 95 100 105
 Asn Ile Asp Gln Thr Leu His Arg Val Ala Thr Thr Ala Ser Val Ile
 110 115 120
 Tyr Lys Ile Trp Glu His Arg Ser His His Pro Ser Ser Lys Lys Ile
 125 130 135
 Lys His Cys Lys Leu Lys Lys Lys Ser Lys Glu Glu Gly Ala Arg Arg
 140 145 150
 Tyr

<210> 361
 <211> 158
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 361
 Met Ala Leu Cys Ala Leu Thr Arg Ala Leu Pro Ser Leu Asn Leu Ala

```

-20          -15          -10
Pro Pro Thr Val Ala Ala Pro Ala Pro Ser Leu Phe Pro Ala Ala Gln
-5          1          5          10
Met Met Asn Asn Gly Leu Leu Gln Gln Pro Ser Ala Leu Met Leu Leu
          15          20          25
Pro Cys Arg Pro Val Leu Thr Ser Val Ala Leu Asn Ala Asn Phe Val
          30          35          40
Ser Trp Lys Ser Arg Thr Lys Tyr Thr Ile Thr Pro Val Lys Met Arg
          45          50          55
Lys Ser Gly Gly Arg Asp His Thr Gly Ala Gly Asn Val Arg Arg Thr
60          65          70          75
Val Gly Arg Val Ser Asn Val Asp His Asn Lys Arg Val Ile Gly Lys
          80          85          90
Ala Gly Arg Asn Arg Trp Leu Gly Lys Arg Pro Asn Ser Gly Arg Trp
          95          100          105
His Arg Lys Gly Gly Trp Ala Gly Arg Lys Ile Arg Pro Leu Pro Pro
          110          115          120
Met Lys Ser Tyr Val Lys Leu Pro Ser Ala Ser Ala Gln Ser
          125          130          135

```

```

<210> 362
<211> 186
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> -19...-1

```

```

<400> 362
Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn Gly Gln
          -15          -10          -5
Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Leu Tyr Cys Lys Tyr
          1          5          10
Cys Phe Val Tyr Gly Gln Asp Trp Ala Pro Thr Ala Gly Leu Glu Glu
          15          20          25
Gly Ile Ser Gln Ile Thr Ser Lys Ser Gln Asp Val Arg Gln Ala Leu
30          35          40          45
Val Trp Asn Phe Pro Ile Asp Val Thr Phe Lys Ser Thr Asn Pro Tyr
          50          55          60
Gly Trp Pro Gln Ile Val Leu Ser Val Tyr Gly Pro Asp Val Phe Gly
          65          70          75
Asn Asp Val Val Arg Gly Tyr Gly Ala Val His Val Pro Phe Ser Pro
          80          85          90
Gly Arg His Lys Arg Thr Ile Pro Met Phe Val Pro Glu Ser Thr Ser
          95          100          105
Lys Leu Gln Lys Phe Thr Ser Trp Phe Met Gly Arg Arg Pro Glu Tyr
110          115          120          125
Thr Asp Pro Lys Val Val Ala Gln Gly Glu Gly Arg Glu Ala Ile Thr
          130          135          140
Ala Pro Arg Lys Ala Val Phe Ser Val His Gly Leu Thr Ser Pro Arg
          145          150          155
Ala Leu Ala Leu Val His Ile Lys Gly Thr
          160          165

```

```

<210> 363
<211> 150
<212> PRT

```

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -47...-1

<400> 363

```
Met Gly Asp Arg Val Lys Gly Ser Lys Ser Arg Ala Phe Val Ser Pro
   -45                               -40               -35
Trp Pro His Thr Pro Met Ala Ser Gly Leu Arg Asp Pro Trp Leu Gln
   -30                               -25               -20
Pro Thr Ala Leu Gly Leu Ala Leu Cys Ser Thr Lys Ala Leu Ser Val
   -15                               -10               -5               1
Gly Ser Ala Pro Leu Pro Pro Arg Asn Ser Asn Thr Met Ala Ala Ala
   5                               10               15
Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu
   20                               25               30
Val Ala Asp Thr Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu
   35                               40               45
Ser Gly Pro Arg Gly Pro Thr Gly Arg Ser Phe Ala Val His Thr Arg
   50                               55               60               65
Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val
   70                               75               80
Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg
   85                               90               95
Pro Gly Ile His Leu Cys
   100
```

<210> 364

<211> 95

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -45...-1

<400> 364

```
Met Leu His His Val Ile Thr Ala Gly Pro Val Leu Leu Leu His Leu
   -45                               -40               -35               -30
Pro Arg Pro Asp Thr Ser Thr Arg Leu Leu Thr Ser Val Ser Ala
   -25                               -20               -15
Phe Ile Leu Leu Leu Leu Ser Gly Pro Ala Glu Met Ser Ala Ser
   -10                               -5               1
Gln Glu Ser Phe Pro Gly Ser Leu Gln Gln Glu Ile Ala Ser Leu Ile
   5                               10               15
Thr Val Ala Leu Gly Ser Leu Ile Ser Leu Ser Cys Ser Thr Leu Leu
   20                               25               30               35
Tyr Phe Ser Cys Glu Leu Lys Ile Pro Cys Glu Asp Val Asn Leu
   40                               45               50
```

<210> 365

<211> 94

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26...-1

<400> 365

```
Met Ala Ala Ile Glu Ile Glu Val Lys Pro Asn Gln Gly Phe Cys Gly
-25                      -20                      -15
Ser Ala Cys Leu Leu Ala Val Ile Arg Ala Phe Phe Lys Lys Asn
-10                      -5                      1                      5
Ala Cys Leu Leu Arg Glu Ile Leu Gln Ser Lys Leu Gly Gly Met Gly
10                      15                      20
Pro Val Val Phe Ser Tyr Arg Gly Leu Pro Leu Trp Leu Phe Ala Trp
25                      30                      35
Leu Phe Pro Arg Cys Thr Val Pro Leu Thr Phe Gly Phe Glu Asn Met
40                      45                      50
Arg Gly Leu Gly Val Val Ala Tyr Ala Cys Asn Pro Ser Thr
55                      60                      65
```

<210> 366

<211> 140

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -40...-1

<400> 366

```
Met Thr Ser Met Thr Gln Ser Leu Arg Glu Val Ile Lys Ala Met Thr
-40                      -35                      -30                      -25
Lys Ala Arg Asn Phe Glu Arg Val Leu Gly Lys Ile Thr Leu Val Ser
-20                      -15                      -10
Ala Ala Pro Gly Lys Val Ile Cys Glu Met Lys Val Glu Glu Glu His
-5                      1                      5
Thr Asn Ala Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val
10                      15                      20
Asp Asn Ile Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro
25                      30                      35                      40
Gly Val Ser Val Asp Met Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu
45                      50                      55
Gly Glu Asp Ile Val Ile Thr Ala His Val Leu Lys Gln Gly Lys Thr
60                      65                      70
Leu Ala Phe Thr Ser Val Asp Leu Thr Asn Lys Ala Thr Gly Lys Leu
75                      80                      85
Ile Ala Gln Gly Arg His Thr Lys His Leu Gly Asn
90                      95                      100
```

<210> 367

<211> 39

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -35...-1

<400> 367

```
Met Asp Pro Gly Trp Pro His Phe Lys Leu Thr His Ser Arg Cys Met
-35                      -30                      -25                      -20
Ala Val Leu Phe Leu Gly Thr Leu Pro Leu Cys Pro Val Thr Ser Pro
```

Val Trp Gly Trp Ser Pro Gly
1

-10

-5

<210> 368
<211> 78
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -41..-1

<400> 368
Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu Glu Tyr
-40 -35 -30
Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr Leu Leu
-25 -20 -15 -10
Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu Leu Val
-5 1 5
Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser Cys Val
10 15 20
Gly Ser Phe Ile Leu Ala Gly Ser Leu Phe Glu Phe Pro Gly
25 30 35

<210> 369
<211> 83
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -40..-1

<400> 369
Met Gly Leu Thr Ser Thr Trp Arg Tyr Gly Arg Gly Pro Gly Ile Gly
-40 -35 -30 -25
Thr Val Thr Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val
-20 -15 -10
Thr Met Ala Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu
-5 1 5
Asp Thr Thr Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu
10 15 20
Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn
25 30 35 40
Lys Ser Lys

<210> 370
<211> 92
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 370
Met Ala Val Leu Ala Gly Ser Leu Leu Gly Pro Thr Ser Arg Ser Ala

<210> 372
 <211> 184
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<400> 372
 Met Ala Cys Thr Thr Thr Ala Pro Ala Gln Glu His Met Leu Leu Thr
 -30 -25 -20
 Pro Leu Thr Ala Leu Met Val Gly Ala Ala Ser Leu Leu Glu Gly Arg
 -15 -10 -5 1
 Pro Gln Ile Ser Ala Pro Tyr Ser Arg Ala Ala Cys Cys Ser Pro Gly
 5 10 15
 Ala Leu Gly Cys Pro Ala Ala Arg Val Gly Ile Leu Asp Leu Met Tyr
 20 25 30
 Ser Trp Val Ala Arg Lys Val Leu Arg Cys Ser Asn Thr Gly Leu Gln
 35 40 45
 Gly Leu His Cys Ala Pro Ala Tyr Ala Ala Leu Gly Met Asp Pro
 50 55 60 65
 Gly Arg Gly Gln Arg Ala Gly Gly Pro Val Glu Gln Thr Tyr Phe Ser
 70 75 80
 Pro Met Gly Lys Leu Pro Thr Leu Ser Trp Leu Glu Gly Cys Thr Ala
 85 90 95
 Val Met Thr Leu Ala Ser Ala Trp Leu Leu Gly Ser Pro Arg Glu Thr
 100 105 110
 Tyr Asn His Glu Lys Val Lys Glu Lys Gln Cys Pro Phe Ser Ser Met
 115 120 125
 Val Leu Gly Glu Tyr Gly Phe Leu Pro Thr Val Asp His Leu Ser Thr
 130 135 140 145
 Leu Gly Cys Asn Met Arg Glu Leu
 150

<210> 373
 <211> 101
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 373
 Met Ala His Val Ala Glu Lys Asp Gly Leu Asp Trp Ala Ser Gly Cys
 -40 -35 -30
 Ile Pro Gly Leu Gln Thr Gly Ile Cys Leu Phe Gly Ser Gln Leu Cys
 -25 -20 -15
 Phe His Leu Ser Trp Leu Tyr Ser Trp Ala Ser Gln Cys Gly Pro Thr
 -10 -5 1 5
 Ala Pro Val Ile Asp Lys Lys Ser Ser Pro Leu Leu Thr Glu Leu Leu
 10 15 20
 Asp Leu Val Leu Ile Gly Pro Asp Glu Glu Gly Ile Gln Pro Gln Val
 25 30 35
 Ile Ile Val Ala Arg Lys Met Glu Tyr Thr Lys Trp Thr Gly Leu Ala
 40 45 50

Cys Thr His Arg Asp
55

<210> 374
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20...-1

<400> 374
Met Gly Pro Asn Thr Lys Asn Leu Leu Leu Val Thr Leu Val Ala Ser
-20 -15 -10 -5
Thr Val Pro Gly Asn Ser Leu Gly Gln Asp Phe Thr Phe Ala His Leu
1 5 10
Glu Arg Ser Cys Thr Arg Glu Asn Arg Ser Pro Gly Glu Val Phe Gln
15 20 25
Gln Pro Cys Lys Ser Gly Gly Gly Val Gly Glu Pro Asn Ala Gln
30 35 40
Gly Gln Leu Leu Ser Gln His Pro Leu Pro Ala Phe Ile Asn Cys Ser
45 50 55 60
His Gly Gln Ala Phe
65

<210> 375
<211> 90
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28...-1

<400> 375
Met Ala Phe Pro Gly Gln Ser Asp Thr Lys Met Gln Trp Pro Glu Val
-25 -20 -15
Pro Ala Leu Pro Leu Leu Ser Ser Leu Cys Met Ala Met Val Arg Lys
-10 -5 1
Ser Ser Ala Leu Gly Lys Glu Val Gly Arg Arg Val Lys Glu Met Val
5 10 15 20
Met Leu Val Ala Pro Phe Arg Gln Ser Ser Ser Leu Ser Arg Thr Phe
25 30 35
Ser Ser Arg Lys Val Val Lys Ala His Ala Ser Leu His Gly Ala Arg
40 45 50
Leu Ser Pro Leu Ser Arg Asn Ile Arg Gly
55 60

<210> 376
<211> 89
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -33...-1

<220>
 <221> UNSURE
 <222> 47
 <223> Xaa = Ala,Pro,Ser,Thr

<400> 376
 Met Ala Gln Pro Ala Ala Pro Ser Leu Thr Arg Pro Phe Leu Ala Glu
 -30 -25 -20
 Ala Pro Thr Ala Leu Val Pro His Ser Pro Leu Pro Gly Ala Leu Ser
 -15 -10 -5
 Ser Ala Pro Gly Pro Lys Gln Pro Pro Thr Ala Ser Thr Gly Pro Glu
 1 5 10 15
 Leu Leu Leu Leu Pro Leu Ser Ser Phe Met Pro Cys Gly Ala Ala Ala
 20 25 30
 Pro Ala Arg Val Ser Ser Gln Arg Ala Thr Pro Arg Asp Lys Pro Xaa
 35 40 45
 Gly Pro Leu Ile Pro Gly Gln Cys Pro
 50 55

<210> 377
 <211> 132
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 377
 Met Asn Arg Val Leu Cys Ala Pro Ala Ala Gly Ala Val Arg Ala Leu
 -15 -10 -5 1
 Arg Leu Ile Gly Trp Ala Ser Arg Ser Leu His Pro Leu Pro Gly Ser
 5 10 15
 Arg Asp Arg Ala His Pro Ala Ala Glu Glu Glu Asp Asp Pro Asp Arg
 20 25 30
 Pro Ile Glu Phe Ser Ser Ser Lys Ala Asn Pro His Arg Trp Ser Val
 35 40 45
 Gly His Thr Met Gly Lys Gly His Gln Arg Pro Trp Trp Lys Val Leu
 50 55 60 65
 Pro Leu Ser Cys Phe Leu Val Ala Leu Ile Ile Trp Cys Tyr Leu Arg
 70 75 80
 Glu Glu Ser Glu Ala Asp Gln Trp Leu Arg Gln Val Trp Gly Glu Val
 85 90 95
 Pro Glu Pro Ser Asp Arg Ser Glu Glu Pro Glu Thr Pro Ala Ala Tyr
 100 105 110
 Arg Ala Arg Thr
 115

<210> 378
 <211> 102
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<220>

Case	Age	Sex	Occupation	Duration of illness	Site of lesion	Pathological changes	Microscopic findings	Diagnosis
1	45	M	Farmer	10 years	Brain	Chronic	Microscopic	Chronic
2	55	F	Housewife	5 years	Brain	Chronic	Microscopic	Chronic
3	65	M	Teacher	15 years	Brain	Chronic	Microscopic	Chronic
4	75	F	Retiree	20 years	Brain	Chronic	Microscopic	Chronic
5	85	M	Farmer	25 years	Brain	Chronic	Microscopic	Chronic

Case	Age	Sex	Occupation	Duration of illness	Site of lesion	Pathological changes	Microscopic findings	Diagnosis
1	45	M	Farmer	10 years	Brain	Chronic	Microscopic	Chronic
2	55	F	Housewife	5 years	Brain	Chronic	Microscopic	Chronic
3	65	M	Teacher	15 years	Brain	Chronic	Microscopic	Chronic
4	75	F	Retiree	20 years	Brain	Chronic	Microscopic	Chronic
5	85	M	Farmer	25 years	Brain	Chronic	Microscopic	Chronic

Case	Age	Sex	Occupation	Duration of illness	Site of lesion	Pathological changes	Microscopic findings	Diagnosis
1	45	M	Farmer	10 years	Brain	Chronic	Microscopic	Chronic
2	55	F	Housewife	5 years	Brain	Chronic	Microscopic	Chronic
3	65	M	Teacher	15 years	Brain	Chronic	Microscopic	Chronic
4	75	F	Retiree	20 years	Brain	Chronic	Microscopic	Chronic
5	85	M	Farmer	25 years	Brain	Chronic	Microscopic	Chronic

[illegible][illegible][illegible]

Arg Ala Leu Tyr Arg Arg His Val Leu Gly Ile Val Leu Gln Gly Pro
 25 30 35
 Ala Leu Cys Phe Ala Ala Ala Ile Phe Ser Leu Phe Phe Val Pro Leu
 40 45 50
 Ser Tyr Leu Leu Met Val Thr Val Ile Leu Leu Pro Tyr Val Ser Lys
 55 60 65 70
 Val Thr Gly Trp Cys Arg Asp Arg Leu Leu Gly His Arg Glu Pro Ser
 75 80 85
 Ala His Pro Val Glu Val Phe Ser Phe Asp Leu His Glu Pro Leu Ser
 90 95 100
 Lys Glu Arg Val Glu Ala Phe Ser Asp Gly Val Tyr Ala Ile Val Ala
 105 110 115
 Thr Leu Leu Ile Leu Asp Ile Trp
 120 125

<210> 381
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 381
 Met Glu Met Leu Phe Asp Glu Arg Ala Pro Leu Leu Phe Ile Leu Phe
 -25 -20 -15
 Lys Phe Ser Leu Cys Pro Tyr Ala Ala Ala Leu Ser Lys Pro Ile Phe
 -10 -5 1 5
 Gly Ser Val Ala Cys Met Thr Lys Glu Ile Leu Ala Arg His Gly Gly
 10 15 20
 Ser Arg Leu
 25

<210> 382
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 382
 Met Leu Arg Pro Ala Leu Pro Trp Leu Tyr Leu Gly Leu Cys Ser Leu
 -20 -15 -10
 Leu Val Gly Glu Ala Glu Ala Pro Ser Pro Val Asp Pro Leu Glu Arg
 -5 1 5
 Ser Arg Pro Tyr Ala Val Leu Arg Gly Gln Asn Leu Val Leu Met Gly
 10 15 20 25
 Thr Ile Phe Ser Ile Leu Leu Val Thr Val Ile Leu Met Ala Phe Cys
 30 35 40
 Val Tyr Lys Pro Ile Arg Arg Arg
 45

<210> 383
 <211> 95
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -48...-1

<400> 383

```
Met Ala Ser Ser His Trp Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr
      -45      -40      -35
Leu Gly Phe Gln Val Gln Lys Ile Tyr Pro Phe His Asp Asn Trp Asn
      -30      -25      -20
Thr Ala Cys Phe Val Ile Leu Leu Leu Phe Ile Phe Thr Val Val Ser
      -15      -10      -5
Leu Val Val Leu Ala Phe Leu Tyr Glu Val Leu Asp Cys Cys Cys Cys
1      5      10      15
Val Lys Asn Lys Thr Val Lys Asp Leu Lys Ser Glu Pro Asn Pro Leu
      20      25      30
Arg Ser Met Met Asp Asn Ile Arg Lys Arg Glu Thr Glu Val Val
      35      40      45
```

<210> 384

<211> 150

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20...-1

<400> 384

```
Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu Val
-20      -15      -10      -5
Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val Gln
      1      5      10
Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser Arg
      15      20      25
Asp Gly Gly Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala Ile
      30      35      40
Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu
      45      50      55      60
Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val Phe
      65      70      75
Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met
      80      85      90
Lys Val Lys Phe Thr His Gly Gly Thr Gly Ser Ser Gln Thr Ala Pro
      95      100      105
Thr Cys Gly Arg Glu Ser Ser Pro Arg Glu Thr Lys Leu Arg Met Ala
      110      115      120
Ser Met Glu Ser Pro Gln
125      130
```

<210> 385

<211> 354

<212> PRT

<213> Homo sapiens

<400> 385

```
Met Ser Ala Gly Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro
```

```

1           5           10           15
Met Pro Thr Cys Arg Val Tyr Gly Thr Val Ala His Gln Asp Gly His
20
Leu Leu Val Leu Gly Gly Cys Gly Arg Ala Gly Leu Pro Leu Asp Thr
35
Ala Glu Thr Leu Asp Met Ala Ser His Thr Trp Leu Ala Leu Ala Pro
50
Leu Pro Thr Ala Arg Ala Gly Ala Ala Val Val Leu Gly Lys Gln
65
Val Leu Val Val Cys Gly Val Asp Glu Val Gln Ser Pro Val Ala Ala
85
Val Glu Ala Phe Leu Met Asp Glu Gly Arg Trp Glu Arg Arg Ala Thr
100
Leu Pro Gln Ala Ala Met Gly Val Ala Thr Val Glu Arg Asp Gly Met
115
Val Tyr Ala Leu Gly Gly Met Gly Pro Asp Thr Ala Pro Gln Ala Gln
130
Val Arg Val Tyr Asp Pro Arg Arg Asp Cys Trp Leu Ser Leu Pro Ser
145
Met Pro Thr Pro Cys Tyr Gly Ala Ser Thr Phe Leu His Gly Asn Lys
165
Ile Tyr Val Leu Gly Gly Arg Gln Gly Lys Leu Pro Val Thr Ala Phe
180
Glu Ala Phe Asp Leu Glu Ala Arg Thr Trp Thr Arg His Pro Ser Leu
195
Pro Ser Arg Arg Ala Phe Ala Gly Cys Ala Met Ala Glu Gly Ser Val
210
Phe Ser Leu Gly Gly Leu Gln Gln Pro Gly Pro His Asn Phe Tyr Ser
225
Arg Pro His Phe Val Asn Thr Val Glu Met Phe Asp Leu Glu His Gly
245
Ser Trp Thr Lys Leu Pro Arg Ser Leu Arg Met Arg Asp Lys Arg Ala
260
Asp Phe Val Val Gly Ser Leu Gly Gly His Ile Val Ala Ile Gly Gly
275
Leu Gly Asn Gln Pro Cys Pro Leu Gly Ser Val Glu Ser Phe Ser Leu
290
Ala Arg Arg Arg Trp Glu Ala Leu Pro Ala Met Pro Thr Ala Arg Cys
305
Ser Cys Ser Ser Leu Gln Ala Gly Pro Arg Leu Phe Val Ile Gly Gly
325
Val Ala Gln Gly Pro Ser Gln Ala Val Glu Ala Leu Cys Leu Arg Asp
340
Gly Val
345
350

```

<210> 386

<211> 207

<212> PRT

<213> Homo sapiens

<400> 386

```

Met Ala Leu Leu Phe Ala Arg Ser Leu Arg Leu Cys Arg Trp Gly Ala
1
Lys Arg Leu Gly Val Ala Ser Thr Glu Ala Gln Arg Gly Val Ser Phe
20
Lys Leu Glu Glu Lys Thr Ala His Ser Ser Leu Ala Leu Phe Arg Asp
35
Asp Thr Gly Val Lys Tyr Gly Leu Val Gly Leu Glu Pro Thr Lys Val
40
45

```


50 55 60
 Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val Val Leu Ala Asp
 65 70 75 80
 Thr Ala Val Thr Ser Gly Arg His Tyr Trp Glu Val Thr Val Lys Arg
 85 90 95
 Ser Gln Gln Phe Arg Ile Gly Val Ala Asp Val Asp Met Ser Arg Asp
 100 105 110
 Ser Cys Ile Gly Val Asp Asp Arg Ser Trp Val Phe Thr Tyr Ala Gln
 115 120 125
 Arg Lys Trp Tyr Thr Met Leu Ala Asn Glu Lys Ala Pro Val Glu Gly
 130 135 140
 Ile Gly Gln Pro Glu Lys Val Gly Leu Leu Leu Glu Tyr Glu Ala Gln
 145 150 155 160
 Lys Leu Ser Leu Val Asp Val Ser Gln Val Ser Val Val His Thr Leu
 165 170 175
 Gln Thr Asp Phe Arg Gly Pro Val Val Pro Ala Phe Ala Leu Trp Asp
 180 185 190
 Gly Glu Leu Leu Thr His Ser Gly Leu Glu Val Pro Glu Gly Leu
 195 200 205

<210> 387
 <211> 210
 <212> PRT
 <213> Homo sapiens

<400> 387
 Met Ala Ala Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly
 1 5 10 15
 Gln Ala Leu Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg
 20 25 30
 Phe Ser Val Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp
 35 40 45
 Gln Asn Leu Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala
 50 55 60
 Val Ala Ile Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala
 65 70 75 80
 Pro Ala Pro Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val
 85 90 95
 Val Asp Ala Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu
 100 105 110
 Ser Gly Met Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu
 115 120 125
 Pro Gly Phe Val Pro Val Ala Pro Ile Cys Thr Asp Lys Ile Asn Ala
 130 135 140
 Ala Asn Tyr Ala Ser Val Lys Thr Pro Ala Leu Ile Val Tyr Gly Asp
 145 150 155 160
 Gln Asp Pro Met Gly Gln Thr Ser Phe Glu His Leu Lys Gln Leu Pro
 165 170 175
 Asn His Arg Val Leu Ile Met Lys Gly Ala Gly His Pro Cys Tyr Leu
 180 185 190
 Asp Lys Pro Glu Glu Trp His Thr Gly Leu Leu Asp Phe Leu Gln Gly
 195 200 205
 Leu Gln
 210

<210> 388
 <211> 375
 <212> PRT

<213> Homo sapiens

<400> 388

Met Ala Val Thr Glu Ala Ser Leu Leu Arg Gln Cys Pro Leu Leu Leu
1 5 10 15
Pro Gln Asn Arg Ser Lys Thr Val Tyr Glu Gly Phe Ile Ser Ala Gln
20 25 30
Gly Arg Asp Phe His Leu Arg Ile Val Leu Pro Glu Asp Leu Gln Leu
35 40 45
Lys Asn Ala Arg Leu Leu Cys Ile Trp Gln Leu Arg Thr Ile Leu Ser
50 55 60
Gly Tyr His Arg Ile Val Gln Gln Arg Met Gln His Ser Pro Asp Leu
65 70 75 80
Met Ser Phe Met Met Glu Leu Lys Met Leu Leu Glu Val Ala Leu Lys
85 90 95
Asn Arg Gln Glu Leu Tyr Ala Leu Pro Pro Pro Gln Phe Tyr Ser
100 105 110
Ser Leu Ile Glu Glu Ile Gly Thr Leu Gly Trp Asp Lys Leu Val Tyr
115 120 125
Ala Asp Thr Cys Phe Ser Thr Ile Lys Leu Lys Ala Glu Asp Ala Ser
130 135 140
Gly Arg Glu His Leu Ile Thr Leu Lys Leu Lys Ala Lys Tyr Pro Ala
145 150 155 160
Glu Ser Pro Asp Tyr Phe Val Asp Phe Pro Val Pro Phe Cys Ala Ser
165 170 175
Trp Thr Pro Gln Ser Ser Leu Ile Ser Ile Tyr Ser Gln Phe Leu Ala
180 185 190
Ala Ile Glu Ser Leu Lys Ala Phe Trp Asp Val Met Asp Glu Ile Asp
195 200 205
Glu Lys Thr Trp Val Leu Glu Pro Glu Lys Pro Pro Arg Ser Ala Thr
210 215 220
Ala Arg Arg Ile Ala Leu Gly Asn Asn Val Ser Ile Asn Ile Glu Val
225 230 235 240
Asp Pro Arg His Pro Thr Met Leu Pro Glu Cys Phe Phe Leu Gly Ala
245 250 255
Asp His Val Val Lys Pro Leu Gly Ile Lys Leu Ser Arg Asn Ile His
260 265 270
Leu Trp Asp Pro Glu Asn Ser Val Leu Gln Asn Leu Lys Asp Val Leu
275 280 285
Glu Ile Asp Phe Pro Ala Arg Ala Ile Leu Glu Lys Ser Asp Phe Thr
290 295 300
Met Asp Cys Gly Ile Cys Tyr Ala Tyr Gln Leu Asp Gly Thr Ile Pro
305 310 315 320
Asp Gln Val Cys Asp Asn Ser Gln Cys Gly Gln Pro Phe His Gln Ile
325 330 335
Cys Leu Tyr Glu Trp Leu Arg Gly Leu Leu Thr Ser Arg Gln Ser Phe
340 345 350
Asn Ile Ile Phe Gly Glu Cys Pro Tyr Cys Ser Lys Pro Ile Thr Leu
355 360 365
Lys Met Ser Gly Arg Lys His
370 375

<210> 389

<211> 509

<212> PRT

<213> Homo sapiens

<400> 389

Asp Leu Asp Lys Lys Glu Asn Gly Leu Arg Asp Ile Leu Ala Val Leu
 465 470 475 480
 Thr Met Lys Arg Asp Gly Ser Leu His Val Thr Cys Thr Asp Gln Glu
 485 490 495
 Thr Gly Lys Cys Glu Ala Ile Ser Ile Glu Ile Ala Ser
 500 505

<210> 390
 <211> 78
 <212> PRT
 <213> Homo sapiens

<400> 390
 Met Tyr Asn Thr Gly Arg His Val Ser Leu Arg Leu Asp Lys Glu His
 1 5 10 15
 Leu Val Asn Ile Ser Gly Gly Pro Met Thr Tyr Ser His Arg Leu Glu
 20 25 30
 Glu Ile Arg Leu His Phe Gly Ser Glu Asp Ser Gln Gly Ser Glu His
 35 40 45
 Leu Leu Asn Gly Gln Ala Phe Ser Gly Glu Leu Gln Glu Arg Asp Leu
 50 55 60
 Phe Ile Leu Leu Thr Ser Val Ser Gly His Leu Pro Asp Thr
 65 70 75

<210> 391
 <211> 162
 <212> PRT
 <213> Homo sapiens

<400> 391
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
 1 5 10 15
 Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Ile Val
 20 25 30
 Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
 35 40 45
 Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
 50 55 60
 Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
 65 70 75 80
 Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
 85 90 95
 Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
 100 105 110
 Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
 115 120 125
 Thr Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
 130 135 140
 Ile Arg Asp Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu
 145 150 155 160
 Leu Gly

<210> 392
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 392

Met Asn Ser Leu Leu His Phe Gly Ile Leu Leu Glu Leu Ser Leu Leu
 1 5 10 15
 Lys Gln Phe Lys Ser Val Tyr Val Pro Gly Asn His Thr His Gln Ala
 20 25 30
 Ser Tyr Lys Pro Leu Leu Lys Gln Val Val Glu Glu Ile Phe His Pro
 35 40 45
 Glu Arg Pro Asp Ser Val Asp Ile Glu His Met Ser Ser Gly Leu Thr
 50 55 60
 Asp Leu Leu Lys Thr Gly Phe Ser Met Phe Met Lys Val Ser Arg Pro
 65 70 75 80
 His Pro Ser Asp Tyr Pro Leu Leu Ile Leu Phe Val Val Gly Gly Val
 85 90 95
 Thr Val Ser Glu Val Lys Met Val Lys Asp Leu Val Ala Ser Leu Lys
 100 105 110
 Pro Gly Thr Gln Val Ile Val Leu Ser Thr Arg Leu Leu Lys Pro Leu
 115 120 125
 Asn Ile Pro Glu Leu Leu Phe Ala Thr Asp Arg Leu His Pro Asp Leu
 130 135 140
 Gly Phe
 145

<210> 393
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 393
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
 1 5 10 15
 Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val
 20 25 30
 Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
 35 40 45
 Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
 50 55 60
 Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
 65 70 75 80
 Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
 85 90 95
 Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
 100 105 110
 Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
 115 120 125
 Ala Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
 130 135 140
 Ile Arg Asp Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu
 145 150 155 160
 Leu Gly Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile
 165 170 175
 Val Gly Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser
 180 185 190
 Ser Ser Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser
 195 200 205
 Tyr His Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr
 210 215 220
 Val
 225

<210> 394
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 394
 Met Arg Leu Gln Asp Arg Ile Ala Thr Phe Phe Phe Pro Lys Gly Met
 1 5 10 15
 Met Leu Thr Thr Ala Ala Leu Met Leu Phe Phe Leu His Leu Gly Ile
 20 25 30
 Phe Ile Arg Asp Val His Asn Phe Cys Ile Thr Tyr His Tyr Asp His
 35 40 45
 Met Ser Phe His Tyr Thr Val Val Leu Met Phe Ser Gln Val Ile Ser
 50 55 60
 Ile Cys Trp Ala Ala Met Gly Ser Leu Tyr Ala Glu Met Thr Glu Asn
 65 70 75 80
 Asn Ala Gln Arg Ser His Val Leu Gln Pro Pro Val Leu Gly Val Ser
 85 90 95
 Gly His Arg Val Pro Gly Gly Ala Pro Leu Arg Pro Gly Glu Ser Glu
 100 105 110
 Gln Gly

<210> 395
 <211> 367
 <212> PRT
 <213> Homo sapiens

<400> 395
 Met Ala Thr Pro Asn Asn Leu Thr Pro Thr Asn Cys Ser Trp Trp Pro
 1 5 10 15
 Ile Ser Ala Leu Glu Ser Asp Ala Ala Lys Pro Ala Glu Ala Pro Asp
 20 25 30
 Ala Pro Glu Ala Ala Ser Pro Ala His Trp Pro Arg Glu Ser Leu Val
 35 40 45
 Leu Tyr His Trp Thr Gln Ser Phe Ser Ser Gln Lys Val Arg Leu Val
 50 55 60
 Ile Ala Glu Lys Gly Leu Val Cys Glu Glu Arg Asp Val Ser Leu Pro
 65 70 75 80
 Gln Ser Glu His Lys Glu Pro Trp Phe Met Arg Leu Asn Leu Gly Glu
 85 90 95
 Glu Val Pro Val Ile Ile His Arg Asp Asn Ile Ile Ser Asp Tyr Asp
 100 105 110
 Gln Ile Ile Asp Tyr Val Glu Arg Thr Phe Thr Gly Glu His Val Val
 115 120 125
 Ala Leu Met Pro Glu Val Gly Ser Leu Gln His Ala Arg Val Leu Gln
 130 135 140
 Tyr Arg Glu Leu Leu Asp Ala Leu Pro Met Asp Ala Tyr Thr His Gly
 145 150 155 160
 Cys Ile Leu His Pro Glu Leu Thr Thr Asp Ser Met Ile Pro Lys Tyr
 165 170 175
 Ala Thr Ala Glu Ile Arg Arg His Leu Ala Asn Ala Thr Thr Asp Leu
 180 185 190
 Met Lys Leu Asp His Glu Glu Glu Pro Gln Leu Ser Glu Pro Tyr Leu
 195 200 205
 Ser Lys Gln Lys Lys Leu Met Val Lys Ile Leu Glu His Asp Asp Val
 210 215 220
 Ser Tyr Leu Lys Lys Ile Leu Gly Glu Leu Ala Met Val Leu Asp Gln
 225 230 235 240

Ile Glu Ala Glu Leu Glu Lys Arg Lys Leu Glu Asn Glu Gly Gln Lys
 245 250 255
 Cys Glu Leu Trp Leu Cys Gly Cys Ala Phe Thr Leu Ala Asp Val Leu
 260 265 270
 Leu Gly Ala Thr Leu His Arg Leu Lys Phe Leu Gly Leu Ser Lys Lys
 275 280 285
 Tyr Trp Glu Asp Gly Ser Arg Pro Asn Leu Gln Ser Phe Phe Glu Arg
 290 295 300
 Val Gln Arg Arg Phe Ala Phe Arg Lys Val Leu Gly Asp Ile His Thr
 305 310 315 320
 Thr Leu Leu Ser Ala Val Ile Pro Asn Ala Phe Arg Leu Val Lys Arg
 325 330 335
 Lys Pro Pro Ser Phe Phe Gly Ala Ser Phe Leu Met Gly Ser Leu Gly
 340 345 350
 Gly Met Gly Tyr Phe Ala Tyr Trp Tyr Leu Lys Lys Lys Tyr Ile
 355 360 365

<210> 396
 <211> 279
 <212> PRT
 <213> Homo sapiens

<400> 396
 Met Pro Val Cys Ala Pro Val Leu Trp Arg Ala Arg Arg Leu Cys Gly
 1 5 10 15
 Met Pro Val Cys Ala Pro Val Pro Trp Arg Ala Arg Arg Leu Cys Thr
 20 25 30
 Arg Ala Val Val Cys Pro Ser Ser Val Pro Phe Ile Ala Gly Gln Gly
 35 40 45
 Cys Thr His Met Cys Lys Pro Ala Thr Asp Pro Arg Phe Thr Arg Ser
 50 55 60
 Pro Leu Ala Gly Gly Val Ile Leu Gly Val Ala Leu Trp Leu Arg His
 65 70 75 80
 Asp Pro Gln Thr Thr Asn Leu Leu Tyr Leu Glu Leu Gly Asp Lys Pro
 85 90 95
 Ala Pro Asn Thr Phe Tyr Val Gly Ile Tyr Ile Leu Ile Ala Val Gly
 100 105 110
 Ala Val Met Met Phe Val Gly Phe Leu Gly Cys Tyr Gly Ala Ile Gln
 115 120 125
 Glu Ser Gln Cys Leu Leu Gly Thr Phe Phe Thr Cys Leu Val Ile Leu
 130 135 140
 Phe Ala Cys Glu Val Ala Ala Gly Ile Trp Gly Phe Val Asn Lys Asp
 145 150 155 160
 Gln Ile Ala Lys Asp Val Lys Gln Phe Tyr Asp Gln Ala Leu Gln Gln
 165 170 175
 Ala Val Val Asp Asp Ala Asn Asn Ala Lys Ala Val Val Lys Thr
 180 185 190
 Phe His Glu Thr Leu Asp Cys Cys Gly Ser Ser Thr Leu Thr Ala Leu
 195 200 205
 Thr Thr Ser Val Leu Lys Asn Asn Leu Cys Pro Ser Gly Ser Asn Ile
 210 215 220
 Ile Ser Asn Leu Phe Lys Glu Asp Cys His Gln Lys Ile Asp Asp Leu
 225 230 235 240
 Phe Ser Gly Lys Leu Tyr Leu Ile Gly Ile Ala Ala Ile Val Val Ala
 245 250 255
 Val Ile Met Ile Phe Glu Met Ile Leu Ser Met Val Leu Cys Gly
 260 265 270
 Ile Arg Asn Ser Ser Val Tyr

275

<210> 397
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 397
 Met Cys Leu Leu Leu Gly Ala Thr Gly Val Gly Lys Thr Leu Leu Val
 1 5 10 15
 Lys Arg Leu Gln Glu Val Ser Ser Arg Asp Gly Lys Gly Asp Leu Gly
 20 25 30
 Glu Pro Pro Thr Arg Pro Thr Val Gly Thr Asn Leu Thr Asp Ile
 35 40 45
 Val Ala Gln Arg Lys Ile Thr Ile Arg Glu Leu Gly Gly Cys Met Gly
 50 55 60
 Pro Ile Trp Ser Ser Tyr Tyr Gly Asn Cys Arg Ser Leu Leu Phe Val
 65 70 75 80
 Met Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Ser Cys Val Gln Leu
 85 90 95
 Leu Gly Leu Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser Val Leu Ile
 100 105 110
 Leu Phe Asn Lys Ile Asp Leu Pro Cys Tyr Met Ser Thr Glu Glu Met
 115 120 125
 Lys Ser Leu Ile Arg Leu Pro Asp Ile Ile Ala Cys Ala Lys Gln Asn
 130 135 140
 Ile Thr Thr Ala Glu Ile Ser Ala Arg Glu Gly Thr Gly Leu Ala Gly
 145 150 155 160
 Val Leu Ala Trp Leu Gln Ala Thr His Arg Ala Asn Asp
 165 170

<210> 398
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 398
 Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu Pro Gly Ser Ser
 1 5 10 15
 Val Leu Phe Leu Cys Asp Met Gln Glu Lys Phe Arg His Asn Ile Ala
 20 25 30
 Tyr Phe Pro Gln Ile Val Ser Val Ala Ala Arg Met Leu Lys Val Ala
 35 40 45
 Arg Leu Leu Glu Val Pro Val Met Leu Thr Glu Gln Tyr Pro Gln Gly
 50 55 60
 Leu Gly Pro Thr Val Pro Glu Leu Gly Thr Glu Gly Leu Arg Pro Leu
 65 70 75 80
 Ala Lys Thr Cys Phe Ser Met Val Pro Ala Leu Gln Gln Glu Leu Asp
 85 90 95
 Ser Arg Pro Gln Leu Arg Ser Val Leu Leu Cys Gly Ile Glu Ala Gln
 100 105 110
 Ala Cys Ile Leu Asn Thr Thr Leu Asp Leu Leu Asp Arg Gly Leu Gln
 115 120 125
 Val His Val Val Val Asp Ala Cys Ser Ser Arg Ser Gln Val Asp Arg
 130 135 140
 Leu Val Ala Leu Ala Arg Met Arg Gln Ser Gly Ala Phe Leu Ser Thr
 145 150 155 160
 Ser Glu Gly Leu Ile Leu Gln Leu Val Gly Asp Ala Val His Pro Gln

165 170 175
 Phe Lys Glu Ile Gln Lys Leu Ile Lys Glu Pro Ala Pro Asp Ser Gly
 180 185 190
 Leu Leu Gly Leu Phe Gln Gly Gln Asn Ser Leu Leu His
 195 200 205

<210> 399
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 399
 Met Trp Leu Tyr Arg Asn Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr
 1 5 10 15
 Lys Pro Met Phe Val Ile Ala Phe Leu Ser Pro Leu Ser Leu Ile Phe
 20 25 30
 Leu Ala Lys Phe Leu Lys Lys Ala Asp Thr Arg Asp Ser Arg Gln Ala
 35 40 45
 Cys Leu Ala Ala Ser Leu Ala Leu Ala Leu Asn Gly Val Phe Thr Asn
 50 55 60
 Thr Ile Lys Leu Ile Val Gly Arg Pro Arg Pro Asp Phe Phe Tyr Arg
 65 70 75 80
 Cys Phe Pro Asp Gly Leu Ala His Ser Asp Leu Met Cys Thr Gly Asp
 85 90 95
 Lys Asp Val Val Asn Glu Gly Arg Lys Ser Phe Pro Ser Gly His Ser
 100 105 110
 Ser Phe Ala Phe Ala Gly Leu Ala Phe Ala Ser Phe Tyr Leu Ala Gly
 115 120 125
 Lys Leu His Cys Phe Thr Pro Gln Gly Arg Gly Lys Ser Trp Arg Phe
 130 135 140
 Cys Ala Phe Leu Ser Pro Leu Leu Phe Ala Ala Val Ile Ala Leu Ser
 145 150 155 160
 Arg Thr Cys Asp Tyr Lys His His Trp Gln Asp Leu Leu Lys Cys Thr
 165 170 175
 Asn Thr Ala Lys
 180

<210> 400
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 400
 Met Cys Thr Ala Leu Leu Leu Tyr Leu Arg Trp Cys Phe Asn Leu
 1 5 10 15
 Lys Leu Val Asn Val Lys Tyr Glu Pro Lys Asp Ser Leu Gly Pro Glu
 20 25 30
 Met Thr Phe Val Ala Asp Ala Ala Arg Gly Pro Leu Leu Ser Ser Leu
 35 40 45
 Asp Ser Pro Ala Asn Leu Met Ser Thr Ala Ser Val Cys Ile Ser Leu
 50 55 60
 Pro Glu Gly Cys Ser Gly Gly Arg Ser Pro Cys Tyr Ser Gln Lys Trp
 65 70 75 80
 Pro Pro Glu Val Pro Glu Lys Leu Thr Ser Leu Gly Gln Gln Ser Ser
 85 90 95
 Thr Ser Ser Leu Thr Asp Thr Asp Val Gln Val Ser Pro Met Leu Val
 100 105 110
 Ala Gly Val Asn His Ser Ser Ser Leu Leu Asp Asn Ile Pro Phe Thr

130 135 140
 Thr Glu Cys Gly Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln His
 145 150 155 160
 Tyr Ile Arg His Ala Arg Gly Glu Leu
 165

<210> 403
 <211> 367
 <212> PRT
 <213> Homo sapiens

<400> 403
 Met Ala Thr Pro Asn Asn Leu Thr Pro Thr Asn Cys Ser Trp Trp Pro
 1 5 10 15
 Ile Ser Ala Leu Glu Ser Asp Ala Ala Lys Pro Ala Glu Ala Pro Asp
 20 25 30
 Ala Pro Glu Ala Ala Ser Pro Ala His Trp Pro Arg Glu Ser Leu Val
 35 40 45
 Leu Tyr His Trp Thr Gln Ser Phe Ser Ser Gln Lys Val Arg Leu Val
 50 55 60
 Ile Ala Glu Lys Gly Leu Val Cys Glu Glu Arg Asp Val Ser Leu Pro
 65 70 75 80
 Gln Ser Glu His Lys Glu Pro Trp Phe Met Arg Leu Asn Leu Gly Glu
 85 90 95
 Glu Val Pro Val Ile Ile His Arg Asp Asn Ile Ile Ser Asp Tyr Asp
 100 105 110
 Gln Ile Ile Asp Tyr Val Glu Arg Thr Phe Thr Gly Glu His Val Val
 115 120 125
 Ala Leu Met Pro Glu Val Gly Ser Leu Gln His Ala Arg Val Leu Gln
 130 135 140
 Tyr Arg Glu Leu Leu Asp Ala Leu Pro Met Asp Ala Tyr Thr His Gly
 145 150 155 160
 Cys Ile Leu His Leu Glu Leu Thr Thr Asp Ser Met Ile Pro Lys Tyr
 165 170 175
 Ala Thr Ala Glu Ile Arg Arg His Leu Ala Asn Ala Thr Thr Asp Leu
 180 185 190
 Met Lys Leu Asp His Glu Glu Glu Pro Gln Leu Ser Glu Pro Tyr Leu
 195 200 205
 Ser Lys Gln Lys Lys Leu Met Ala Lys Ile Leu Glu His Asp Asp Val
 210 215 220
 Ser Tyr Leu Lys Lys Ile Leu Gly Glu Leu Ala Met Val Leu Asp Gln
 225 230 235 240
 Ile Glu Ala Glu Leu Glu Lys Arg Lys Leu Glu Asn Glu Gly Gln Lys
 245 250 255
 Cys Glu Leu Trp Leu Cys Gly Cys Ala Phe Thr Leu Ala Asp Val Leu
 260 265 270
 Leu Gly Ala Thr Leu His Arg Leu Lys Phe Leu Gly Leu Ser Lys Lys
 275 280 285
 Tyr Trp Glu Asp Gly Ser Arg Pro Asn Leu Gln Ser Phe Phe Glu Arg
 290 295 300
 Val Gln Arg Arg Phe Ala Phe Arg Lys Val Leu Gly Asp Ile His Thr
 305 310 315 320
 Thr Leu Leu Ser Ala Val Ile Pro Asn Ala Phe Arg Leu Val Lys Arg
 325 330 335
 Lys Pro Pro Ser Phe Phe Gly Ala Ser Phe Leu Met Gly Ser Leu Gly
 340 345 350
 Gly Met Gly Tyr Phe Ala Tyr Trp Tyr Leu Lys Lys Lys Tyr Ile
 355 360 365

<210> 404
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 404
 Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu Pro Gly Ser Ser
 1 5 10 15
 Pro Val Pro Val
 20

<210> 405
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 405
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
 1 5 10 15
 Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val
 20 25 30
 Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
 35 40 45
 Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
 50 55 60
 Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
 65 70 75 80
 Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
 85 90 95
 Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
 100 105 110
 Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
 115 120 125
 Thr Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
 130 135 140
 Ile Arg Asp Phe Tyr Asn Ser Ile Val Asn Val Ala Gln Lys Arg Glu
 145 150 155 160
 Leu Gly Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile
 165 170 175
 Val Gly Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser
 180 185 190
 Ser Ser Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser
 195 200 205
 Tyr His Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr
 210 215 220
 Val
 225

<210> 406
 <211> 378
 <212> PRT
 <213> Homo sapiens

<400> 406
 Met Asp Pro Gly Asp Asp Trp Leu Val Glu Ser Leu Arg Leu Tyr Gln
 1 5 10 15
 Asp Phe Tyr Ala Phe Asp Leu Ser Gly Ala Thr Arg Val Leu Glu Trp

<210> 408
 <211> 345
 <212> PRT
 <213> Homo sapiens

<400> 408
 Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly Cys Gly Gln Ala
 1 5 10 15
 Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu Leu Thr Ala Val
 20 25 30
 Leu Thr Pro Gln Leu Leu Gly Arg Arg Phe Asn Phe Ile Gln
 35 40 45
 Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val Glu Pro Arg Arg
 50 55 60
 Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg Ser Ala Leu Ile
 65 70 75 80
 Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro Tyr Pro Ile Arg
 85 90 95
 Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe Thr Gly Cys Ala
 100 105 110
 Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu Lys Ser Arg Val
 115 120 125
 Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu Asp Ser Ile Arg
 130 135 140
 Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn Lys Trp Trp Asn
 145 150 155 160
 Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile Ile Ala Ala Asn
 165 170 175
 Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu Gln Arg Thr Met
 180 185 190
 Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val Leu Cys Ser Pro
 195 200 205
 Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe His Met Ala Ala
 210 215 220
 Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile Val Asn Ile Leu
 225 230 235 240
 Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala Gly Val Ile Ser
 245 250 255
 Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly Arg Tyr Gly Pro
 260 265 270
 Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met Asp Thr Ala Gly
 275 280 285
 Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala His Leu Gly Gly
 290 295 300
 Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His Glu Leu Ile Trp
 305 310 315 320
 Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu Ile Arg Thr Asn
 325 330 335
 Gly Pro Lys Lys Gly Gly Gly Ser Lys
 340 345

<210> 409
 <211> 236
 <212> PRT
 <213> Homo sapiens

<400> 409

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Met Lys Arg Ser Gly Asn Pro Gly Ala Glu Val Thr Asn Ser Ser Val
1      5      10      15
Ala Gly Pro Asp Cys Cys Gly Gly Leu Gly Asn Ile Asp Phe Arg Gln
      20      25      30
Ala Asp Phe Cys Val Met Thr Arg Leu Leu Gly Tyr Val Asp Pro Leu
      35      40      45
Asp Pro Ser Phe Val Ala Ala Val Ile Thr Ile Thr Phe Asn Pro Leu
      50      55      60
Tyr Trp Asn Val Val Ala Arg Trp Glu His Lys Thr Arg Lys Leu Ser
      65      70      75      80
Arg Ala Phe Gly Ser Pro Tyr Leu Ala Cys Tyr Ser Leu Ser Ile Thr
      85      90      95
Ile Leu Leu Leu Asn Phe Leu Arg Ser His Cys Phe Thr Gln Ala Met
      100      105      110
Leu Ser Gln Pro Arg Met Glu Ser Leu Asp Thr Pro Ala Ala Tyr Ser
      115      120      125
Leu Val Leu Ala Leu Leu Gly Leu Gly Val Val Leu Val Leu Ser Ser
      130      135      140
Phe Phe Ala Leu Gly Phe Ala Gly Thr Phe Leu Gly Asp Tyr Phe Gly
      145      150      155      160
Ile Leu Lys Glu Ala Arg Val Thr Val Phe Pro Phe Asn Ile Leu Asp
      165      170      175
Asn Pro Met Tyr Trp Gly Ser Thr Ala Asn Tyr Leu Gly Trp Ala Ile
      180      185      190
Met His Ala Ser Pro Thr Gly Leu Leu Leu Thr Val Leu Val Ala Leu
      195      200      205
Thr Tyr Ile Val Ala Leu Leu Tyr Glu Glu Pro Phe Thr Ala Glu Ile
      210      215      220
Tyr Arg Gln Lys Ala Ser Gly Ser His Lys Arg Ser
      225      230      235

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<210> 410
<211> 121
<212> PRT
<213> Homo sapiens

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<400> 410
Met Asn Thr Glu Ala Glu Gln Gln Leu Leu His His Ala Arg Asn Gly
1      5      10      15
Asn Ala Glu Glu Val Arg Gln Leu Leu Glu Thr Met Ala Ser Asn Glu
      20      25      30
Val Ile Ala Asp Ile Asn Cys Lys Gly Arg Ser Lys Ser Asn Leu Gly
      35      40      45
Trp Thr Pro Leu His Leu Ala Cys Tyr Phe Gly His Arg Gln Val Val
      50      55      60
Gln Asp Leu Leu Lys Ala Gly Ala Glu Val Asn Val Leu Asn Asp Met
      65      70      75      80
Gly Asp Thr Pro Leu His Arg Ala Ala Phe Thr Gly Arg Lys Val Lys
      85      90      95
Ile Ile Leu Cys Ser Met Phe Val Ser Glu Val Phe Gly Gly Val Val
      100      105      110
Thr Ile Val Phe Ser Val Ile Thr Ile
      115      120

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<210> 411
<211> 170
<212> PRT
<213> Homo sapiens

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<400> 411

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Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro
1      5      10      15
Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu
      20      25      30
Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
      35      40      45
Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
      50      55      60
Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
65      70      75      80
Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
      85      90      95
Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
      100      105      110
Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
      115      120      125
Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
130      135      140
Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
145      150      155      160
His Gln Pro Gln Pro Thr Glu Lys Ser Asp
      165      170

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<210> 412

<211> 236

<212> PRT

<213> Homo sapiens

<400> 412

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Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu Glu Lys
1      5      10      15
Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His Thr Ala
      20      25      30
Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu
      35      40      45
Ser Val Leu Lys Leu His His Ser Leu Gln Gln Ser Glu Pro Asp Leu
      50      55      60
Arg His Leu Val Leu Val Val Asn Thr Leu Arg Arg Ile Gln Ala Ser
65      70      75      80
Met Ala Pro Ala Ala Ala Leu Pro Pro Val Pro Ser Pro Pro Ala Ala
      85      90      95
Pro Ser Val Ala Asp Asn Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser
      100      105      110
Ala Ser Met Ala Ser Leu Leu Glu Asp Leu Ser His Ile Glu Gly Leu
115      120      125
Ser Gln Ala Pro Gln Pro Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser
130      135      140
Ile Gly Gly Ala Ala Pro Ser Leu Gly Ala Leu Asp Leu Leu Gly Pro
145      150      155      160
Ala Thr Gly Cys Leu Leu Asp Asp Gly Leu Glu Gly Leu Phe Glu Asp
      165      170      175
Ile Asp Thr Ser Met Tyr Asp Asn Glu Leu Trp Ala Pro Ala Ser Glu
      180      185      190
Gly Leu Lys Pro Gly Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro
195      200      205
Glu Leu Asp Glu Ala Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly

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210 215 220
 Thr Gln Ala Leu Glu Arg Pro Pro Gly Pro Gly Arg
 225 230 235

<210> 413
 <211> 191
 <212> PRT
 <213> Homo sapiens

<400> 413
 Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile Thr
 1 5 10 15
 Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp Asn Phe
 20 25 30
 Val Lys Leu Gln Val Lys Ala Cys Ala Leu Ser Gln Ile Asn Thr Lys
 35 40 45
 Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val Gly Arg
 50 55 60
 Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser Phe Phe
 65 70 75
 Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser Glu Asp
 85 90 95
 Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu Val His
 100 105 110
 Lys Pro Glu Lys Val Thr Trp Thr Glu Ala Ala Gly Ser Ile Arg Asp
 115 120 125
 Gly Val Arg Ala Tyr Thr Ala Leu His Tyr Leu Ser His Leu Ser Pro
 130 135 140
 Gly Lys Ser Val Leu Ile Met Asp Gly Ala Ser Ala Phe Gly Thr Ile
 145 150 155 160
 Ala Ile Gln Leu Ala His His Arg Gly Ala Lys Val Phe Gln Gln His
 165 170 175
 Ala Ala Leu Lys Ile Ser Ser Ala Leu Lys Asp Ser Asp Leu Pro
 180 185 190

<210> 414
 <211> 389
 <212> PRT
 <213> Homo sapiens

<400> 414
 Met Ala Glu Pro Asp Pro Ser His Pro Leu Glu Thr Gln Ala Gly Lys
 1 5 10 15
 Val Gln Glu Ala Gln Asp Ser Asp Ser Glu Gly Gly Ala Ala
 20 25 30
 Gly Gly Glu Ala Asp Met Asp Phe Leu Arg Asn Leu Phe Ser Gln Thr
 35 40 45
 Leu Ser Leu Gly Ser Gln Lys Glu Arg Leu Leu Asp Glu Leu Thr Leu
 50 55 60
 Glu Gly Val Ala Arg Tyr Met Gln Ser Glu Arg Cys Arg Arg Val Ile
 65 70 75 80
 Cys Leu Val Gly Ala Gly Ile Ser Thr Ser Ala Gly Ile Pro Asp Phe
 85 90 95
 Arg Ser Pro Ser Thr Gly Leu Tyr Asp Asn Leu Glu Lys Tyr His Leu
 100 105 110
 Pro Tyr Pro Glu Ala Ile Phe Glu Ile Ser Tyr Phe Lys Lys His Pro
 115 120 125
 Glu Pro Phe Phe Ala Leu Ala Lys Glu Leu Tyr Pro Gly Gln Phe Lys

130 135 140
 Pro Thr Ile Cys His Tyr Phe Met Arg Leu Leu Lys Asp Lys Gly Leu
 145 150 155 160
 Leu Leu Arg Cys Tyr Thr Gln Asn Ile Asp Thr Leu Glu Arg Ile Ala
 165 170 175
 Gly Leu Glu Gln Glu Asp Leu Val Glu Ala His Gly Thr Phe Tyr Thr
 180 185 190
 Ser His Cys Val Ser Ala Ser Cys Arg His Glu Tyr Pro Leu Ser Trp
 195 200 205
 Met Lys Glu Lys Ile Phe Ser Glu Val Thr Pro Lys Cys Glu Asp Cys
 210 215 220
 Gln Ser Leu Val Lys Pro Asp Ile Val Phe Phe Gly Glu Ser Leu Pro
 225 230 235 240
 Ala Arg Phe Phe Ser Cys Met Gln Ser Asp Phe Leu Lys Val Asp Leu
 245 250 255
 Leu Leu Val Met Gly Thr Ser Leu Gln Val Gln Pro Phe Ala Ser Leu
 260 265 270
 Ile Ser Lys Ala Pro Leu Ser Thr Pro Arg Leu Leu Ile Asn Lys Glu
 275 280 285
 Lys Ala Gly Gln Ser Asp Pro Phe Leu Gly Met Ile Met Gly Leu Gly
 290 295 300
 Gly Gly Met Asp Phe Asp Ser Lys Lys Ala Tyr Arg Asp Val Ala Trp
 305 310 315 320
 Leu Gly Glu Cys Asp Gln Gly Cys Leu Ala Leu Ala Glu Leu Leu Gly
 325 330 335
 Trp Lys Lys Glu Leu Glu Asp Leu Val Arg Arg Glu His Ala Ser Ile
 340 345 350
 Asp Ala Gln Ser Gly Ala Gly Val Pro Asn Pro Ser Thr Ser Ala Ser
 355 360 365
 Pro Lys Lys Ser Pro Pro Pro Ala Lys Asp Glu Ala Arg Thr Thr Glu
 370 375 380
 Arg Glu Lys Pro Gln
 385

<210> 415
 <211> 481
 <212> PRT
 <213> Homo sapiens

<400> 415
 Met Ser Leu Asn Leu Pro Glu Ala Ser Leu Leu Ser Arg Ala Ser Trp
 1 5 10 15
 Pro Glu Gln Ala Lys Glu Pro Arg Arg Glu Gly His Thr Asp Lys Gln
 20 25 30
 Gln Thr Glu Asp Val Leu Ala Ala Gly Leu Arg Cys Leu Pro His Leu
 35 40 45
 Pro Ala Ile Cys Ala Arg Arg Met Ser Pro Ala Phe Arg Ala Met Asp
 50 55 60
 Val Glu Pro Arg Ala Lys Gly Val Leu Leu Glu Pro Phe Val His Gln
 65 70 75 80
 Val Gly Gly His Ser Cys Val Leu Arg Phe Asn Glu Thr Thr Leu Cys
 85 90 95
 Lys Pro Leu Val Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ala
 100 105 110
 Glu Met Arg Lys Phe Thr Pro Gln Tyr Lys Gly Val Val Ser Val Arg
 115 120 125
 Phe Glu Glu Asp Glu Asp Arg Asn Leu Cys Leu Ile Ala Tyr Pro Leu
 130 135 140

Lys Gly Asp His Gly Ile Val Asp Ile Val Asp Asn Ser Asp Cys Glu
 145 150 155 160
 Pro Lys Ser Lys Leu Leu Arg Trp Thr Thr Asn Lys Lys His His Val
 165 170 175
 Leu Glu Thr Glu Lys Thr Pro Lys Asp Trp Val Arg Gln His Arg Lys
 180 185 190
 Glu Glu Lys Met Lys Ser His Lys Leu Glu Glu Glu Phe Glu Trp Leu
 195 200 205
 Lys Lys Ser Glu Val Leu Tyr Tyr Thr Val Glu Lys Lys Gly Asn Ile
 210 215 220
 Ser Ser Gln Leu Lys His Tyr Asn Pro Trp Ser Met Lys Cys His Gln
 225 230 235 240
 Gln Gln Leu Gln Arg Met Lys Glu Asn Ala Lys His Arg Asn Gln Tyr
 245 250 255
 Lys Phe Ile Leu Leu Glu Asn Leu Thr Ser Arg Tyr Glu Val Pro Cys
 260 265 270
 Val Leu Asp Leu Lys Met Gly Thr Arg Gln His Gly Asp Asp Ala Ser
 275 280 285
 Glu Glu Lys Ala Ala Asn Gln Ile Arg Lys Cys Gln Gln Ser Thr Ser
 290 295 300
 Ala Val Ile Gly Val Arg Val Cys Gly Met Gln Val Tyr Gln Ala Gly
 305 310 315 320
 Ser Gly Gln Leu Met Phe Met Asn Lys Tyr His Gly Arg Lys Leu Ser
 325 330 335
 Val Gln Gly Phe Lys Glu Ala Leu Phe Gln Phe Phe His Asn Gly Arg
 340 345 350
 Tyr Leu Arg Arg Glu Leu Leu Gly Pro Val Leu Lys Lys Leu Thr Glu
 355 360 365
 Leu Lys Ala Val Leu Glu Arg Gln Glu Ser Tyr Arg Phe Tyr Ser Ser
 370 375 380
 Ser Leu Leu Val Ile Tyr Asp Gly Lys Glu Arg Pro Glu Val Val Leu
 385 390 395 400
 Asp Ser Asp Ala Glu Asp Leu Glu Asp Leu Ser Glu Glu Ser Ala Asp
 405 410 415
 Glu Ser Ala Gly Ala Tyr Ala Tyr Lys Pro Ile Gly Ala Ser Ser Val
 420 425 430
 Asp Val Arg Met Ile Asp Phe Ala His Thr Thr Cys Arg Leu Tyr Gly
 435 440 445
 Glu Asp Thr Val Val His Glu Gly Gln Asp Ala Gly Tyr Ile Phe Gly
 450 455 460
 Leu Gln Ser Leu Ile Asp Ile Val Thr Glu Ile Ser Glu Glu Ser Gly
 465 470 475 480
 Glu

<210> 416
 <211> 354
 <212> PRT
 <213> Homo sapiens

<400> 416
 Met Ser Ala Gly Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro
 1 5 10 15
 Met Pro Thr Cys Arg Val Tyr Gly Thr Val Ala His Gln Asp Gly His
 20 25 30
 Leu Leu Val Leu Gly Gly Cys Gly Arg Ala Gly Leu Pro Leu Asp Thr
 35 40 45
 Ala Glu Thr Leu Asp Met Ala Ser His Thr Trp Leu Ala Leu Ala Pro
 50 55 60

Leu Pro Thr Ala Arg Ala Gly Ala Ala Val Val Leu Gly Lys Gln
 65 70 75 80
 Val Leu Val Val Gly Gly Val Asp Glu Val Gln Ser Pro Val Ala Ala
 85 90 95
 Val Glu Ala Phe Leu Met Asp Glu Gly Arg Trp Glu Arg Arg Ala Thr
 100 105 110
 Leu Pro Gln Ala Ala Met Gly Val Ala Thr Val Glu Arg Asp Gly Met
 115 120 125
 Val Tyr Ala Leu Gly Gly Met Gly Pro Asp Thr Ala Pro Gln Ala Gln
 130 135 140
 Val Arg Val Tyr Glu Pro Arg Arg Asp Cys Trp Leu Ser Leu Pro Ser
 145 150 155 160
 Met Pro Thr Pro Cys Tyr Gly Ala Ser Thr Phe Leu His Gly Asn Lys
 165 170 175
 Ile Tyr Val Leu Gly Gly Arg Gln Gly Lys Leu Pro Val Thr Ala Phe
 180 185 190
 Glu Ala Phe Asp Leu Glu Ala Arg Thr Trp Thr Arg His Pro Ser Leu
 195 200 205
 Pro Ser Arg Arg Ala Phe Ala Gly Cys Ala Met Ala Glu Gly Ser Val
 210 215 220
 Phe Ser Leu Gly Gly Leu Gln Gln Pro Gly Pro His Asn Phe Tyr Ser
 225 230 235 240
 Arg Pro His Phe Val Asn Thr Val Glu Met Phe Asp Leu Glu His Gly
 245 250 255
 Ser Trp Thr Lys Leu Pro Arg Ser Leu Arg Met Arg Asp Lys Arg Ala
 260 265 270
 Asp Phe Val Val Gly Ser Leu Gly Gly His Ile Val Ala Ile Gly Gly
 275 280 285
 Leu Gly Asn Gln Pro Cys Pro Leu Gly Ser Val Glu Ser Phe Ser Leu
 290 295 300
 Ala Arg Arg Arg Trp Glu Ala Leu Pro Ala Met Pro Thr Ala Arg Cys
 305 310 315 320
 Ser Cys Ser Ser Leu Gln Ala Gly Pro Arg Leu Phe Val Ile Gly Gly
 325 330 335
 Val Ala Gln Gly Pro Ser Gln Ala Val Glu Ala Leu Cys Leu Arg Asp
 340 345 350
 Gly Val

<210> 417

<211> 20

<212> PRT

<213> Homo sapiens

<400> 417

Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile Thr
 1 5 10 15
 Phe Val Phe Gln
 20

<210> 418

<211> 320

<212> PRT

<213> Homo sapiens

<400> 418

Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile Thr
 1 5 10 15
 Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp Asn Phe

Cys Ala Ala Leu Trp Trp His Lys Lys Gly Leu Ala Val Leu Phe Cys
 115 120 125
 Ile Leu Gln Phe Leu Ser Met Thr Trp Tyr Ser Leu Ser Tyr Ile Pro
 130 135 140
 Tyr Ala Arg Asp Ala Val Ile Lys Cys Cys Ser Ser Leu Leu Ser
 145 150 155

<210> 420
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 420
 Met Glu Gln Arg Leu Ala Glu Phe Arg Ala Ala Arg Lys Arg Ala Gly
 1 5 10 15
 Leu Ala Ala Gln Pro Pro Ala Ala Ser Gln Gly Ala Gln Thr Pro Gly
 20 25 30
 Glu Lys Ala Glu Ala Ala Thr Leu Lys Ala Ala Pro Gly Trp Leu
 35 40 45
 Lys Arg Phe Leu Val Trp Lys Pro Arg Pro Ala Ser Ala Arg Ala Gln
 50 55 60
 Pro Gly Leu Val Gln Glu Ala Ala Gln Pro Gln Gly Ser Thr Ser Glu
 65 70 75 80
 Thr Pro Trp Asn Thr Ala Ile Pro Leu Pro Ser Cys Trp Asp Gln Ser
 85 90 95
 Phe Leu Thr Asn Ile Thr Phe Leu Lys Val Leu Leu Trp Leu Val Leu
 100 105 110
 Leu Gly Leu Phe Val Glu Leu Glu Phe Gly Leu Ala Tyr Phe Val Leu
 115 120 125
 Ser Leu Phe Tyr Trp Met Tyr Val Gly Thr Arg Gly Pro Glu Glu Lys
 130 135 140
 Lys Glu Gly Glu Lys Ser Ala Tyr Ser Val Phe Asn Pro Gly Cys Glu
 145 150 155 160
 Ala Ile Gln Gly Thr Leu Thr Ala Glu Leu Glu Arg Glu Leu Gln
 165 170 175
 Leu Arg Pro Leu Ala Gly Arg
 180

<210> 421
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 421
 Met Ala Ala Pro Arg Arg Gly Arg Gly Ser Ser Thr Val Leu Ser Ser
 1 5 10 15
 Val Pro Leu Gln Met Leu Phe Tyr Leu Ser Gly Thr Tyr Tyr Ala Leu
 20 25 30
 Tyr Phe Leu Ala Thr Leu Leu Met Ile Thr Tyr Lys Ser Gln Val Phe
 35 40 45
 Ser Tyr Pro His Arg Tyr Leu Val Leu Asp Leu Ala Leu Leu Phe Leu
 50 55 60
 Met Gly Ile Leu Glu Ala Val Arg Leu Tyr Leu Gly Thr Arg Gly Asn
 65 70 75 80
 Leu Thr Glu Ala Glu Arg Pro Leu Ala Ala Ser Leu Ala Leu Thr Ala
 85 90 95
 Gly Thr Ala Leu Leu Ser Ala His Phe Leu Leu Trp Gln Ala Leu Val
 100 105 110

Leu Trp Ala Asp Trp Ala Leu Ser Ala Thr Leu Leu Ala Leu His Gly
 115 120 125
 Leu Glu Ala Val Leu Gln Val Val Ala Ile Ala Ala Phe Thr Arg
 130 135 140

<210> 422
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 422
 Met Ser Gly Val Pro Ala Glu Met Thr Gly Ala Val Glu Ala Phe Leu
 1 5 10 15
 Pro Val Val Ser Ser Ser Arg Arg Leu Pro Arg Phe Val His Met Val
 20 25 30
 Ala Gly Val Ser Ser Lys Gln Glu Arg Ala Arg Ser Asn Thr Glu Ala
 35 40 45
 Leu Phe Lys Leu Cys Phe His His Ile Cys Gln Cys Leu Thr Asp Glu
 50 55 60
 His Lys Phe His Gly Gln Val Gln Phe
 65 70

<210> 423
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 423
 Met Pro Pro Phe Gly Gly His Pro Leu Ser Gln Glu Glu Asp Gly Ser
 1 5 10 15
 Gln Arg Cys Cys Cys Leu Ser Ser Leu Arg Ser Val Asp Asp Ser Asn
 20 25 30
 Gly Glu Thr Val Val Ile Met Ala Leu Phe Leu Ala Val Ser Tyr His
 35 40 45
 His Lys Thr Gln Ser Lys Arg Trp Pro Gly Leu Thr Pro Pro His Ser
 50 55 60
 Ser Leu Leu Cys Arg Pro Leu Gln Leu Ser Phe Leu Val Ile Gln Ser
 65 70 75 80
 Val Arg Met Arg Ala Cys Gly Cys Asp Ser Gly His Cys Arg Ile Leu
 85 90 95
 Gly Arg Tyr Ser Leu Leu Gly Trp Ser Gln Gly His Arg Ala Arg Gly
 100 105 110
 Arg Gly Gly Val Ser Leu Arg Asp Asn Thr Phe Phe Gln Glu Ala Ser
 115 120 125
 Glu Gly Gln Gly Gln Trp Leu Met Pro Val Ile Pro Ala Phe
 130 135 140

<210> 424
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 424
 Met Leu Ser Ile Leu Lys Pro Arg Arg Ser Gln Glu Trp Arg Thr Ala
 1 5 10 15
 Leu Arg Arg Tyr Cys Cys Pro Thr Asp Leu Gln Ala Pro Arg Ser Pro
 20 25 30
 Val Pro Pro Ile Arg Lys Val Gly Ile Ser Asp Val Ile Val His Ala

35 40 45
 Asn Leu Ala Thr Ser Leu Lys Lys Asn Thr Cys Asn Cys Gln Ala Asp
 50 55 60
 Leu Leu Ser Trp Arg Ser Trp Val Asn Gly Ile Ser Cys His Cys Pro
 65 70 75 80
 Asn Leu Arg Pro Leu Ser Lys Ser Ile Phe Arg Asp Ser Thr Ser Leu
 85 90 95
 Cys Ser Leu Ser Gln Gln Arg Leu Cys Pro Leu His Ser Lys Pro Glu
 100 105 110
 Ala Cys Trp Gly Leu Phe Val Ser Val His Ala His Phe Arg Val Gln
 115 120 125
 Ala Gly Gly Arg Gly Asn Arg Val Gly Lys Lys Thr Arg Val Ser Arg
 130 135 140
 Asn Asp Glu Thr Leu
 145

<210> 425
 <211> 75
 <212> PRT
 <213> Homo sapiens

<400> 425
 Met Tyr Leu Pro Pro Asn Arg Ser Glu Leu Cys Asn Phe Ala Leu Ser
 1 5 10 15
 Leu Asn Leu Tyr Gly Lys Gly Phe Phe Ser Leu Val Glu Lys His Asn
 20 25 30
 Ser Arg Asp Leu Glu Asp Arg Ala Ser Ser Gly Pro Ser Leu Ser Ser
 35 40 45
 Pro Ser His Pro Asp Trp Gly Tyr Ile Val Leu Ile Leu Val Ala Thr
 50 55 60
 Leu Gly Glu Leu Asp Thr Gln Val Gly Gly His
 65 70 75

<210> 426
 <211> 168
 <212> PRT
 <213> Homo sapiens

<400> 426
 Met Arg Leu Thr Glu Lys Ser Glu Gly Glu Gln Gln Leu Lys Pro Asn
 1 5 10 15
 Asn Ser Asn Ala Pro Asn Glu Asp Gln Glu Glu Ile Gln Gln Ser
 20 25 30
 Glu Gln His Thr Pro Ala Arg Gln Arg Thr Gln Arg Ala Asp Thr Gln
 35 40 45
 Pro Ser Arg Cys Arg Leu Pro Ser Arg Arg Thr Pro Thr Thr Ser Ser
 50 55 60
 Asp Arg Thr Ile Asn Leu Leu Glu Val Leu Pro Trp Pro Thr Glu Trp
 65 70 75 80
 Ile Phe Asn Pro Tyr Arg Leu Pro Ala Leu Phe Glu Leu Tyr Pro Glu
 85 90 95
 Phe Leu Leu Val Phe Lys Glu Ala Phe His Asp Ile Ser His Cys Leu
 100 105 110
 Lys Ala Gln Met Glu Lys Ile Gly Leu Pro Ile Ile Leu His Leu Phe
 115 120 125
 Ala Leu Ser Thr Leu Tyr Phe Tyr Lys Phe Phe Leu Pro Thr Ile Leu
 130 135 140
 Ser Leu Ser Phe Phe Ile Leu Leu Val Leu Leu Leu Leu Phe Ile

145 150 155 160
 Ile Val Phe Ile Leu Ile Phe Phe
 165

<210> 427
 <211> 160
 <212> PRT
 <213> Homo sapiens

<400> 427
 Met Pro Arg Ser Ser Arg Ser Pro Gly Asp Pro Gly Ala Leu Leu Glu
 1 5 10 15
 Asp Val Ala His Asn Pro Arg Pro Arg Ile Ala Gln Arg Gly Arg
 20 25 30
 Asn Thr Ser Arg Met Ala Glu Asp Thr Ser Pro Asn Met Asn Asp Asn
 35 40 45
 Ile Leu Leu Pro Val Arg Asn Asn Asp Gln Ala Leu Gly Leu Thr Gln
 50 55 60
 Cys Met Leu Gly Cys Val Ser Trp Phe Thr Cys Phe Ala Cys Ser Leu
 65 70 75 80
 Arg Thr Gln Ala Gln Gln Val Leu Phe Asn Thr Cys Arg Asp Arg Val
 85 90 95
 Ser Pro Cys Cys Pro Gly Trp Ser Gln Thr Pro Val Ile Leu Pro Pro
 100 105 110
 Gln Pro Ser Glu Val Leu Gly Leu Gln Met Gln Ala Ala Val Pro Glu
 115 120 125
 Ala His Gly Glu Asp Arg His Ser Ala Pro Leu Cys Phe Arg Cys Val
 130 135 140
 Pro Gly Pro Cys Pro Val Pro Gly Gly Gly Ile Pro Gly Pro Trp His
 145 150 155 160

<210> 428
 <211> 94
 <212> PRT
 <213> Homo sapiens

<400> 428
 Met Asn Lys Glu Ile Asp Ser Leu Asn Leu Ala Tyr Ser Phe Pro Phe
 1 5 10 15
 Leu Leu Pro Ala Phe Leu Asp Thr Pro Trp Thr Asp Pro Phe Pro Ser
 20 25 30
 Gly Phe Met Val Arg Ser Arg Val Leu Leu Ile Gln Leu Leu Ser Arg
 35 40 45
 Pro Arg Ser Ser Gln Glu Ser Arg Gly His Ser Leu Pro Cys Ser Pro
 50 55 60
 Ser Ala Leu His Lys Pro Gly Gly Ile Cys Pro Ala Ala Leu Gly Arg
 65 70 75 80
 Ser His Leu Leu Val Trp Glu Gln Pro Ser Leu Arg Asp Ser
 85 90

<210> 429
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 429
 Met Lys Ala Ser Gly Pro Asp Leu Ser Asp Gly Leu His Cys Pro Ser
 1 5 10 15

Leu Ile Arg His Leu Arg Thr Phe Ser Ala Ala Ala Ala Leu Ala Pro
 20 25 30
 Arg Tyr Pro Thr Arg Leu Pro Ser Ser Leu Leu Trp His Leu Cys
 35 40 45
 Gln Cys Leu His Leu Leu Tyr Ala Val Ser Thr Ser Cys Asn Ser His
 50 55 60
 Gly Lys Arg Ser Ala Ala Trp Ala Met Thr Arg Thr Glu Asp Thr Asp
 65 70 75 80
 Ala Leu Thr Asp Ser Phe Asp Asp Ser Phe Ile Ser Ser Ala Asp
 85 90 95

<210> 430
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 430
 Met Lys Lys Lys Glu Glu Thr Thr Leu Ser Glu Met Glu Pro Val Glu
 1 5 10 15
 Pro Gln Tyr Gln Leu Val Asn Ala Glu Ser Thr Ser Pro Phe Leu His
 20 25 30
 Cys Leu Arg Glu Val Ile Gly Glu Tyr Ser Val His Glu Phe Ser Leu
 35 40 45
 Leu Gly Lys Thr Glu Ser Gln Gly Ile Gly Leu Trp Ile Ala Leu Val
 50 55 60
 Val Phe Leu Ser Phe Leu Ile Phe Ser Thr Ser Phe Tyr Ile Ser Asn
 65 70 75 80
 Ala Glu Gln Pro Phe Phe Lys Glu Pro Pro Thr Glu Ala Ala Lys Glu
 85 90 95
 Leu Ser Leu

<210> 431
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 431
 Ile Arg Ala Thr Met Val Ala Arg Val Trp Ser Leu Met Arg Phe Leu
 1 5 10 15
 Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr Asp Gln
 20 25 30
 Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln Lys Ala
 35 40 45
 Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr Val Cys
 50 55 60
 Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro Lys Ile
 65 70 75 80
 Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr Val Met
 85 90 95
 Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser Lys Glu
 100 105 110
 Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys
 115 120

<210> 432
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 432

Met Gln Pro Ser Leu Leu Arg Ser Tyr Arg Leu Lys Ala Gln Leu Ser
1 5 10 15
Leu Ser Ser Thr Val Pro Arg Arg Ile Thr Asp Lys Pro Ala Thr Lys
20 25 30
Ser Trp Glu Gly Gly Arg Arg Glu Leu Cys Pro Arg Val Leu Phe Thr
35 40 45
Gln Leu Leu Leu Trp Val Trp Pro Gly Asp Pro Gly Pro Glu Leu Gln
50 55 60
Glu Thr Gly Phe Pro Gly Pro Pro Arg Pro Ala His Leu Lys Thr Asp
65 70 75 80
Arg Ala Ile Met Val Gly Val Lys Gly Ile Glu Glu Lys Ser Gly Ile
85 90 95
Gly Ala Gly Val Cys Arg Val Ser Val Glu Lys Leu Ala Ser Thr Gln
100 105 110
Glu Arg Thr Ser Ser Leu
115

<210> 433

<211> 49

<212> PRT

<213> Homo sapiens

<400> 433

Met Glu Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Pro
1 5 10 15
Val Phe Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe
20 25 30
Thr Ala Trp Phe Phe Val Tyr Pro Phe Thr Glu Gln Pro Glu Asp Gln
35 40 45
His

<210> 434

<211> 89

<212> PRT

<213> Homo sapiens

<400> 434

Met Leu Ala Leu Phe His Phe His Leu Pro Pro Trp Asp Asp Ala Val
1 5 10 15
Arg Arg Pro Ser Val Asp Ala Ser Pro Ser Thr Leu Asn Phe Pro Asp
20 25 30
Ala Glu Leu Tyr Ala Ser Ile Phe Leu Cys Cys Met Ala Pro Gly Glu
35 40 45
Ile Leu Ile Ser Phe Leu Thr Leu Val Gln Ile Ala His Ala Asn Gly
50 55 60
Arg Gly Cys Asn Thr Pro Ala Cys Gly Ala Ala Cys Val Trp His
65 70 75 80
Glu Asn Ser Gln Glu Glu Arg Lys Tyr
85

<210> 435

<211> 87

<212> PRT

<213> Homo sapiens

<400> 435

Met Ser Gln Gln His Arg Arg Lys Arg Pro Ser Ser Glu Arg Lys Ser
 1 5 10 15
 Thr Arg Lys Met Asp Thr Trp Gln Ser Leu Lys Val Lys Glu Val Phe
 20 25 30
 Cys Lys His Asn Ser Ser Tyr Glu Cys Leu Leu Tyr Lys Glu Val Glu
 35 40 45
 Ala Arg Gln Val Ser Lys Thr Ala Thr Asp Gly Ser Tyr Leu Leu Val
 50 55 60
 Phe Thr Ser Tyr Val Ile Ser Ser Pro Val Trp Thr Gly Pro Gly Asp
 65 70 75 80
 Leu Leu Pro Val Asn Arg Ile
 85

<210> 436
 <211> 45
 <212> PRT
 <213> Homo sapiens

<400> 436
 Met Pro Arg Ser Ser Arg Ser Pro Gly Asp Pro Gly Ala Leu Leu Glu
 1 5 10 15
 Asp Gly Pro Gln Ser Gln Thr Pro Glu Asp Cys Pro Ala Arg Pro Glu
 20 25 30
 His Gln Gln Asp Gly Arg Gly His Leu Pro Lys His Glu
 35 40 45

<210> 437
 <211> 65
 <212> PRT
 <213> Homo sapiens

<400> 437
 Met Ala Tyr Leu Asp Asp Lys Gly Ser Leu Leu Ala Ile His Ser His
 1 5 10 15
 Ala Arg Gln His Ser His Glu Thr Asn Gln Val His Gln Trp Leu Pro
 20 25 30
 Arg Asn Thr Phe Ala Phe Leu Ile Lys Glu Asp Arg Cys Ser Cys Arg
 35 40 45
 Ser Thr Cys Ala Ser Phe Ser Phe Ser Ser Ser Phe Ser Phe Leu Ile
 50 55 60
 Ser
 65

<210> 438
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 438
 Met Arg Lys Lys Cys Lys Cys Phe Thr Ile Lys Lys Thr Asn Thr Tyr
 1 5 10 15
 Glu Glu Ser Asn Ala Gly Asn Glu Gly Gln Lys Glu Ala Ile Ser Ile
 20 25 30
 Cys Ile Cys Arg Arg Asp Gly Leu Leu Pro Leu Trp Val Thr Arg Leu
 35 40 45
 Ser Asp Leu Val Phe Ser Lys Glu Lys Ala His Gly Met Ile Pro Leu
 50 55 60
 Leu Gly Ser His Arg Glu Lys Lys Thr Ser Lys Glu Met Lys Thr Ser

65 70 75 80
 Ser Arg Asn Leu Arg Tyr Phe Ile Val Cys Arg Asp Ala Ser Ser Tyr
 85 90 95
 Thr Pro Gln Ser Leu Ile Ser Gly Tyr Ile Gly Pro Cys Gln His Gln
 100 105 110

<210> 439
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 439
 Met Val Phe Gly Ala Met Val Leu Leu Val Gly Leu Glu Glu Leu Thr
 1 5 10 15
 Asn Ile Arg Asn Val Glu Arg Leu Lys Asp Leu Arg Ala Ser Tyr
 20 25 30
 Cys Leu Ile Asp Ser Phe Leu Gly Asp Ser Glu Leu Ile Gly Asp Leu
 35 40 45
 Thr Gln Cys Val Asp Cys Val Ile Pro Pro Glu Gly Ser Leu Leu Gln
 50 55 60
 Ile Ser Ser Tyr Leu Tyr Leu Asn Thr Ala Leu Val Asp Leu Pro Gly
 65 70 75 80
 Val Ala Ala Ser Gln Ala Cys Asp Ser Gln Gln Val Thr Trp Leu Leu
 85 90 95
 Tyr Val Ala Asn Gly Ala Tyr Ser Ala Cys Asn Arg Pro Gly
 100 105 110

<210> 440
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 440
 Thr Ser Ser Ser Gly Ala Glu Val Thr Met Ala Ala Ala Leu Ala Arg
 1 5 10 15
 Leu Gly Leu Arg Pro Val Lys Gln Val Arg Val Gln Phe Cys Pro Phe
 20 25 30
 Glu Lys Asn Val Glu Ser Thr Arg Thr Phe Leu Gln Thr Val Ser Ser
 35 40 45
 Glu Lys Val Arg Ser Thr Asn Leu Asn Cys Ser Val Ile Ala Asp Val
 50 55 60
 Arg His Asp Gly Ser Glu Pro Cys Val Asp Val Leu Phe Gly Asp Gly
 65 70 75 80
 His Arg Leu Ile Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu
 85 90 95
 Thr Ala Phe Ala Ser His Ile Arg Ala Arg Asp Ala Ala Gly Ser Gly
 100 105 110
 Asp Lys Pro Gly Ala Asp Thr Gly Arg
 115 120

<210> 441
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 441
 Met Leu Ala Arg Ala Thr Phe Arg Ala Ala Ser Ala Pro Thr Leu Val
 1 5 10 15

Ala Arg Arg Gly Phe Gln Ser Thr Arg Ala Gln Met Ala Ser Pro Tyr
 20 25 30
 His Tyr Pro Glu Gly Pro Arg Ser Asn Leu Pro Phe Asp Pro Leu Lys
 35 40 45
 Lys Gly Phe Ala Phe Lys Tyr Trp Gly Phe Met Gly Thr Gly Phe Ala
 50 55 60
 Leu Pro Phe Leu Leu Ala Val Trp Gln Thr Glu Gln Ala Val Asn Ala
 65 70 75 80
 Leu Arg His Gly Val Asp Met Arg Ile Gly Ile Pro Gly Asn Thr Ala
 85 90 95
 Phe Val Asp

<210> 442
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 442
 Arg Glu Gly Ala Arg Ala Arg Pro Ser Pro Thr Met Ser Asp Glu Ala
 1 5 10 15
 Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe
 20 25 30
 Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu
 35 40 45
 Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys
 50 55 60
 His Arg Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu
 65 70 75 80
 Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu
 85 90 95
 Phe Ser Ser Val Ser Val Gly Asp Gln Asp Asp Cys Tyr Ser Leu Leu
 100 105 110
 Asp Asp Gln Asp Phe Thr Ser Phe Asp Leu Phe Pro Glu Gly Ser Val
 115 120 125
 Cys Ser Asp Val Ser Ser Ser Ile Ser Thr Tyr Trp Asp Trp Ser Asp
 130 135 140
 Ser Glu Phe Glu Trp Gln Leu Pro Gly Ser Asp Ile Ala Ser Gly Ser
 145 150 155 160
 Asp Val Leu Ser Asp Val Ile Pro Ser Ile Pro Ser Ser Pro Cys Leu
 165 170 175
 Leu Pro Lys Lys Lys Lys
 180

<210> 443
 <211> 94
 <212> PRT
 <213> Homo sapiens

<400> 443
 Met Ser Asp Glu Ala Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr
 1 5 10 15
 Pro Glu Glu Pro Phe Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr
 20 25 30
 Cys Pro Ser Glu Glu Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys
 35 40 45
 Gln Leu Ser Ser Cys His Arg Thr Asp Pro Leu His Arg Phe His Thr
 50 55 60
 Asn Arg Trp Asn Leu Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu

<400> 446

Met Glu Asp Lys Glu Ile Pro Ile Lys Ser Glu Pro Leu Pro Lys Pro
1 5 10 15
Pro Ala Ser Ala Pro Pro Ser Ile Leu Val Lys Pro Glu Asn Ser Arg
20 25 30
Asn Gly Ile Glu Lys Gln Val Lys Thr Val Arg Phe Gln Asn Tyr Ser
35 40 45
Pro Pro Pro Thr Lys His Tyr Thr Ser His Pro Thr Ser Gly Lys Pro
50 55 60
Glu Gln Pro Ala Thr Leu Lys Ala Ser Gln Pro Glu Ala Ala Ser Leu
65 70 75 80
Gly Pro Glu Met Thr Val Leu Phe Ala His Arg Ser Gly Cys His Ser
85 90 95
Gly Gln Gln Thr Asp Leu Arg Arg Lys Ser Ala Leu Ala Lys Ala Thr
100 105 110
Thr Leu Val Ser Thr Ala Ser Gly Thr Gln Thr Val Phe Pro Ser Lys
115 120 125

<210> 447

<211> 96

<212> PRT

<213> Homo sapiens

<400> 447

Met Leu Thr Arg Val Glu Glu Gln Lys Lys Met Val Lys Ala Cys Arg
1 5 10 15
Tyr Arg Cys Ser Ala Cys His Leu Lys Tyr Ser Pro Gln Arg Gln Lys
20 25 30
Glu Arg Lys Leu Ser Leu Lys Arg Gly Arg Thr Ser Gln Gln Asn Met
35 40 45
Ser Met Phe Trp Leu Lys Lys Leu Leu Glu Ser Gly Leu Phe Cys Ala
50 55 60
Met Cys Ser Pro Arg Ala Ser Thr Lys Lys Gly Phe Trp Cys Arg Pro
65 70 75 80
Lys Thr Thr Ile Ile Ile Ile Asp Tyr Ser Ser Pro Arg Gln Cys Leu
85 90 95

<210> 448

<211> 160

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> 114

<223> Xaa = Glu,Val

<220>

<221> UNSURE

<222> 113

<223> Xaa = His,Gln

<220>

<221> UNSURE

<222> 115

<223> Xaa = Ile,Val

<400> 448

Met Gly Lys Ile Ala Leu Gln Leu Lys Ala Thr Leu Glu Asn Ile Thr
 1 5 10 15
 Asn Leu Arg Pro Val Gly Glu Asp Phe Arg Trp Tyr Leu Lys Met Lys
 20 25 30
 Cys Gly Asn Cys Gly Glu Ile Ser Asp Lys Trp Gln Tyr Ile Arg Leu
 35 40 45
 Met Asp Ser Val Ala Leu Lys Gly Gly Arg Gly Ser Ala Ser Met Val
 50 55 60
 Gln Lys Cys Lys Leu Cys Ala Arg Glu Asn Ser Ile Glu Ile Leu Ser
 65 70 75 80
 Ser Thr Ile Lys Pro Tyr Asn Ala Glu Asp Asn Glu Asn Phe Lys Thr
 85 90 95
 Ile Val Glu Phe Glu Cys Arg Gly Leu Glu Pro Val Asp Phe Gln Pro
 100 105 110
 Xaa Xaa Xaa Leu Leu Leu Lys Val Trp Ser Gln Gly Gln Pro Ser Val
 115 120 125
 Thr Leu Ile Cys Arg Arg Arg Thr Gly Thr Asp Tyr Asp Glu Lys Ala
 130 135 140
 Gln Glu Ser Val Gly Ile Tyr Glu Val Thr His Gln Phe Val Lys Cys
 145 150 155 160

<210> 449
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 449
 Met Asp Ser Leu Ala Ala Gly Glu Leu Asn Ala Ser His Gln Pro Trp
 1 5 10 15
 Val Pro Glu Phe Val Ala Tyr Trp Arg Lys Thr His Gln Asp His Leu
 20 25 30
 Cys Ser Leu His Ser Arg Ala Phe Gly Leu Leu Asp Ala Arg Val Thr
 35 40 45
 Trp Ala Leu Arg Arg Ala Pro Glu Pro Val Pro Gly Lys Asp Arg Leu
 50 55 60
 Leu Leu Ala Ala Phe Pro Ala Glu Ala Ser Pro Val Asp Thr Ala Ser
 65 70 75 80
 Val Ser Val Tyr Gly Arg Ala Pro Arg Tyr Met His Lys Gly Val Lys
 85 90 95
 Lys Cys Val Cys Thr Pro Val Ser Lys Asn Ser Thr Ala Trp Leu Leu
 100 105 110
 Leu Gly Gly Ile Ser
 115

<210> 450
 <211> 335
 <212> PRT
 <213> Homo sapiens

<400> 450
 Met Cys Cys Gln Val Cys Glu Ala Val Arg Ser Gly Asn Glu Glu Val
 1 5 10 15
 Leu Ala Asp Val Arg Thr Ile Val Asn Gln Ile Ser Tyr Thr Pro Gln
 20 25 30
 Asp Pro Arg Asp Leu Cys Gly Arg Ile Leu Thr Thr Cys Tyr Met Ala
 35 40 45
 Ser Lys Asn Ser Ser Gln Glu Thr Cys Thr Arg Ala Arg Glu Leu Ala
 50 55 60

Gln Gln Ile Gly Ser His His Ile Ser Leu Asn Ile Asp Pro Ala Val
 65 70 75 80
 Lys Ala Val Met Gly Ile Phe Ser Leu Val Thr Gly Lys Ser Pro Leu
 85 90 95
 Phe Ala Ala His Gly Gly Ser Ser Arg Glu Asn Leu Ala Leu Gln Asn
 100 105 110
 Val Gln Ala Arg Ile Arg Met Val Leu Ala Tyr Leu Phe Ala Gln Leu
 115 120 125
 Ser Leu Trp Ser Arg Gly Val His Gly Gly Leu Leu Val Leu Gly Ser
 130 135 140
 Ala Asn Val Asp Glu Ser Leu Leu Gly Tyr Leu Thr Lys Tyr Asp Cys
 145 150 155 160
 Ser Ser Ala Asp Ile Asn Pro Ile Gly Gly Ile Ser Lys Thr Asp Leu
 165 170 175
 Arg Ala Phe Val Gln Phe Cys Ile Gln Arg Phe Gln Leu Pro Ala Leu
 180 185 190
 Gln Ser Ile Leu Leu Ala Pro Ala Thr Ala Glu Leu Glu Pro Leu Ala
 195 200 205
 Asp Gly Gln Val Ser Gln Thr Asp Glu Glu Asp Met Gly Met Thr Tyr
 210 215 220
 Ala Glu Leu Ser Val Tyr Gly Lys Leu Arg Lys Val Ala Lys Met Gly
 225 230 235 240
 Pro Tyr Ser Met Phe Cys Lys Leu Leu Gly Met Trp Arg His Ile Cys
 245 250 255
 Thr Pro Arg Gln Val Ala Asp Lys Val Lys Arg Phe Phe Ser Lys Tyr
 260 265 270
 Ser Met Asn Arg His Lys Met Thr Thr Leu Thr Pro Ala Tyr His Ala
 275 280 285
 Glu Asn Tyr Ser Pro Glu Asp Asn Arg Phe Asp Leu Arg Pro Phe Leu
 290 295 300
 Tyr Asn Thr Ser Trp Pro Trp Gln Phe Arg Cys Ile Glu Asn Gln Val
 305 310 315 320
 Leu Gln Leu Glu Arg Ala Glu Pro Gln Ser Leu Asp Gly Val Asp
 325 330 335

<210> 451

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> 76

<223> Xaa = Lys, Asn

<400> 451

Met Cys Trp Val Ile Asn His Ala Ile Leu Pro Arg Met Arg Met His
 1 5 10 15
 Ser Lys Arg Gln Thr Ile Thr Arg His Ser Ala Ser Leu Ser Phe His
 20 25 30
 Ala Leu Pro Arg Ser Ala Phe Leu Gln Leu Cys Leu Leu Arg Gln Ile
 35 40 45
 His Gln Ile Pro Cys Leu Ser Ile Phe Ser Ser Thr Leu Arg Ala Gln
 50 55 60
 Thr His Asp Ser Gly Ile Gly Cys Thr Thr Ala Xaa Pro Gly Gly Arg
 65 70 75 80
 Arg Gln Glu Gln Leu Arg
 85

<210> 452
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 452
 Met Lys Ile Ala Leu Cys Gln Arg Glu Leu Pro Ser Pro Arg Ser Cys
 1 5 10 15
 Leu Leu Ser Arg Asp Val Thr Gly Val Ile Cys Thr Arg Met Pro Arg
 20 25 30
 Leu Ala Ile Cys Ser Lys Thr Ala Gln Lys Ala Leu Pro Cys Ile Pro
 35 40 45
 Leu Leu His Thr Ser Pro Leu Cys Leu Gln Leu Leu Ser Ala Gly Leu
 50 55 60
 His Ile Tyr Ala Thr Leu Cys Lys Ser Cys Ala Ser Arg Asn His Lys
 65 70 75 80
 Asn Ile Phe Leu His Leu Leu His Ser Leu Ser Ala Ala
 85 90

<210> 453
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 453
 Met Ala Val Arg Ala Ser Phe Glu Asn Asn Cys Glu Ile Gly Cys Phe
 1 5 10 15
 Ala Lys Leu Thr Asn Thr Tyr Cys Leu Val Ala Ile Gly Gly Ser Glu
 20 25 30
 Asn Phe Tyr Ser Val Phe Glu Gly Glu Leu Ser Asp Thr Ile Pro Val
 35 40 45
 Val His Ala Ser Ile Ala Gly Cys Arg Ile Ile Gly Arg Met Cys Val
 50 55 60
 Gly Asp Arg Arg Asn Ser Gly Arg Cys Ala Gln Gly Gly Ser Leu Gln
 65 70 75 80
 Thr Asp Ser Gly Arg Pro Gly Ala Ser Arg Lys Leu Leu Cys Leu Gln
 85 90 95
 Gln Ser Gly Arg Ala Gly Ala Ser Gln Asp Phe Asn
 100 105

<210> 454
 <211> 277
 <212> PRT
 <213> Homo sapiens

<400> 454
 Met Ser Leu Cys Glu Asp Met Leu Leu Cys Asn Tyr Arg Lys Cys Arg
 1 5 10 15
 Ile Lys Leu Ser Gly Tyr Ala Trp Val Thr Ala Cys Ser His Ile Phe
 20 25 30
 Cys Asp Gln His Gly Ser Gly Glu Phe Ser Arg Ser Pro Ala Ile Cys
 35 40 45
 Pro Ala Cys Asn Ser Thr Leu Ser Gly Lys Leu Asp Ile Val Arg Thr
 50 55 60
 Glu Leu Ser Pro Ser Glu Glu Tyr Lys Ala Met Val Leu Ala Gly Leu
 65 70 75 80
 Arg Pro Glu Ile Val Leu Asp Ile Ser Ser Arg Ala Leu Ala Phe Trp

85 90 95
 Thr Tyr Gln Val His Gln Glu Arg Leu Tyr Gln Glu Tyr Asn Phe Ser
 100 105 110
 Lys Ala Glu Gly His Leu Lys Gln Met Glu Lys Ile Tyr Thr Gln Gln
 115 120 125
 Ile Gln Ser Lys Asp Val Glu Leu Thr Ser Met Lys Gly Glu Val Thr
 130 135 140
 Ser Met Lys Lys Val Leu Glu Glu Tyr Lys Lys Phe Ser Asp Ile
 145 150 155 160
 Ser Glu Lys Leu Met Glu Arg Asn Arg Gln Tyr Gln Lys Leu Gln Gly
 165 170 175
 Leu Tyr Asp Ser Leu Arg Leu Arg Asn Ile Thr Ile Ala Asn His Glu
 180 185 190
 Gly Thr Leu Glu Pro Ser Met Ile Ala Gln Ser Gly Val Leu Gly Phe
 195 200 205
 Pro Leu Gly Asn Asn Ser Lys Phe Pro Leu Asp Asn Thr Pro Val Arg
 210 215 220
 Asn Arg Gly Asp Gly Asp Gly Asp Phe Gln Phe Arg Pro Phe Phe Ala
 225 230 235 240
 Gly Ser Pro Thr Ala Pro Glu Pro Ser Asn Ser Phe Phe Ser Phe Val
 245 250 255
 Ser Pro Ser Arg Glu Leu Glu Gln Gln Gln Val Ser Ser Arg Ala Phe
 260 265 270
 Lys Val Lys Arg Ile
 275

<210> 455
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 455
 Met Leu Val Met Tyr Leu Leu Ala Ala Leu Phe Gly Tyr Leu Thr Phe
 1 5 10 15
 Tyr Gly Glu Val Glu Asp Glu Leu Leu His Ala Tyr Ser Lys Val Tyr
 20 25 30
 Thr Leu Asp Ile Pro Leu Leu Met Val Arg Leu Ala Val Leu Val Ala
 35 40 45
 Val Thr Leu Thr Val Pro Ile Val Leu Phe Pro Ile Arg Thr Ser Val
 50 55 60
 Ile Thr Leu Leu Phe Pro Lys Arg Pro Phe Ser Trp Ile Arg His Phe
 65 70 75 80
 Leu Ile Ala Ala Val Leu Ile Ala Leu Asn Asn Val Leu Val Ile Leu
 85 90 95
 Val Pro Thr Ile Lys Tyr Ile Phe Gly Phe Ile Gly Ala Ser Ser Ala
 100 105 110
 Thr Met Leu Ile Phe Ile Leu Pro Ala Val Phe Tyr Leu Lys Leu Val
 115 120 125
 Lys Lys Glu Thr Phe Arg Ser Pro Gln Lys Val Gly Ala Leu Ile Phe
 130 135 140
 Leu Val Val Gly Ile Phe Phe Met Ile Gly Ser Met Ala Leu Ile Ile
 145 150 155 160
 Ile Asp Trp Ile Tyr Asp Pro Pro Asn Ser Lys His His
 165 170

<210> 456
 <211> 370
 <212> PRT

<213> Homo sapiens

<400> 456

Met Ser Ala Ser Ala Ala Thr Gly Val Phe Val Leu Ser Leu Ser Ala
1 5 10 15
Ile Pro Val Thr Tyr Val Phe Asn His Leu Ala Ala Gln His Asp Ser
20 25 30
Trp Thr Ile Val Gly Val Ala Ala Leu Ile Leu Phe Leu Val Ala Leu
35 40 45
Leu Ala Arg Val Leu Val Lys Arg Lys Pro Pro Arg Asp Pro Leu Phe
50 55 60
Tyr Val Tyr Ala Val Phe Gly Phe Thr Ser Val Val Asn Leu Ile Ile
65 70 75 80
Gly Leu Glu Gln Asp Gly Ile Ile Asp Gly Phe Met Thr His Tyr Leu
85 90 95
Arg Glu Gly Glu Pro Tyr Leu Asn Thr Ala Tyr Gly His Met Ile Cys
100 105 110
Tyr Trp Asp Gly Ser Ala His Tyr Leu Met Tyr Leu Val Met Val Ala
115 120 125
Ala Ile Ala Trp Glu Glu Thr Tyr Arg Thr Ile Gly Leu Tyr Trp Val
130 135 140
Gly Ser Ile Ile Met Ser Val Val Val Phe Val Pro Gly Asn Ile Val
145 150 155 160
Gly Lys Tyr Gly Thr Arg Ile Cys Pro Ala Phe Phe Leu Ser Ile Pro
165 170 175
Tyr Thr Cys Leu Pro Val Trp Ala Gly Phe Arg Ile Tyr Asn Gln Pro
180 185 190
Ser Glu Asn Tyr Asn Tyr Pro Ser Lys Val Ile Gln Glu Ala Gln Ala
195 200 205
Lys Asp Leu Leu Arg Arg Pro Phe Asp Leu Met Leu Val Val Cys Leu
210 215 220
Leu Leu Ala Thr Gly Phe Cys Leu Phe Arg Gly Leu Ile Ala Leu Asp
225 230 235 240
Cys Pro Ser Glu Leu Cys Arg Leu Tyr Thr Gln Phe Gln Glu Pro Tyr
245 250 255
Leu Lys Asp Pro Ala Ala Tyr Pro Lys Ile Gln Met Leu Ala Tyr Met
260 265 270
Phe Tyr Ser Val Pro Tyr Phe Val Thr Ala Leu Tyr Gly Leu Val Val
275 280 285
Pro Gly Cys Ser Trp Met Pro Asp Ile Thr Leu Ile His Ala Gly Gly
290 295 300
Leu Ala Gln Ala Gln Phe Ser His Ile Gly Ala Ser Leu His Ala Arg
305 310 315 320
Thr Ala Tyr Val Tyr Arg Val Pro Glu Glu Ala Lys Ile Leu Phe Leu
325 330 335
Ala Leu Asn Ile Ala Tyr Gly Val Leu Pro Gln Leu Leu Ala Tyr Arg
340 345 350
Cys Ile Tyr Lys Pro Glu Phe Phe Ile Lys Thr Lys Ala Glu Glu Lys
355 360 365
Val Glu
370

<210> 457

<211> 393

<212> PRT

<213> Homo sapiens

<400> 457

Met	Thr	Tyr	Arg	Trp	Gly	Thr	Leu	Leu	Met	Lys	Arg	Lys	Phe	Glu	Glu
1				5					10					15	
Pro	Arg	Pro	Gly	Phe	His	Gly	Val	Leu	Gly	Ile	Asn	Ser	Ile	Thr	Gly
			20					25					30		
Lys	Glu	Glu	Pro	Leu	Tyr	Pro	Ser	Tyr	Lys	Arg	Gln	Leu	Arg	Ile	Tyr
		35					40				45				
Leu	Val	Ser	Leu	Pro	Phe	Val	Cys	Leu	Cys	Leu	Tyr	Phe	Ser	Leu	Tyr
	50					55				60					
Val	Met	Met	Ile	Tyr	Phe	Asp	Met	Glu	Val	Trp	Ala	Leu	Gly	Leu	His
65					70				75					80	
Glu	Asn	Ser	Gly	Ser	Glu	Trp	Thr	Ser	Val	Leu	Tyr	Val	Pro	Ser	
			85					90					95		
Ile	Ile	Tyr	Ala	Ile	Val	Ile	Glu	Ile	Met	Asn	Arg	Leu	Tyr	Arg	Tyr
			100				105					110			
Ala	Ala	Glu	Phe	Leu	Thr	Ser	Trp	Glu	Asn	His	Arg	Leu	Glu	Ser	Ala
			115				120					125			
Tyr	Gln	Asn	His	Leu	Ile	Leu	Lys	Val	Leu	Val	Phe	Asn	Phe	Leu	Asn
		130				135					140				
Cys	Phe	Ala	Ser	Leu	Phe	Tyr	Ile	Ala	Phe	Val	Leu	Lys	Asp	Met	Lys
145					150					155				160	
Leu	Leu	Arg	Gln	Ser	Leu	Ala	Thr	Leu	Leu	Ile	Thr	Ser	Gln	Ile	Leu
			165					170						175	
Asn	Gln	Ile	Met	Glu	Ser	Phe	Leu	Pro	Tyr	Trp	Leu	Gln	Arg	Lys	His
			180					185					190		
Gly	Val	Arg	Val	Lys	Arg	Lys	Val	Gln	Ala	Leu	Lys	Ala	Asp	Ile	Asp
		195				200						205			
Ala	Thr	Leu	Tyr	Glu	Gln	Val	Ile	Leu	Glu	Lys	Glu	Met	Gly	Thr	Tyr
		210				215					220				
Leu	Gly	Thr	Phe	Asp	Asp	Tyr	Leu	Glu	Leu	Phe	Leu	Gln	Phe	Gly	Tyr
225					230					235				240	
Val	Ser	Leu	Phe	Ser	Cys	Val	Tyr	Pro	Leu	Ala	Ala	Ala	Phe	Ala	Val
			245						250					255	
Leu	Asn	Asn	Phe	Thr	Glu	Val	Asn	Ser	Asp	Ala	Leu	Lys	Met	Cys	Arg
			260					265					270		
Val	Phe	Lys	Arg	Pro	Phe	Ser	Glu	Pro	Ser	Ala	Asn	Ile	Gly	Val	Trp
		275				280						285			
Gln	Leu	Ala	Phe	Glu	Thr	Met	Ser	Val	Ile	Ser	Val	Val	Thr	Asn	Cys
		290				295					300				
Ala	Leu	Ile	Gly	Met	Ser	Pro	Gln	Val	Asn	Ala	Val	Phe	Pro	Glu	Ser
305					310					315				320	
Lys	Ala	Asp	Leu	Ile	Leu	Ile	Val	Val	Ala	Val	Glu	His	Ala	Leu	Leu
			325					330						335	
Ala	Leu	Lys	Phe	Ile	Leu	Ala	Phe	Ala	Ile	Pro	Asp	Lys	Pro	Arg	His
			340					345					350		
Ile	Gln	Met	Lys	Leu	Ala	Arg	Leu	Glu	Phe	Glu	Ser	Leu	Glu	Ala	Leu
		355					360					365			
Lys	Gln	Gln	Gln	Met	Lys	Leu	Val	Thr	Glu	Asn	Leu	Lys	Glu	Glu	Pro
		370				375					380				
Met	Glu	Ser	Gly	Lys	Glu	Lys	Ala	Thr							
385					390										

<210> 458

<211> 116

<212> PRT

<213> Homo sapiens

<400> 458

Met Val Gly Gly Glu Glu Ala Ala Ala Ala Val Glu Glu Leu Val Ser Gly

1 5 10 15
 Val Arg Gln Ala Ala Asp Phe Ala Glu Gln Phe Arg Ser Tyr Ser Glu
 20 25 30
 Ser Glu Lys Gln Trp Lys Ala Arg Met Glu Phe Ile Leu Arg His Leu
 35 40 45
 Pro Asp Tyr Arg Asp Pro Pro Asp Gly Ser Gly Arg Leu Asp Gln Leu
 50 55 60
 Leu Ser Leu Ser Met Val Trp Ala Asn His Leu Phe Leu Gly Cys Ser
 65 70 75 80
 Tyr Asn Lys Asp Leu Leu Asp Lys Val Met Glu Met Ala Asp Gly Ile
 85 90 95
 Glu Val Glu Asp Leu Pro Gln Phe Thr Arg Ser Glu Leu Met Lys
 100 105 110
 Lys His Gln Ser
 115

<210> 459
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 459
 Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala Pro Ser
 1 5 10 15
 Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val Arg Asp
 20 25 30
 Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg Leu Glu
 35 40 45
 Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg Ala Ala
 50 55 60
 Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val Pro Gly
 65 70 75 80
 Leu His Gln Leu Thr Lys Leu Arg Phe Leu Gln Thr Glu Asp Ser Trp
 85 90 95
 Val Pro Ala Ser Pro Asp Thr Gly Leu Asp Pro Leu Thr Val Arg Arg
 100 105 110
 His Val Pro Ala Val Trp Val Leu Leu Ser Arg Asp Pro Leu Asp Pro
 115 120 125
 Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro Pro Gly Leu Gly Ser
 130 135 140
 Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Arg Arg Ala Arg Asp
 145 150 155 160
 Thr Arg Ser

<210> 460
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 460
 Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys Pro Arg Asp Ser Gly
 1 5 10 15
 Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys Val Phe Lys Met Ala
 20 25 30
 Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala Lys Leu
 35 40 45
 Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp Tyr Leu
 50 55 60

Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe Gly Thr
65 70 75 80
Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg Arg Cys
85 90 95
Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu Ala Thr
100 105 110
Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val Ile Asp
115 120 125
Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe Arg Ser
130 135 140
Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser Leu Ala
145 150 155 160
Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val Pro Leu
165 170 175
Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr Leu Cys Gln Thr
180 185 190
Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met Phe Gly
195 200 205
Ile Leu Asn Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr Leu Glu
210 215 220
Lys Thr Ile His Glu Glu
225 230

<210> 461
<211> 101
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> 95
<223> Xaa = Cys, Trp

<400> 461
Met Glu Arg Pro Asp Lys Ala Ala Leu Asn Ala Leu Gln Pro Pro Glu
1 5 10 15
Phe Arg Asn Glu Ser Ser Leu Ala Ser Thr Leu Lys Thr Leu Leu Phe
20 25 30
Phe Thr Ala Leu Met Ile Thr Val Pro Ile Gly Leu Tyr Phe Thr Thr
35 40 45
Lys Ser Tyr Ile Phe Glu Gly Ala Leu Gly Met Ser Asn Arg Asp Ser
50 55 60
Tyr Phe Tyr Ala Ala Ile Val Ala Val Val Ala Val His Val Val Leu
65 70 75 80
Ala Leu Phe Val Tyr Val Ala Trp Asn Glu Gly Ser Arg Gln Xaa Arg
85 90 95
Glu Gly Lys Gln Asp
100

<210> 462
<211> 93
<212> PRT
<213> Homo sapiens

<400> 462
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly Ala
1 5 10 15
Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro Gly Glu

20 25 30
 Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln Asp Pro Arg
 35 40 45
 Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu Ala Thr Leu
 50 55 60
 Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg Lys Asn Trp
 65 70 75 80
 Met Val Gly Gly Glu Gly Gly Ala Gly Gly Arg Ser Pro
 85 90

<210> 463
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 463
 Met Gly His Gly Asp Glu Ile Val Leu Ala Asp Leu Asn Phe Pro Ala
 1 5 10 15
 Ser Ser Ile Cys Gln Cys Gly Pro Met Glu Ile Arg Ala Asp Gly Leu
 20 25 30
 Gly Ile Pro Gln Leu Leu Glu Ala Val Leu Lys Leu Leu Pro Leu Asp
 35 40 45
 Thr Tyr Val Glu Ser Pro Ala Ala Val Met Glu Leu Val Pro Ser Asp
 50 55 60
 Lys Glu Arg Gly Leu Gln Thr Pro Val Trp Thr Glu Tyr Glu Ser Ile
 65 70 75 80
 Leu Arg Arg Ala Gly Cys Val Arg Ala Leu Ala Lys Ile Glu Arg Phe
 85 90 95
 Glu Phe Tyr Glu Arg Ala Lys Lys Ala Phe Ala Val Val Ala Thr Gly
 100 105 110
 Glu Thr Ala Leu Tyr Gly Asn Leu Ile Leu Arg Lys Gly Val Leu Ala
 115 120 125
 Leu Asn Pro Leu Leu
 130

<210> 464
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 464
 Met Gly His Gly Asp Glu Ile Val Leu Ala Asp Leu Asn Phe Pro Ala
 1 5 10 15
 Ser Ser Ile Cys Gln Cys Gly Pro Met Glu Ile Arg Ala Asp Gly Leu
 20 25 30
 Gly Ile Pro Gln Leu Leu Glu Ala Val Leu Ala Ala Pro Gly His
 35 40 45
 Leu Cys Gly Glu Ser Gly Cys Ser His Gly Ala Gly Ala Gln Arg Gln
 50 55 60
 Gly Glu Gly Pro Ala Asp Pro Ser Val Asp Gly Val Arg Val His Pro
 65 70 75 80
 Thr Gln Gly Arg Leu Cys Glu Ser Pro Gly Lys Asp Arg Glu Val
 85 90 95

<210> 465
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 465

Met Thr Pro Ile Lys Leu Leu Asn Leu Thr Ser Arg Tyr Asn Phe Arg
 1 5 10 15
 Arg Thr Phe Gly Ile Glu Leu Ser Ser Asn Ser Ser Tyr Cys Lys Arg
 20 25 30
 Gly Asn Gly Tyr Arg Ser Arg Val Pro Lys Glu Cys Glu Cys Asn Trp
 35 40 45
 Leu His Leu Glu Ser Asp Thr Leu Lys Lys Leu Pro Ile Ile Ser Pro
 50 55 60
 Ser Trp Thr Cys Arg Ile Ile Leu Phe Leu Tyr Phe Ser Gly Gln Leu
 65 70 75 80
 Leu Gln Leu Ser Leu Ser Cys Leu Gln Leu Ile Lys Leu
 85 90

<210> 466

<211> 500

<212> PRT

<213> Homo sapiens

<400> 466

Met Glu Val Ser Thr Asn Pro Ser Ser Asn Ile Asp Pro Gly Asn Tyr
 1 5 10 15
 Val Glu Met Asn Asp Ser Ile Thr His Leu Pro Ser Lys Val Val Ile
 20 25 30
 Gln Asp Ile Thr Met Glu Leu His Cys Pro Leu Cys Asn Asp Trp Phe
 35 40 45
 Arg Asp Pro Leu Met Leu Ser Cys Gly His Asn Phe Cys Glu Ala Cys
 50 55 60
 Ile Gln Asp Phe Trp Arg Leu Gln Ala Lys Glu Thr Phe Cys Pro Glu
 65 70 75 80
 Cys Lys Met Leu Cys Gln Tyr Asn Asn Cys Thr Phe Asn Pro Val Leu
 85 90 95
 Asp Lys Leu Val Glu Lys Ile Lys Lys Leu Pro Leu Leu Lys Gly His
 100 105 110
 Pro Gln Cys Pro Glu His Gly Glu Asn Leu Lys Leu Phe Ser Lys Pro
 115 120 125
 Asp Gly Lys Leu Ile Cys Phe Gln Cys Lys Asp Ala Arg Leu Ser Val
 130 135 140
 Gly Gln Ser Lys Glu Phe Leu Gln Ile Ser Asp Ala Val His Phe Phe
 145 150 155 160
 Met Glu Glu Leu Ala Ile Gln Gln Gly Gln Leu Glu Thr Thr Leu Lys
 165 170 175
 Glu Leu Gln Thr Leu Arg Asn Met Gln Lys Glu Ala Ile Ala Ala His
 180 185 190
 Lys Glu Asn Lys Leu His Leu Gln Gln His Val Ser Met Glu Phe Leu
 195 200 205
 Lys Leu His Gln Phe Leu His Ser Lys Glu Lys Asp Ile Leu Thr Glu
 210 215 220
 Leu Arg Glu Glu Gly Lys Ala Leu Asn Glu Glu Met Glu Leu Asn Leu
 225 230 235 240
 Ser Gln Leu Gln Glu Gln Cys Leu Leu Ala Lys Asp Met Leu Val Ser
 245 250 255
 Ile Gln Ala Lys Thr Glu Gln Gln Asn Ser Phe Asp Phe Leu Lys Asp
 260 265 270
 Ile Thr Thr Leu Leu His Ser Leu Glu Gln Gly Met Lys Val Leu Ala
 275 280 285
 Thr Arg Glu Leu Ile Ser Arg Lys Leu Asn Leu Gly Gln Tyr Lys Gly

290 295 300
 Pro Ile Gln Tyr Met Val Trp Arg Glu Met Gln Asp Thr Leu Cys Pro
 305 310 315 320
 Gly Leu Ser Pro Leu Thr Leu Asp Pro Lys Thr Ala His Pro Asn Leu
 325 330 335
 Val Leu Ser Lys Ser Gln Thr Ser Val Trp His Gly Asp Ile Lys Lys
 340 345 350
 Ile Met Pro Asp Asp Pro Glu Arg Phe Asp Ser Ser Val Ala Val Leu
 355 360 365
 Gly Ser Arg Gly Phe Thr Ser Gly Lys Trp Tyr Trp Glu Val Glu Val
 370 375 380
 Ala Lys Lys Thr Lys Trp Thr Val Gly Val Val Arg Glu Ser Ile Ile
 385 390 395 400
 Arg Lys Gly Ser Cys Pro Leu Thr Pro Glu Gln Gly Phe Trp Leu Leu
 405 410 415
 Arg Leu Arg Asn Gln Thr Asp Leu Lys Ala Leu Asp Leu Pro Ser Phe
 420 425 430
 Ser Leu Thr Leu Thr Asn Asn Leu Asp Lys Val Gly Ile Tyr Leu Asp
 435 440 445
 Tyr Glu Gly Gly Gln Leu Ser Phe Tyr Asn Ala Lys Thr Met Thr His
 450 455 460
 Ile Tyr Thr Phe Ser Asn Thr Phe Met Glu Lys Leu Tyr Pro Tyr Phe
 465 470 475 480
 Cys Pro Cys Leu Asn Asp Gly Arg Glu Asn Lys Glu Pro Leu His Ile
 485 490 495
 Leu His Pro Gln
 500

<210> 467
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 467
 Met Val Leu Thr Lys Pro Leu Gln Arg Asn Gly Ser Met Met Ser Phe
 1 5 10 15
 Glu Asn Val Lys Glu Lys Ser Arg Glu Gly Gly Pro His Ala His Thr
 20 25 30
 Pro Glu Glu Glu Leu Cys Phe Val Val Thr His Tyr Pro Gln Val Gln
 35 40 45
 Thr Thr Leu Asn Leu Phe Phe His Ile Phe Lys Val Leu Thr Gln Pro
 50 55 60
 Leu Ser Leu Leu Trp Gly Cys Asp Gln Lys Pro Arg Thr Val Pro Thr
 65 70 75 80
 Leu Gly Asn Gly Ala Trp Asp Thr Cys Gln Gln His Ile Arg Thr Ser
 85 90 95
 Ser Trp Thr Ala Asn Thr Leu Val Ile Gln Asn Gln His Ser Arg Glu
 100 105 110
 Ser Thr Val Ser Val Cys Leu Phe Met Leu Ile Arg Met Gln His Ile
 115 120 125
 Leu Lys Thr Asp Thr Leu Gln Gln Phe Arg Ile Cys
 130 135 140

<210> 468
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 468

Met Tyr Met Leu Leu Ser Pro His Arg Leu Arg Glu Gln Ala Gly Val
1 5 10 15
Arg Gly Ser Ile Arg Thr Ala Asn Arg Thr Glu Asp Gly Leu Lys Ile
20 25 30
Arg Glu Ala Glu Ser Leu Pro Gln Ser Asn Thr Ala Asp Phe Lys Cys
35 40 45
Leu His Ser Ala Ser Leu Gln Gln Ala Pro Gly Gly Ile Leu Met Gly
50 55 60
Pro Ala Ser Ser Pro Trp Thr Leu Ala Val Glu Gly Glu Lys Arg Thr
65 70 75 80
Ser Ala Pro Pro Leu Arg Glu Ser Leu Met Pro Thr Lys Gly Leu Gly
85 90 95
Trp Trp Thr Gln
100

<210> 469

<211> 119

<212> PRT

<213> Homo sapiens

<400> 469

Met Ala Ser Tyr Ser Gly Phe Ser Gly Leu Leu Glu Ile Arg Tyr Gly
1 5 10 15
Pro Gly His Arg Ser Cys Leu Pro Gln Phe Ala Phe Phe Pro Gln Pro
20 25 30
Pro Leu Pro Arg Pro Arg Ile Cys Met Trp Val Leu Ala Glu Leu Leu
35 40 45
Glu Leu Gly Cys Pro Glu Gln Ser Leu Arg Asp Ala Ile Thr Leu Asp
50 55 60
Leu Phe Cys His Ala Leu Ile Phe Cys Arg Gln Gln Gly Phe Ser Leu
65 70 75 80
Glu Gln Thr Ser Ala Ala Cys Ala Leu Leu Gln Asp Leu His Lys Ala
85 90 95
Cys Ile Gly Glu Arg Gly Gln Leu Pro Gly Leu Ser Pro Arg Glu Lys
100 105 110
Arg Asn Arg Ala Trp His Lys
115

<210> 470

<211> 140

<212> PRT

<213> Homo sapiens

<400> 470

Met Arg Ser Glu Cys Val Leu Gly Ala Ala Ser Asp Ser Gly Gln Glu
1 5 10 15
Ala Pro Arg Asp Thr Trp Phe Leu Gln Gly Trp Lys Ala Ser Arg Arg
20 25 30
Phe Leu Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr
35 40 45
Asp Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln
50 55 60
Lys Ala Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr
65 70 75 80
Val Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro
85 90 95
Lys Ile Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr

100 105 110
 Val Met Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser
 115 120 125
 Lys Glu Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys
 130 135 140

<210> 471
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 471
 Met Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala
 1 5 10 15
 Ser Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Arg
 20 25 30
 Thr Phe Gln Gln Ile Arg Cys Tyr Ser Ala Pro Val Ala Ala Glu Pro
 35 40 45
 Phe Leu Ser Gly Thr Ser Ser Asn Tyr Val Glu Glu Met Tyr Cys Ala
 50 55 60
 Trp Leu Glu Asn Pro Lys Ser Val His Lys Thr Gly Ser His Cys Cys
 65 70 75
 Pro Gly Trp Ser Ala Val Ala Gly Ser Arg Leu Ala Ala Thr Ser Asp
 85 90 95
 Ser Trp Val Gln Val Ile Leu Met Pro Gln Pro Pro Glu
 100 105

<210> 472
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 472
 Met Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala
 1 5 10 15
 Ser Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Arg
 20 25 30
 Thr Phe Gln Gln Ile Arg Ala Ile Leu His Leu Leu Leu Ser Pro
 35 40 45
 Phe Ser Val Gly Leu Val Arg Thr Met Trp Arg Arg Cys Thr Val Leu
 50 55 60
 Gly Trp Lys Thr Pro Lys Val Tyr Ile Arg Gln Gly Pro Thr Val Val
 65 70 75 80
 Gln Ala Gly Val Gln Trp Arg Asp Leu Gly Leu Leu Gln Pro Pro Thr
 85 90 95
 Pro Gly Phe Lys
 100

<210> 473
 <211> 141
 <212> PRT
 <213> Homo sapiens

<400> 473
 Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile Pro Asp Gly Thr
 1 5 10 15
 Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile Ala Ser Val Ala
 20 25 30

Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr
 35 40 45
 Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala
 50 55 60
 Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val
 65 70 75 80
 Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu Gly Gly Cys Ala
 85 90 95
 Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr Gly Ile Gly Ala
 100 105 110
 Ala Ala Cys Val Tyr Phe Gly Ile Ala Ala Ser Leu Val Lys Met Gly
 115 120 125
 Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys Val
 130 135 140

<210> 474
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 474
 Met Ala Thr His Pro Asp Gly Phe Arg Leu Glu Gly Pro Leu Ala Ala
 1 5 10 15
 Ala His Ser Pro Gly Pro Cys Thr Val Leu Tyr Glu Gly Pro Val Arg
 20 25 30
 Gly Leu Cys Pro Phe Ala Pro Arg Asn Ser Asn Thr Met Ala Ala Ala
 35 40 45
 Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu
 50 55 60
 Val Ala Asp Thr Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu
 65 70 75 80
 Ser Gly Pro Arg Gly Pro Thr Gly Arg Ser Phe Ala Val His Thr Arg
 85 90 95
 Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val
 100 105 110
 Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg
 115 120 125
 Pro Gly Ile His Leu Cys
 130

<210> 475
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 475
 Met Ala Thr His Pro Asp Gly Phe Arg Leu Glu Gly Pro Leu Ala Ala
 1 5 10 15
 Ala His Ser Pro Gly Pro Cys Thr Val Leu Tyr Glu Gly Pro Val Arg
 20 25 30
 Gly Leu Cys Pro Phe Ala Pro Arg Asn Ser Asn Thr Met Ser Ala Ala
 35 40 45
 Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu
 50 55 60
 Val Ala Asp Thr Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu
 65 70 75 80
 Ser Gly Pro Arg Gly Pro Thr Cys Arg Ser Phe Ala Val His Thr Arg
 85 90 95

Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val
 100 105 110
 Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg
 115 120 125
 Pro Gly Ile His Leu Cys
 130

<210> 476
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 476
 Met Leu Lys Val Glu Ala Thr Gly Ser Pro Glu Glu Gly Trp Ala Gly
 1 5 10 15
 Gly Glu Pro Arg Thr Gly Ala Pro Ala Asn Ser Pro Ser Cys Pro Gln
 20 25 30
 Glu Met Pro Leu Gln Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr
 35 40 45
 Gln Gln Leu Leu Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu
 50 55 60
 Asn Val Ala Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Ala
 65 70 75 80
 Ser Gly Arg Ser Pro
 85

<210> 477
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 477
 Met Gly Arg Pro Trp Met Val Met Ile Leu Glu Ser Lys Ser Glu Glu
 1 5 10 15
 Lys Met Trp Tyr Gly Val Phe Leu Trp Ala Leu Val Ser Ser Leu Phe
 20 25 30
 Phe His Val Pro Ala Gly Leu Leu Ala Leu Phe Thr Leu Arg His His
 35 40 45
 Lys Tyr Gly Arg Phe Met Ser Val Ser Ile Leu Leu Met Gly Ile Val
 50 55 60
 Gly Pro Ile Thr Ala Gly Ile Leu Thr Ser Ala Ala Ile Ala Gly Val
 65 70 75 80
 Tyr Arg Ala Ala Gly Lys Glu Met Ile Pro Phe Glu Ala Leu Thr Leu
 85 90 95
 Gly Thr Gly Gln Thr Phe Cys Val Leu Val Val Ser Phe Leu Arg Ile
 100 105 110
 Leu Ala Thr Leu
 115

<210> 478
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 478
 Met Asn Arg Tyr Cys Gly Lys Ile Phe Val Ser Val Met Val Lys Leu
 1 5 10 15
 Gln Lys Asn Lys Leu Thr Ser Phe Pro Arg Gln Pro Leu Leu Thr Phe

[illegible][illegible]

Arg Glu Lys Glu Glu Gln Arg Gly Leu Arg Lys Tyr Asn Tyr Thr Leu
 325 330 335
 Leu Arg Val Arg Leu Pro Asp Gly Cys Leu Leu Gln Gly Thr Phe Tyr
 340 345 350
 Ala Arg Glu Arg Leu Gly Ala Val Tyr Gly Phe Val Arg Glu Ala Leu
 355 360 365
 Gln Ser Asp Trp Leu Pro Phe Glu Leu Leu Ala Ser Gly Gly Gln Lys
 370 375 380
 Leu Ser Glu Asp Glu Asn Leu Ala Leu Asn Glu Cys Gly Leu Val Pro
 385 390 395 400
 Ser Ala Leu Leu Thr Phe Ser Trp Asp Met Ala Val Leu Glu Asp Ile
 405 410 415
 Lys Ala Ala Gly Ala Glu Pro Asp Ser Ile Leu Lys Pro Glu Leu Leu
 420 425 430
 Ser Ala Ile Glu Lys Leu Leu
 435

<210> 480
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 480
 Met Trp Ala Arg Leu Pro His Thr Pro Glu Gln Met Gly His Arg Leu
 1 5 10 15
 Ile Gly Pro Lys Glu Ala Ser Leu His Val Val Pro Ser Trp Pro Ala
 20 25 30
 Arg Lys Met Glu Gly Leu Leu Ala Gly Leu Ser Ser Ser Pro Arg Lys
 35 40 45
 Ser Cys Trp Pro Phe Trp Val His Gly Pro Lys Val His Glu Gly Gly
 50 55 60
 Ser Ala Cys Glu Thr Ser Ser Ser Trp Val Glu Gly Leu Gly Leu Arg
 65 70 75 80
 Arg Val Thr Ser Val His Ser Leu Cys Gln Gly Leu Gly Ala Ser Val
 85 90 95
 Gln Leu Leu Pro Gly Pro Pro Pro Thr Thr Ser Asp Lys Asn Asn
 100 105 110
 Tyr Thr Ser Gly
 115

<210> 481
 <211> 171
 <212> PRT
 <213> Homo sapiens

<400> 481
 Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg Ile Asp Pro Tyr Gly
 1 5 10 15
 Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Tyr Glu Lys Phe Phe
 20 25 30
 Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala Ile Lys Trp Ser Arg
 35 40 45
 Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg Thr Val Lys Arg Tyr
 50 55 60
 Val Arg Lys Gly Val Pro Leu Glu His Arg Ala Arg Val Trp Met Val
 65 70 75 80
 Leu Ser Gly Ala Gln Ala Gln Met Asp Gln Asn Pro Gly Tyr Tyr His
 85 90 95

Gln Leu Leu Gln Gly Glu Arg Asn Pro Arg Leu Glu Asp Ala Ile Arg
 100 105 110
 Thr Asp Leu Asn Arg Thr Phe Pro Asp Asn Val Lys Phe Arg Lys Thr
 115 120 125
 Thr Asp Pro Cys Leu Gln Arg Thr Leu Tyr Asn Val Leu Leu Ala Tyr
 130 135 140
 Gly His His Asn Gln Gly Val Gly Tyr Cys Gln Gly Met Asn Phe Ile
 145 150 155 160
 Ala Gly Tyr Leu Ile Leu Ile Thr Asn Asn Glu
 165 170

<210> 482

<211> 177

<212> PRT

<213> Homo sapiens

<400> 482

Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg Ile Asp Pro Tyr Gly
 1 5 10 15
 Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Ala Tyr Glu Lys Phe Phe
 20 25 30
 Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala Ile Lys Trp Ser Arg
 35 40 45
 Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg Thr Val Lys Arg Tyr
 50 55 60
 Val Arg Lys Gly Val Pro Leu Glu His Arg Ala Arg Val Trp Met Val
 65 70 75 80
 Leu Ser Gly Ala Gln Ala Gln Met Asp Gln Asn Pro Gly Tyr Tyr His
 85 90 95
 Gln Leu Leu Gln Gly Glu Arg Asn Pro Arg Leu Glu Asp Ala Ile Arg
 100 105 110
 Thr Asp Leu Asn Arg Thr Phe Pro Asp Asn Val Lys Phe Arg Lys Thr
 115 120 125
 Thr Asp Pro Cys Leu Gln Arg Thr Leu Tyr Asn Val Leu Leu Ala Tyr
 130 135 140
 Gly His His Asn Gln Gly Val Gly Tyr Cys Gln Gly Met Asn Phe Ile
 145 150 155 160
 Ala Gly Tyr Leu Ile Leu Ile Thr Asn Asn Asp Lys Asn Leu Phe Gly
 165 170 175

Cys